

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
11 November 2004 (11.11.2004)

PCT

(10) International Publication Number
WO 2004/096992 A2

(51) International Patent Classification⁷: C12N

HAMRICK, Alice [US/US]; 1610 Fifth Street, Los Osos, California 93402 (US).

(21) International Application Number:
PCT/US2004/012717

(74) Agent: MYERS BIGEL SIBLEY & SAJOVEC, P.A.;
P.O. Box 37428, Raleigh, North Carolina 27627 (US).

(22) International Filing Date: 23 April 2004 (23.04.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/465,621 25 April 2003 (25.04.2003) US

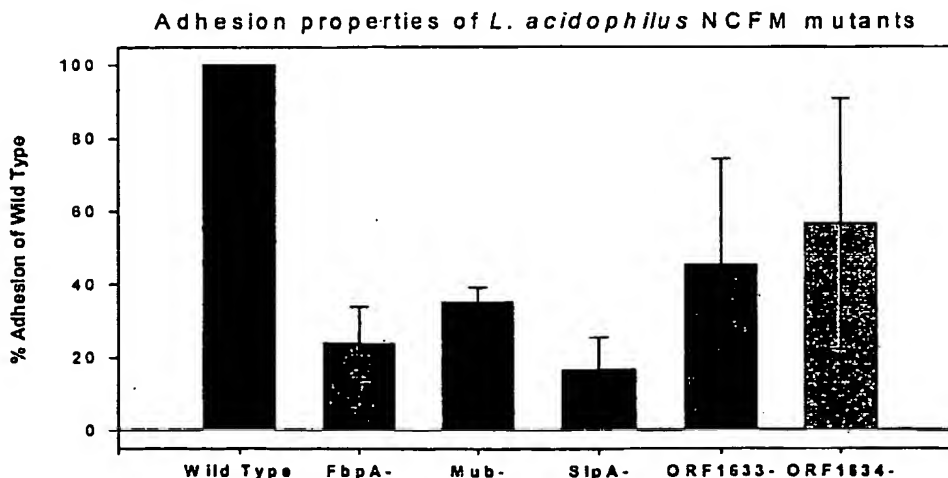
(71) Applicant (for all designated States except US): NORTH
CAROLINA STATE UNIVERSITY [US/US]; 2401 Re-
search Drive, Campus Box 8210, Raleigh, North Carolina
27695-8210 (US).

(81) Designated States (unless otherwise indicated, for every
kind of national protection available): AE, AG, AL, AM,
AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI,
GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE,
KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD,
MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG,
PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM,
TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM,
ZW.

(84) Designated States (unless otherwise indicated, for every
kind of regional protection available): ARIPO (BW, GH,
GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW),
Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), Euro-
pean (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR,
GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK,
TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW,
ML, MR, NE, SN, TD, TG).

[Continued on next page]

(54) Title: LACTOBACILLUS ACIDOPHILUS NUCLEIC ACID SEQUENCES ENCODING CELL SURFACE PROTEIN HO-
MOLOGUES AND USES THEREFORE



(57) Abstract: Cell wall, cell surface and secreted protein nucleic acid molecules and polypeptides and fragments and variants thereof are disclosed in the current invention. In addition, cell wall, cell surface and secreted fusion proteins, antigenic peptides, and anti-cell wall, cell surface and secreted antibodies are encompassed. The invention also provides recombinant expression vectors containing a nucleic acid molecule of the invention and host cells into which the expression vectors have been introduced. Methods for producing the polypeptides of the invention and methods for their use are further disclosed.

RECT AVAILABLE COPY

WO 2004/096992 A2

431



Published:

— *without international search report and to be republished
upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

10 CROSS REFERENCE TO RELATED APPLICATION

15 FIELD OF THE INVENTION

20 BACKGROUND OF THE INVENTION

- 1 -

the environment where the organism is cultured. Acidified environments (e.g., food, vagina, and regions within the gastrointestinal tract) can interfere with the growth of undesirable bacteria, pathogens, and yeasts. The organism is well known for its acid tolerance, survival in cultured dairy products, and viability during passage through the stomach and gastrointestinal tract. *Lactobacilli* and other commensal bacteria, some of which are considered as probiotic bacteria that "favor life," have been studied extensively for their effects on human health, particularly in the prevention or treatment of enteric infections, diarrheal disease, prevention of cancer, and stimulation of the immune system.

The cell wall of Gram-positive bacteria consists of a peptidoglycan macromolecule, with attached accessory molecules such as teichoic acids, teichuronic acids, lipoteichoic acids, lipoglycans, polyphosphates, and carbohydrates (Hancock (1997) *Biochem. Soc. Trans.* 25:183-187; Salton (1994) *The bacterial cell envelope-a historical perspective*, p. 1-22. In J.-M. Ghuysen and R. Hakenbeck (ed.) *Bacterial cell wall*. Elsevier Science BV, Amsterdam, The Netherlands). Proteins associated with the cell surface of Gram-positive bacteria include hydrolases and proteases, polysaccharides, surface exclusion proteins and aggregation-promoting proteins (thought to be involved in mating), S-layer proteins (subunits of crystalline arrays covering the outer surface of many single-celled organisms), sortase (a transpeptidase responsible for cleaving surface proteins at the LPXTG-like (SEQ ID NO:308) motifs), proteins with LPXTG-like motifs, and MSCRAMMs (microbial surface components recognizing adhesive matrix molecules) such as fibronectin-binding proteins, fibrinogen-binding proteins, and mucus-binding proteins.

Cell wall, cell surface, and secreted proteins of Gram-positive bacteria serve many diverse functions, including adhering to other cells or compounds, providing structural stability, and responding to environmental stimuli. Surface proteins of bacteria are important for survival within a host, and for cell growth and division. Furthermore, surface proteins are often recognized by a host's immune system to initiate immunostimulation, -modulation, or -enhancement. The isolation and characterization of these proteins will aid in developing essential probiotic products with numerous applications, including those that benefit human or animal health, and those concerned with food production and safety.

BRIEF SUMMARY OF THE INVENTION

Compositions and methods for modifying *Lactobacillus* organisms are provided. Compositions of the invention include isolated nucleic acid molecules from *Lactobacillus*

5 *acidophilus* encoding cell wall, cell surface, and secreted proteins. Specifically, the present invention provides for isolated nucleic acid molecules comprising the nucleotide sequences found in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119,

10 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299,

15 301, 303, 305 and 307, and isolated nucleic acid molecules encoding the amino acid sequences found in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156,

20 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 and 306. Also provided are isolated or recombinant polypeptides having an

25 amino acid sequence encoded by a nucleic acid molecule described herein. Variant nucleic acid molecules and polypeptides sufficiently identical to the nucleotide and amino acid sequences set forth in the sequence listings are encompassed by the present invention. Additionally, fragments and sufficiently identical fragments of the nucleotide and amino acid sequences are encompassed. Nucleotide sequences that are

30 complementary to a nucleotide sequence of the invention, or that hybridize to a sequence of the invention, are also encompassed.

Compositions further include vectors and host cells for recombinant expression of the nucleic acid molecules described herein, as well as transgenic microbial populations comprising the vectors. Also included in the invention are methods for making the vectors and host cells described herein, as well as methods for the recombinant
5 production of the polypeptides of the invention, and methods for their use. Further included are methods and kits for detecting the presence of a nucleic acid or polypeptide sequence of the invention in a sample, and antibodies that bind to a polypeptide of the invention.

The cell wall, cell surface, and secreted polypeptides encoded by the inventive
10 sequences, and the transgenic microbes expressing them, have health-related benefits. The microbes transformed with these polynucleotide sequences may be taken internally as a pharmaceutical or probiotic composition or alternatively, the microbes or their encoded polypeptides may be administered separately or added to products to provide health-related benefits. The nucleic acid molecules of the invention may also enhance the
15 stability of microorganisms expressing them, and therefore may be useful in the production and processing of various foods.

DESCRIPTION OF FIGURES

Figure 1 shows the percent adhesion of wild-type *L. acidophilus* NCFM
20 versus mutant bacteria lacking FpbA (SEQ ID NO:58), Mub (SEQ ID NO:18), SlpA (SEQ ID NO: 60), or streptococcal R28 proteins (SEQ ID NO:76 and SEQ ID NO:78, designated as ORF 1633 and ORF 1634, respectively).

DETAILED DESCRIPTION OF THE INVENTION

25 The present invention relates to cell wall, cell surface and secreted molecules from *Lactobacillus acidophilus*. Nucleotide and amino acid sequences of the molecules are provided. The sequences find use in modifying organisms to have enhanced benefits.

By "cell wall, cell surface and secreted molecules" is intended novel cell wall, cell surface and secreted proteins from *L. acidophilus*. By "cell wall" is intended a
30 protein found in association with the cell wall of a bacterial cell. By "cell surface" as it relates to a polypeptide or polynucleotide of the current invention is intended a protein

found in association with the bacterial cell membrane. By "secreted" is intended a protein that is released from the cell it is expressed in. A protein of the invention may be classified as either a cell wall, a cell surface or a secreted protein, or may be included in more than one of these classifications. Furthermore, the term "cell wall, cell surface, or
5 secreted" may be used to describe a single protein as well as more than one protein. See Table 1 for specific cell wall, cell surface and secreted protein molecules of the present invention.

These novel cell wall, cell surface and secreted proteins include cell components selected from the group consisting of peptidoglycans; teichoic acids; lipoteichoic acids;
10 polysaccharides, including homopolysaccharides and heteropolysaccharides; adhesion proteins; secreted proteins; surface (s)-layer proteins; collagen-binding proteins and other cell surface proteins, and may include steroid binding proteins; lemA-like proteins; aggregation-promoting proteins; surface-exclusion proteins; myosin cross-reactive proteins; mucus binding precursors and proteins; fibronectin-binding proteins; sortases;
15 biofilm-associated surface proteins; fibrinogen-binding proteins; tropomyosin-like proteins; FmtB-like surface proteins; psaA-like adhesins; lysM-like proteins; autolysins; cell shape-determining proteins; and rod shape-determining proteins. The full-length gene sequences are referred to as "cell wall, cell surface and secreted molecule sequences," indicating that they have similarity to cell wall, cell surface and secreted
20 genes. The invention further provides fragments and variants of these cell wall, cell surface and secreted sequences, which can also be used to practice the methods of the present invention.

As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame, particularly those encoding a cell wall, cell
25 surface or secreted protein. Isolated nucleic acid molecules of the present invention comprise nucleic acid sequences encoding cell wall, cell surface and secreted proteins, nucleic acid sequences encoding the amino acid sequences set forth in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98,
30 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170,

172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 and 306 (hereinafter
5 designated "even SEQ ID NOS:1-307"), the nucleic acid sequences set forth in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167,
10 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 and 307 (hereinafter designated "odd SEQ ID NOS:1-307"), and variants and fragments thereof.
15 The present invention also encompasses antisense nucleic acid molecules, as described below.

In addition, isolated polypeptides and proteins associated with the cell wall, cell surface or that are secreted, and variants and fragments thereof, are encompassed. For purposes of the present invention, the terms "protein" and "polypeptide" are used
20 interchangeably.

The compositions and methods of the present invention can be used to modulate the function of the cell wall, cell surface and secreted molecules of *L. acidophilus*. By "modulate," "alter," or "modify" is intended the up- or down-regulation of a target biological activity. Proteins of the invention are useful in modifying the biological
25 activities of lactic acid bacteria, and also in modifying the nutritional or health-promoting characteristics of foods fermented by lactic acid bacteria. Nucleotide molecules of the invention are useful in modulating cell wall, cell surface and secreted protein expression by lactic acid bacteria. Up- or down-regulation of expression from a polynucleotide of the present invention is encompassed. Up- regulation may be accomplished by providing
30 multiple gene copies, modulating expression by modifying regulatory elements, promoting transcriptional or translational mechanisms, or other means. Down-regulation

may be accomplished by using known antisense and gene silencing techniques. Thus, proteins of the invention are useful in modulating the immune system, expression of host proteins, therapeutic benefits, stability, and other activities of lactic acid bacteria. By "lactic acid bacteria" is intended bacteria from a genus selected from the following:

- 5 *Aerococcus, Carnobacterium, Enterococcus, Lactococcus, Lactobacillus, Leuconostoc, Oenococcus, Pediococcus, Streptococcus, Melissococcus, Alloiococcus, Dolosigranulum, Lactosphaera, Tetragenococcus, Vagococcus, and Weissella* (Holzapfel *et al.* (2001) *Am. J. Clin. Nutr.* 73:365S-373S; *Bergey's Manual of Systematic Bacteriology*, Vol. 2 (Williams and Wilkins, Baltimore (1986) pp. 1075-1079).

- 10 The polypeptides of the present invention or microbes expressing them are useful as nutritional additives or supplements, and as additives in dairy and fermentation processing. The polynucleotide sequences, encoded polypeptides, and microorganisms expressing them are useful in the manufacture of milk-derived products, such as cheeses, yogurt, fermented milk products, sour milks, and buttermilk. Microorganisms that
- 15 express polypeptides of the invention may be probiotic organisms. By "probiotic" is intended a live microorganism that survives passage through the gastrointestinal tract and has a beneficial effect on the host. By "host" is intended an organism that comes into contact with a polypeptide disclosed in the present invention or a microorganism expressing such a protein. Host may refer to humans and other animals as well as
- 20 bacteria.

- The polynucleotides and polypeptides of the present invention are useful in modifying the health-related benefits of milk-derived products. These uses include, but are not limited to modulating the immune system of a host; altering the expression of a host protein or compound; treating a gastrointestinal disorder; preventing or reducing the
- 25 occurrence of an infection; binding, inactivating, removing, sequestering, degrading, digesting, cleaving or modifying detrimental compounds in a subject; enabling a microorganism to possess modified adherence properties; reducing the occurrence of dental caries in a subject; increasing feed conversion in production animals; enabling microorganisms or polypeptides to antagonize other microorganisms; protecting food
- 30 from contamination; treating a wound; modulating the antibiotic sensitivity of a microorganism; enabling a microorganism to form a biofilm, or interfering with such an

ability; treating or preventing cancer; treating heart disease; and lowering cholesterol. The uses also include modifying the texture of a food product produced by a lactic acid bacteria.

The polynucleotides and polypeptides of the present invention are also useful in enhancing the stability of a microorganism during industrial fermentation processes including storage, where exposure to various stresses can lead to reduced microbial viability, impaired metabolic activity and sub-optimal fermentation conditions. Stresses are also present in the gastrointestinal tract. Possible stresses include oxidative stress, pH, osmotic stress, dehydration, carbon starvation, phosphate starvation, nitrogen starvation, amino acid starvation, mechanical stress, altered pressure, heat or cold shock and mutagenic stress.

The nucleic acid molecules of the invention encode cell wall, cell surface and secreted proteins. They encode transcripts having the DNA sequences set forth in odd SEQ ID NOS:1-307. The amino acid sequences encoded by the nucleotide sequences of the invention are set forth in even SEQ ID NOS:1-307.

In addition to the cell wall, cell surface and secreted nucleotide sequences disclosed herein, and fragments and variants thereof, the isolated nucleic acid molecules of the current invention also encompass homologous DNA sequences identified and isolated from other organisms or cells by hybridization with entire or partial sequences obtained from the cell wall, cell surface and secreted nucleotide sequences disclosed herein, or variants and fragments thereof.

The nucleic acid and protein compositions encompassed by the present invention are isolated or substantially purified. By "isolated" or "substantially purified" is intended that the nucleic acid or protein molecules, or biologically active fragments or variants, are substantially or essentially free from components normally found in association with the nucleic acid or protein in its natural state. Such components include other cellular material, culture media from recombinant production, and various chemicals used in chemically synthesizing the proteins or nucleic acids. Preferably, an "isolated" nucleic acid of the present invention is free of nucleic acid sequences that flank the nucleic acid of interest in the genomic DNA of the organism from which the nucleic acid was derived (such as coding sequences present at the 5' or 3' ends). However, the molecule may

include some additional bases or moieties that do not deleteriously affect the basic characteristics of the composition. For example, in various embodiments, the isolated nucleic acid contains less than 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleic acid sequence normally associated with the genomic DNA in the cells from which it was derived. Similarly, a substantially purified protein has less than about 30%, 20%, 10%, 5%, or 1% (by dry weight) of contaminating protein, or non-cell wall, cell surface or secreted protein. When the protein is recombinantly produced, preferably culture medium represents less than 30%, 20%, 10%, or 5% of the volume of the protein preparation, and when the protein is produced chemically, preferably the preparations have less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors, or non-cell wall, cell surface or secreted protein chemicals.

Fragments and Variants

The invention provides isolated nucleic acid molecules comprising nucleotide sequences encoding cell wall, cell surface and secreted proteins, as well as the cell wall, cell surface and secreted proteins encoded thereby. By "cell wall, cell surface and secreted proteins" is intended proteins having the amino acid sequences set forth in even SEQ ID NOS:1-307. Fragments and variants of these nucleotide sequences and encoded proteins are also provided. By "fragment" of a nucleotide sequence or protein is intended a portion of the nucleotide or amino acid sequence.

Fragments of the nucleic acid molecules disclosed herein can be used as hybridization probes to identify cell wall, cell surface and secreted protein-encoding nucleic acids, or can be used as primers in PCR amplification or mutation of cell wall, cell surface and secreted protein nucleic acid molecules. Fragments of nucleic acids can also be bound to a physical substrate to comprise what may be considered a macro- or microarray (see, for example, U.S. Patent No. 5,837,832; U.S. Patent No. 5,861,242; WO 89/10977; WO 89/11548; WO 93/17126; U.S. Patent No. 6,309,823). Such arrays of nucleic acids may be used to study gene expression or to identify nucleic acid molecules with sufficient identity to the target sequences. By "polynucleotide" or "nucleic acid molecule" is intended both sense and antisense strands of DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA

generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. A fragment of a nucleic acid molecule encoding a cell wall, cell surface and secreted protein may encode a protein fragment that is biologically active, or it may be used as a hybridization probe or PCR primer as described below. A biologically active fragment of a polypeptide disclosed herein can be prepared by isolating a portion of one of the nucleotide sequences of the invention, expressing the encoded portion of the cell wall, cell surface or secreted protein (e.g., by recombinant expression *in vitro*), and assessing the activity of the encoded portion of the cell wall, cell surface or secreted protein. Fragments of nucleic acid molecules encoding cell wall, cell surface and secreted proteins comprise at least about 15, 20, 50, 75, 100, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000 nucleotides or up to the total number of nucleotides present in a full-length cell wall, cell surface or secreted nucleotide sequence as disclosed herein (for example, 918 for SEQ ID NO:1, 573 for SEQ ID NO:3, 7617 for SEQ ID NO:5, etc.).

15 Fragments of the nucleotide sequences of the present invention will encode protein fragments that retain the biological activity of the cell surface, cell membrane or secreted protein and, hence, retain cell surface, cell membrane or secreted protein activity. By "retains activity" is intended that the fragment will have at least about 30%, preferably at least about 50%, more preferably at least about 70%, even more preferably at least about 80% of the activity of the cell surface, cell membrane or secreted protein disclosed in even SEQ ID NOS:1-307. Methods for measuring cell surface, cell membrane or secreted activity are well known in the art. See, for example, the Example section below as well as the section entitled "Methods of Use" for examples of functional assays.

25 Fragments of amino acid sequences include polypeptide fragments suitable for use as immunogens to raise anti-cell wall, cell surface and secreted antibodies. Fragments include peptides comprising amino acid sequences sufficiently identical to or derived from the amino acid sequence of a cell wall, cell surface or secreted protein, or partial-length protein, of the invention and exhibiting at least one activity of a cell wall, cell surface or secreted protein, but which include fewer amino acids than the full-length cell wall, cell surface and secreted proteins disclosed herein. Typically, biologically

30

active portions comprise a domain or motif with at least one activity of the cell wall, cell surface or secreted protein. A biologically active portion of a cell wall, cell surface or secreted protein can be a polypeptide that is, for example, 10, 25, 50, 100, 150, 200 contiguous amino acids in length, or up to the total number of amino acids present in a full-length cell wall, cell surface or secreted protein of the current invention (for example, 306 for SEQ ID NO:2, 191 for SEQ ID NO:4, 2539 for SEQ ID NO:6, etc.). Such biologically active portions can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native cell wall, cell surface or secreted protein. As used herein, a fragment comprises at least 5 contiguous amino acids of any of even SEQ ID NOS:1-307. The invention encompasses other fragments, however, such as any fragment in the protein greater than 6, 7, 8, or 9 amino acids.

Variants of the nucleotide and amino acid sequences are encompassed in the present invention. By "variant" is intended a sufficiently identical sequence. Accordingly, the invention encompasses isolated nucleic acid molecules that are sufficiently identical to the nucleotide sequences encoding cell wall, cell surface and secreted proteins in even SEQ ID NOS:1-307, or nucleic acid molecules that hybridize to a nucleic acid molecule of odd SEQ ID NOS:1-307, or a complement thereof, under stringent conditions. Variants also include polypeptides encoded by the variant nucleotide sequences of the present invention. In addition, polypeptides of the current invention have an amino acid sequence that is sufficiently identical to an amino acid sequence put forth in even SEQ ID NOS:1-307. By "sufficiently identical" is intended that one amino acid or nucleotide sequence contains a sufficient or minimal number of equivalent or identical amino acid residues as compared to a second amino acid or nucleotide sequence, thus providing a common structural domain and/or indicating a common functional activity. By "sufficiently identical" is intended an amino acid or nucleotide sequence that has at least about 45%, 55%, or 65% identity, preferably at least about 70% or 75% identity, more preferably at least about 80%, 85% or 90%, most preferably at least about 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence set forth in even SEQ ID NOS:1-307, or a nucleotide sequences set forth in odd SEQ ID NOS:1-307 using one of the alignment programs described herein using standard parameters. One of skill in the art will recognize that

these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like.

Variant proteins encompassed by the present invention are biologically active, that is they retain the desired biological activity of the native protein, that is, one or more of the functional activities of a native cell wall, cell surface or secreted protein as described herein. By "retains activity" is intended that the variant will have at least about 30%, preferably at least about 50%, more preferably at least about 70%, even more preferably at least about 80% of the activity of the cell surface, cell membrane or secreted protein disclosed in even SEQ ID NOS:1-307. Methods for measuring cell surface, cell membrane or secreted activity are well known in the art. See, for example, the Example section below as well as the section entitled "Methods of Use" for examples of functional assays. A biologically active variant of a protein of the invention may differ from that protein by as few as 1-15 amino acid residues, as few as 1-10, such as 6-10, as few as 5, as few as 4, 3, 2, or even 1 amino acid residue.

Naturally occurring variants may exist within a population (e.g., the *L. acidophilus* population). Such variants can be identified by using well-known molecular biology techniques, such as the polymerase chain reaction (PCR), and hybridization as described below. Synthetically derived nucleotide sequences, for example, sequences generated by site-directed mutagenesis or PCR-mediated mutagenesis that still encode a cell wall, cell surface or secreted protein, are also included as variants. One or more nucleotide or amino acid substitutions, additions, or deletions can be introduced into a nucleotide or amino acid sequence disclosed herein, such that the substitutions, additions, or deletions are introduced into the encoded protein. The additions (insertions) or deletions (truncations) may be made at the N-terminal or C-terminal end of the native protein, or at one or more sites in the native protein. Similarly, a substitution of one or more nucleotides or amino acids may be made at one or more sites in the native protein.

For example, conservative amino acid substitutions may be made at one or more predicted, preferably nonessential amino acid residues. A "nonessential" amino acid residue is a residue that can be altered from the wild-type sequence of a protein without altering the biological activity, whereas an "essential" amino acid is required for

biological activity. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue with a similar side chain. Families of amino acid residues having similar side chains are known in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Such substitutions would not be made for conserved amino acid residues, or for amino acid residues residing within a conserved motif, where such residues are essential for protein activity.

Alternatively, mutations can be made randomly along all or part of the length of the cell wall, cell surface or secreted coding sequence, such as by saturation mutagenesis. The mutants can be expressed recombinantly, and screened for those that retain biological activity by assaying for one or more of the functional activities of a native cell wall, cell surface or secreted protein using standard assay techniques. Methods for mutagenesis and nucleotide sequence alterations are known in the art. See, for example, Kunkel (1985) *Proc. Natl. Acad. Sci. USA* 82:488-492; Kunkel *et al.* (1987) *Methods in Enzymol. Molecular Biology* (MacMillan Publishing Company, New York) and the references cited therein. Obviously the mutations made in the DNA encoding the variant must not disrupt the reading frame and preferably will not create complimentary regions that could produce secondary mRNA structure. See, EP Patent Application Publication No. 75,444. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be found in the model of Dayhoff *et al.* (1978) *Atlas of Protein Sequence and Structure* (Natl. Biomed. Res. Found., Washington, D.C.), herein incorporated by reference.

The deletions, insertions, and substitutions of the protein sequences encompassed herein are not expected to produce radical changes in the characteristics of the protein. However, when it is difficult to predict the exact effect of the substitution, deletion, or insertion in advance of doing so, one skilled in the art will appreciate that the effect will be evaluated by routine screening assays. That is, the activity can be evaluated by

comparing the activity of the modified sequence with the activity of the original sequence. For example, the modification of gusA has produced alterations in enzyme activity and enzyme stability. (see, Matsumura and Ellington (2001) *J. Mol. Biol.* 305:331-9; Flores and Ellington (2002) *J. Mol. Biol.*, 315:325-37). Similar work has
5 been done with lactase.

Variant nucleotide and amino acid sequences of the present invention also encompass sequences derived from mutagenic and recombinogenic procedures such as DNA shuffling. With such a procedure, one or more different cell wall, cell surface and secreted protein coding regions can be used to create a new cell wall, cell surface or
10 secreted protein possessing the desired properties. In this manner, libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. For example, using this approach, sequence motifs encoding a domain of interest may be shuffled between the cell wall, cell
15 surface or secreted gene of the invention and other known cell wall, cell surface or secreted genes to obtain a new gene coding for a protein with an improved property of interest, such as an increased K_m in the case of an enzyme. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer (1994) *Proc. Natl. Acad. Sci. USA* 91:10747-10751; Stemmer (1994) *Nature* 370:389-391; Cramer *et al.* (1997)
20 *Nature Biotech.* 15:436-438; Moore *et al.* (1997) *J. Mol. Biol.* 272:336-347; Zhang *et al.* (1997) *Proc. Natl. Acad. Sci. USA* 94:4504-4509; Cramer *et al.* (1998) *Nature* 391:288-291; and U.S. Patent Nos. 5,605,793 and 5,837,458.

Variants of the cell wall, cell surface and secreted proteins can function as either cell wall, cell surface or secreted protein agonists (mimetics) or as cell wall, cell surface
25 or secreted protein antagonists. An agonist of a cell wall, cell surface or secreted protein can retain substantially the same, or a subset, of the biological activities of a naturally occurring form of the cell wall, cell surface or secreted protein. An antagonist of a cell wall, cell surface or secreted protein can inhibit one or more of the activities of a naturally occurring form of the cell wall, cell surface or secreted protein by, for example,
30 competitively binding to a downstream or upstream member of a cellular signaling cascade that includes the cell wall, cell surface or secreted protein.

5 Variants of a cell wall, cell surface or secreted protein that function as either agonists or antagonists can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of cell wall, cell surface and secreted proteins for cell wall, cell surface and secreted protein agonist or antagonist activity. In one embodiment, a
10 variegated library of cell wall, cell surface and secreted variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of cell wall, cell surface and secreted variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential cell wall, cell surface and
15 secreted sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display) containing the set of cell wall, cell surface and secreted sequences therein. There are a variety of methods that can be used to produce libraries of potential cell wall, cell surface and secreted variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence
20 can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential cell wall, cell surface or secreted protein sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (*see*, e.g., Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477).

In addition, libraries of fragments of cell wall, cell surface and secreted protein coding sequences can be used to generate a variegated population of cell wall, cell surface and secreted fragments for screening and subsequent selection of variants of cell
25 wall, cell surface and secreted proteins. In one embodiment, a library of coding sequence fragments can be generated by treating a double-stranded PCR fragment of a cell wall, cell surface or secreted coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double-stranded DNA, renaturing the DNA to form double-stranded DNA which can include sense/antisense
30 pairs from different nicked products, removing single-stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into

an expression vector. By this method, one can derive an expression library that encodes N-terminal and internal fragments of various sizes of cell wall, cell surface and secreted proteins.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of cell wall, cell surface and secreted proteins. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify cell wall, cell surface or secreted variants (Arkin and Yourvan (1992) *Proc. Natl. Acad. Sci. USA* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

Sequence Identity

The cell wall, cell surface and secreted sequences of Gram-positive bacteria, even though they have a diverse range of functions, and are from multiple protein families, have several common themes in their design (see, Navarre and Schneewind (1999) *Micro. Mol. Biol. Rev.* 63:174-229). N-terminal domains, which usually contain binding or catalytic activities are often followed by a number of repeat domains of various sizes, which may or may not have activity (Navarre and Schneewind (1999) *Micro. Mol. Biol. Rev.* 63:174-229). A proline-rich stretch of amino acid residues that may introduce random coils in the protein structure, and aid in traversing the peptidoglycan complex, is frequently found immediately preceding the LPXTG motif (SEQ ID NO:308, Navarre and Schneewind (1999) *Micro. Mol. Biol. Rev.* 63:174-229).

By "family" is intended two or more proteins or nucleic acid molecules having sufficient nucleotide or amino acid sequence identity. By "sequence identity" is intended

the nucleotide or amino acid residues that are the same when aligning two sequences for maximum correspondence over a specified comparison window. By "comparison window" is intended a contiguous segment of the two nucleotide or amino acid sequences for optimal alignment, wherein the second sequence may contain additions or deletions (i.e., gaps) as compared to the first sequence. Generally, for nucleic acid alignments, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. For amino acid sequence alignments, the comparison window is at least 6 contiguous amino acids in length, and optionally can be 10, 15, 20, 30, or longer. Those of skill in the art understand that to avoid a high similarity due to inclusion of gaps, a gap penalty is typically introduced and is subtracted from the number of matches.

Family members may be from the same or different species, and can include homologues as well as distinct proteins. Often, members of a family display common functional characteristics. Homologues can be isolated based on their identity to the *Lactobacillus acidophilus* cell wall, cell surface or secreted protein nucleic acid sequences disclosed herein using the cDNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions as disclosed below.

To determine the percent identity of two amino acid or nucleotide sequences, an alignment is performed. Percent identity of the two sequences is a function of the number of identical residues shared by the two sequences in the comparison window (i.e., $\text{percent identity} = \text{number of identical residues} / \text{total number of residues} \times 100$). In one embodiment, the sequences are the same length. Methods similar to those mentioned below can be used to determine the percent identity between two sequences. The methods can be used with or without allowing gaps. Alignment may also be performed manually by inspection.

When amino acid sequences differ in conservative substitutions, the percent identity may be adjusted upward to correct for the conservative nature of the substitution. Means for making this adjustment are known in the art. Typically the conservative substitution is scored as a partial, rather than a full mismatch, thereby increasing the percentage sequence identity.

Mathematical algorithms can be used to determine the percent identity of two sequences. Non-limiting examples of mathematical algorithms are the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877; the algorithm of Myers and Miller (1988) *CABIOS* 4:11-17; the local alignment algorithm of Smith *et al.* (1981) *Adv. Appl. Math.* 2:482; the homology alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443-453; and the search-for-similarity-method of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85:2444-2448.

Various computer implementations based on these mathematical algorithms have been designed to enable the determination of sequence identity. The BLAST programs of Altschul *et al.* (1990) *J. Mol. Biol.* 215:403 are based on the algorithm of Karlin and Altschul (1990) *supra*. Searches to obtain nucleotide sequences that are homologous to nucleotide sequences of the present invention can be performed with the BLASTN program, score = 100, wordlength = 12. To obtain amino acid sequences homologous to sequences encoding a protein or polypeptide of the current invention, the BLASTX program may be used, score = 50, wordlength = 3. Gapped alignments may be obtained by using Gapped BLAST as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389. To detect distant relationships between molecules, PSI-BLAST can be used. See, Altschul *et al.* (1997) *supra*. For all of the BLAST programs, the default parameters of the respective programs can be used. See, www.ncbi.nlm.nih.gov.

Another program that can be used to determine percent sequence identity is the ALIGN program (version 2.0), which uses the mathematical algorithm of Myers and Miller (1988) *supra*. A PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used with this program when comparing amino acid sequences.

In addition to the ALIGN and BLAST programs, the BESTFIT, GAP, FASTA and TFASTA programs are part of the Wisconsin Genetics Software Package (from GCG, Madison, Wisconsin), and can be used for performing sequence alignments. The preferred program is GAP version 10, which used the algorithm of Needleman and Wunsch (1970) *supra*. Unless otherwise stated the sequence identity similarity values provided herein refer to the value obtained using GAP Version 10 with the following parameters: % identity and % similarity for a nucleotide sequence using GAP Weight of

50 and Length Weight of 3, and the nwsgapdna.cmp scoring matrix; % identity and % similarity for an amino acid sequence using GAP Weight of 8 and Length Weight of 2, and the BLOSUM62 scoring matrix; or any equivalent program. By "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by GAP Version 10.

Identification and Isolation of Homologous Sequences

10 Cell wall, cell surface and secreted nucleotide sequences identified based on their sequence identity to the cell wall, cell surface and secreted nucleotide sequences set forth herein or to fragments and variants thereof are encompassed by the present invention. Methods such as PCR or hybridization can be used to identify sequences from a cDNA or genomic library, for example, that are substantially identical to a sequence of the invention. See, for example, Sambrook *et al.* (1989) *Molecular Cloning: Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York) and Innis, *et al.* (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, New York). Methods for construction of such cDNA and genomic libraries are generally known in the art and are also disclosed in the above reference.

20 In hybridization techniques, the hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may consist of all or part of a known nucleotide sequence disclosed herein. In addition, they may be labeled with a detectable group such as ^{32}P , or any other detectable marker, such as other radioisotopes, a fluorescent compound, an enzyme, or an enzyme co-factor. Probes for hybridization can be made by labeling synthetic oligonucleotides based on the known cell wall, cell surface and secreted nucleotide sequences disclosed herein. Degenerate primers designed on the basis of conserved nucleotides or amino acid residues in a known cell wall, cell surface and secreted nucleotide sequence or encoded amino acid sequence can additionally be used. The hybridization probe typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 10, preferably about 20, more preferably about 50, 75, 100, 125, 150, 175, 200, 250, 300,

350, or 400 consecutive nucleotides of a cell wall, cell surface or secreted protein nucleotide sequence of the invention or a fragment or variant thereof. To achieve specific hybridization under a variety of conditions, such probes include sequences that are unique among cell wall, cell surface or secreted protein sequences. Preparation of probes for hybridization is generally known in the art and is disclosed in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York), herein incorporated by reference.

In one embodiment, the entire nucleotide sequence encoding a cell wall, cell surface or secreted protein is used as a probe to identify novel cell wall, cell surface or secreted sequences and messenger RNAs. In another embodiment, the probe is a fragment of a nucleotide sequence disclosed herein. In some embodiments, the nucleotide sequence that hybridizes under stringent conditions to the probe can be at least about 300, 325, 350, 375, 400, 425, 450, 500, 550, 600, 650, 700, 800, 900, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10,000, 11,000, 12,000, or 12,500 nucleotides in length.

Substantially identical sequences will hybridize to each other under stringent conditions. By "stringent conditions" is intended conditions under which a probe will hybridize to its target sequence to a detectably greater degree than to other sequences (e.g., at least 2-fold over background). Generally, stringent conditions encompass those conditions for hybridization and washing under which nucleotides having at least about 60%, 65%, 70%, preferably 75% sequence identity typically remain hybridized to each other. Stringent conditions are known in the art and can be found in *Current Protocols in Molecular Biology* (John Wiley & Sons, New York (1989)), 6.3.1-6.3.6. Hybridization typically occurs for less than about 24 hours, usually about 4 to about 12 hours.

Stringent conditions are sequence-dependent and will differ in different circumstances. Full-length or partial nucleic acid sequences may be used to obtain homologues and orthologs encompassed by the present invention. By "orthologs" is intended genes derived from a common ancestral gene and which are found in different species as a result of speciation. Genes found in different species are considered orthologs when their nucleotide sequences and/or their encoded protein sequences share

substantial identity as defined elsewhere herein. Functions of orthologs are often highly conserved among species.

When using probes, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides).

The post-hybridization washes are instrumental in controlling specificity. The two critical factors are ionic strength and temperature of the final wash solution. For the detection of sequences that hybridize to a full-length or approximately full-length target sequence, the temperature under stringent conditions is selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. However, stringent conditions would encompass temperatures in the range of 1°C to 20°C lower than the T_m , depending on the desired degree of stringency as otherwise qualified herein. For DNA-DNA hybrids, the T_m can be determined using the equation of Meinkoth and Wahl (1984) *Anal. Biochem.* 138:267-284: $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe.

The ability to detect sequences with varying degrees of homology can be obtained by varying the stringency of the hybridization and/or washing conditions. To target sequences that are 100% identical (homologous probing), stringency conditions must be obtained that do not allow mismatching. By allowing mismatching of nucleotide residues to occur, sequences with a lower degree of similarity can be detected (heterologous probing). For every 1% of mismatching, the T_m is reduced about 1°C; therefore, hybridization and/or wash conditions can be manipulated to allow hybridization of sequences of a target percentage identity. For example, if sequences with $\geq 90\%$ sequence identity are preferred, the T_m can be decreased by 10°C. Two nucleotide

sequences could be substantially identical, but fail to hybridize to each other under stringent conditions, if the polypeptides they encode are substantially identical. This situation could arise, for example, if the maximum codon degeneracy of the genetic code is used to create a copy of a nucleic acid.

- 5 Exemplary low stringency conditions include hybridization with a buffer solution of 30-35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulfate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C.
- 10 Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C. Optionally, wash buffers may comprise about 0.1% to about 1% SDS. Duration of hybridization is generally less than about 24 hours, usually about 4 to about 12 hours. An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in*
- 15 *Biochemistry and Molecular Biology – Hybridization with Nucleic Acid Probes*, Part I, Chapter 2 (Elsevier, New York); and Ausubel *et al.*, eds. (1995) *Current Protocols in Molecular Biology*, Chapter 2 (Greene Publishing and Wiley-Interscience, New York). See Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed.; Cold Spring Harbor Laboratory Press, Plainview, New York).
- 20 In a PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or genomic DNA extracted from any organism of interest. PCR primers are preferably at least about 10 nucleotides in length, and most preferably at least about 20 nucleotides in length. Methods for designing PCR primers and PCR cloning are generally known in the art and
- 25 are disclosed in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York). See also Innis *et al.*, eds. (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, New York); Innis and Gelfand, eds. (1995) *PCR Strategies* (Academic Press, New York); and Innis and Gelfand, eds. (1999) *PCR Methods Manual* (Academic Press, New York).
- 30 Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers,

vector-specific primers, partially-mismatched primers, and the like.

Assays

Diagnostic assays to detect expression of the disclosed polypeptides and/or nucleic acid molecules as well as their disclosed activity in a sample are disclosed. An exemplary method for detecting the presence or absence of a disclosed nucleic acid or protein comprising the disclosed polypeptide in a sample involves obtaining a sample from a food/dairy/feed product, starter culture (mother, seed, bulk/set, concentrated, dried, lyophilized, frozen), cultured food/dairy/feed product, dietary supplement, bioprocessing fermentate, or a subject that has ingested a probiotic material and contacting the sample with a compound or an agent capable of detecting the disclosed polypeptides or nucleic acids (e.g., an mRNA or genomic DNA comprising the disclosed nucleic acid or fragment thereof) such that the presence of the disclosed sequence is detected in the sample. Results obtained with a sample from the food, supplement, culture, product, or subject may be compared to results obtained with a sample from a control culture, product, or subject.

One agent for detecting the mRNA or genomic DNA comprising a disclosed nucleotide sequence is a labeled nucleic acid probe capable of hybridizing to the disclosed nucleotide sequence of the mRNA or genomic DNA. The nucleic acid probe can be, for example, a disclosed nucleic acid molecule, such as the nucleic acid of odd SEQ ID NOS:1-307, or a portion thereof, such as a nucleic acid molecule of at least 15, 30, 50, 100, 250, or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to the mRNA or genomic DNA comprising the disclosed nucleic acid sequence. Other suitable probes for use in the diagnostic assays of the invention are described herein.

One agent for detecting a protein comprising a disclosed polypeptide sequence is an antibody capable of binding to the disclosed polypeptide, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (e.g., Fab or F(ab')₂) can be used. The term "labeled," with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically linking) a detectable substance to

the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end labeling of a DNA probe with biotin such that it can be detected with fluorescently
5 labeled streptavidin.

The term "sample" is intended to include tissues, cells, and biological fluids present in or isolated from a subject, as well as cells from starter cultures or food products carrying such cultures, or derived from the use of such cultures. That is, the detection method of the invention can be used to detect mRNA, protein, or genomic DNA
10 comprising a disclosed sequence in a sample both *in vitro* and *in vivo*. *In vitro* techniques for detection of mRNA comprising a disclosed sequence include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of a protein comprising a disclosed polypeptide include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection
15 of genomic DNA comprising the disclosed nucleotide sequences include Southern hybridizations. Furthermore, *in vivo* techniques for detection of a protein comprising a disclosed polypeptide include introducing into a subject a labeled antibody against the disclosed polypeptide. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging
20 techniques.

In one embodiment, the sample contains protein molecules from a test subject that has consumed a probiotic material. Alternatively, the sample can contain mRNA or genomic DNA from a starter culture.

The invention also encompasses kits for detecting the presence of disclosed
25 nucleic acids or proteins comprising disclosed polypeptides in a sample. Such kits can be used to determine if a microbe expressing a specific polypeptide of the invention is present in a food product or starter culture, or in a subject that has consumed a probiotic material. For example, the kit can comprise a labeled compound or agent capable of detecting a disclosed polypeptide or mRNA in a sample and means for determining the
30 amount of a disclosed polypeptide in the sample (e.g., an antibody that recognizes the disclosed polypeptide or an oligonucleotide probe that binds to DNA encoding a

disclosed polypeptide, e.g., any of even SEQ ID NOS:1-307. Kits can also include instructions detailing the use of such compounds.

For antibody-based kits, the kit can comprise, for example: (1) a first antibody (e.g., attached to a solid support) that binds to a disclosed polypeptide; and, optionally,
5 (2) a second, different antibody that binds to the disclosed polypeptide or the first antibody and is conjugated to a detectable agent. For oligonucleotide-based kits, the kit can comprise, for example: (1) an oligonucleotide, e.g., a detectably labeled oligonucleotide, that hybridizes to a disclosed nucleic acid sequence or (2) a pair of primers useful for amplifying a disclosed nucleic acid molecule.

10 The kit can also comprise, e.g., a buffering agent, a preservative, or a protein-stabilizing agent. The kit can also comprise components necessary for detecting the detectable agent (e.g., an enzyme or a substrate). The kit can also contain a control sample or a series of control samples that can be assayed and compared to the test sample contained. Each component of the kit is usually enclosed within an individual container,
15 and all of the various containers are within a single package along with instructions for use.

In one embodiment, the kit comprises multiple probes in an array format, such as those described, for example, in U.S. Patent Nos. 5,412,087 and 5,545,531, and International Publication No. WO 95/00530, herein incorporated by reference. Probes for
20 use in the array may be synthesized either directly onto the surface of the array, as disclosed in International Publication No. WO 95/00530, or prior to immobilization onto the array surface (Gait, ed. (1984) *Oligonucleotide Synthesis a Practical Approach* IRL Press, Oxford, England). The probes may be immobilized onto the surface using techniques well known to one of skill in the art, such as those described in U.S. Patent
25 No. 5,412,087. Probes may be a nucleic acid or peptide sequence, preferably purified, or an antibody.

The arrays may be used to screen organisms, samples, or products for differences in their genomic, cDNA, polypeptide, or antibody content, including the presence or absence of specific sequences or proteins, as well as the concentration of those materials.
30 Binding to a capture probe is detected, for example, by signal generated from a label attached to the nucleic acid molecule comprising the disclosed nucleic acid sequence, a

polypeptide comprising the disclosed amino acid sequence, or an antibody. The method can include contacting the molecule comprising the disclosed nucleic acid, polypeptide, or antibody with a first array having a plurality of capture probes and a second array having a different plurality of capture probes. The results of each hybridization can be compared to analyze differences in expression between a first and second sample. The first plurality of capture probes can be from a control sample, e.g., a wild type lactic acid bacteria, or control subject, e.g., a food, dietary supplement, starter culture sample, or a biological fluid. The second plurality of capture probes can be from an experimental sample, e.g., a mutant type lactic acid bacteria, or subject that has consumed a probiotic material, e.g., a starter culture sample or a biological fluid.

These assays may be especially useful in microbial selection and quality control procedures where the detection of unwanted materials is essential. The detection of particular nucleotide sequences or polypeptides may also be useful in determining the genetic composition of food, fermentation products, or industrial microbes, or microbes present in the digestive system of animals or humans that have consumed probiotics.

Antisense Nucleotide Sequences

The present invention also encompasses antisense nucleic acid molecules, i.e., molecules that are complementary to a sense nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule, or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire cell wall, cell surface or secreted protein coding strand, or to only a portion thereof, e.g., all or part of the protein-coding region (or open reading frame). An antisense nucleic acid molecule can be antisense to a noncoding region of the coding strand of a nucleotide sequence encoding a cell wall, cell surface or secreted protein. The noncoding regions are the 5' and 3' sequences that flank the coding region and are not translated into amino acids. Antisense nucleotide sequences are useful in disrupting the expression of the target gene. Antisense constructions having 70%, preferably 80%, more preferably 85% sequence identity to the corresponding sequence may be used.

Given the coding-strand sequence encoding a cell wall, cell surface or secreted protein disclosed herein (e.g., odd SEQ ID NOS:1-307), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of cell wall, cell surface or secreted protein mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of cell wall, cell surface or secreted protein mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of cell wall, cell surface or secreted protein mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 nucleotides in length, or it can be 100, 200 nucleotides, or greater in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation procedures known in the art.

For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, including, but not limited to, for example e.g., phosphorothioate derivatives and acridine substituted nucleotides. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest).

An antisense nucleic acid molecule of the invention can be an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

The invention also encompasses ribozymes, which are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Ribozymes (e.g.,

hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave cell wall, cell surface and secreted mRNA transcripts to thereby inhibit translation of cell wall, cell surface and secreted mRNA. A ribozyme having specificity for a cell wall, cell surface or secreted protein-encoding nucleic acid can be designed based upon the nucleotide sequence of a cell wall, cell surface or secreted protein cDNA disclosed herein (e.g., odd SEQ ID NOS:1-307). See, e.g., U.S. Patent No. 4,987,071; and U.S. Patent No. 5,116,742. Alternatively, cell wall, cell surface and secreted protein mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel and Szostak (1993) *Science* 261:1411-1418.

The invention also encompasses nucleic acid molecules that form triple helical structures. For example, cell wall, cell surface or secreted protein gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the cell wall, cell surface or secreted protein (e.g., the cell wall, cell surface or secreted promoters and/or enhancers) to form triple helical structures that prevent transcription of the cell wall, cell surface or secreted protein gene in target cells. See generally Helene (1991) *Anticancer Drug Des.* 6(6):569; Helene (1992) *Ann. N.Y. Acad. Sci.* 660:27; and Maher (1992) *Bioassays* 14(12):807.

In some embodiments, the nucleic acid molecules of the invention can be modified at the base moiety, sugar moiety, or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorganic & Medicinal Chemistry* 4:5). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid-phase peptide synthesis protocols as described, for example, in Hyrup *et al.* (1996) *supra*; Perry-O'Keefe *et al.* (1996) *Proc. Natl. Acad. Sci. USA* 93:14670.

PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA-directed PCR clamping; as artificial
5 restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup (1996) *supra*); or as probes or primers for DNA sequence and hybridization (Hyrup (1996) *supra*; Perry-O'Keefe *et al.* (1996) *supra*).

In another embodiment, PNAs of a cell wall, cell surface or secreted molecule can be modified, e.g., to enhance their stability, specificity, or cellular uptake, by attaching
10 lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) *supra*; Finn *et al.* (1996) *Nucleic Acids Res.* 24(17):3357-63; Mag *et al.* (1989) *Nucleic Acids Res.* 17:5973; and Peterson *et al.* (1975) *Bioorganic Med. Chem. Lett.* 5:1119.

15

Fusion Proteins

The invention also includes cell wall, cell surface and secreted chimeric or fusion proteins. A cell wall, cell surface or secreted "chimeric protein" or "fusion protein" comprises a cell wall, cell surface or secreted polypeptide operably linked to a non-cell
20 wall, cell surface or secreted polypeptide. A "cell wall, cell surface or secreted polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a cell wall, cell surface or secreted protein, whereas a "non-cell wall, cell surface or secreted polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially identical to the cell wall, cell surface
25 or secreted protein, and which is derived from the same or a different organism. Within a cell wall, cell surface or secreted fusion protein, the cell wall, cell surface or secreted polypeptide can correspond to all or a portion of a cell wall, cell surface or secreted protein, preferably including at least one biologically active portion of a cell wall, cell surface or secreted protein. Within the fusion protein, the term "operably linked" is
30 intended to indicate that the cell wall, cell surface or secreted polypeptide and the non-cell wall, cell surface or secreted polypeptide are fused in-frame to each other. The non-

cell wall, cell surface or secreted polypeptide can be fused to the N-terminus or C-terminus of the cell wall, cell surface or secreted polypeptide.

Expression of the linked coding sequences results in two linked heterologous amino acid sequences that form the fusion protein. The carrier sequence (the non-cell
5 wall, cell surface or secreted polypeptide) can encode a carrier polypeptide that potentiates or increases expression of the fusion protein in the bacterial host. The portion of the fusion protein encoded by the carrier sequence, i.e., the carrier polypeptide, may be a protein fragment, an entire functional moiety, or an entire protein sequence. The carrier region or polypeptide may additionally be designed to be used in purifying the fusion
10 protein, either with antibodies or with affinity purification specific for that carrier polypeptide. Likewise, physical properties of the carrier polypeptide can be exploited to allow selective purification of the fusion protein.

Particular carrier polypeptides of interest include superoxide dismutase (SOD), maltose-binding protein (MBP), glutathione-S-transferase (GST), an N-terminal histidine
15 (His) tag, and the like. This list is not intended to be limiting, as any carrier polypeptide that potentiates expression of the cell wall, cell surface or secreted protein as a fusion protein can be used in the methods of the invention.

In one embodiment, the fusion protein is a GST-cell wall, cell surface or secreted fusion protein in which the cell wall, cell surface or secreted sequence is fused to the C-
20 terminus of the GST sequence. In another embodiment, the fusion protein is a cell wall, cell surface or secreted-immunoglobulin fusion protein in which all or part of a cell wall, cell surface or secreted protein is fused to sequences derived from a member of the immunoglobulin protein family. The cell wall, cell surface or secreted protein-immunoglobulin fusion proteins of the invention can be used as immunogens to produce
25 anti-cell wall, cell surface or secreted antibodies in a subject, to purify cell wall, cell surface or secreted protein ligands, and in screening assays to identify molecules that inhibit the interaction of a cell wall, cell surface or secreted protein with a cell wall, cell surface or secreted protein ligand.

One of skill in the art will recognize that the particular carrier polypeptide is
30 chosen with the purification scheme in mind. For example, His tags, GST, and maltose-binding protein represent carrier polypeptides that have readily available affinity columns

to which they can be bound and eluted. Thus, where the carrier polypeptide is an N-terminal His tag such as hexahistidine (His₆ tag), the cell wall, cell surface or secreted fusion protein can be purified using a matrix comprising a metal-chelating resin, for example, nickel nitrilotriacetic acid (Ni-NTA), nickel iminodiacetic acid (Ni-IDA), and cobalt-containing resin (Co-resin). See, for example, Steinert *et al.* (1997) *QIAGEN News* 4:11-15, herein incorporated by reference in its entirety. Where the carrier polypeptide is GST, the cell wall, cell surface or secreted fusion protein can be purified using a matrix comprising glutathione-agarose beads (Sigma or Pharmacia Biotech); where the carrier polypeptide is a maltose-binding protein (MBP), the cell wall, cell surface or secreted fusion protein can be purified using a matrix comprising an agarose resin derivatized with amylose.

Preferably, a chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences may be ligated together in-frame, or the fusion gene can be synthesized, such as with automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments, which can subsequently be annealed and re-amplified to generate a chimeric gene sequence (see, e.g., Ausubel *et al.*, eds. (1995) *Current Protocols in Molecular Biology* (Greene Publishing and Wiley-Interscience, New York). Moreover, a cell wall, cell surface or secreted protein-encoding nucleic acid can be cloned into a commercially available expression vector such that it is linked in-frame to an existing fusion moiety.

The fusion protein expression vector is typically designed for ease of removing the carrier polypeptide to allow the cell wall, cell surface or secreted protein to retain the native biological activity associated with it. Methods for cleavage of fusion proteins are known in the art. See, for example, Ausubel *et al.*, eds. (1998) *Current Protocols in Molecular Biology* (John Wiley & Sons, Inc.). Chemical cleavage of the fusion protein can be accomplished with reagents such as cyanogen bromide, 2-(2-nitrophenylsulphenyl)-3-methyl-3'-bromoindolenine, hydroxylamine, or low pH. Chemical cleavage is often accomplished under denaturing conditions to cleave otherwise insoluble fusion proteins.

Where separation of the cell wall, cell surface or secreted polypeptide from the carrier polypeptide is desired and a cleavage site at the junction between these fused polypeptides is not naturally occurring, the fusion construct can be designed to contain a specific protease cleavage site to facilitate enzymatic cleavage and removal of the carrier polypeptide. In this manner, a linker sequence comprising a coding sequence for a peptide that has a cleavage site specific for an enzyme of interest can be fused in-frame between the coding sequence for the carrier polypeptide (for example, MBP, GST, SOD, or an N-terminal His tag) and the coding sequence for the cell wall, cell surface or secreted polypeptide. Suitable enzymes having specificity for cleavage sites include, but are not limited to, factor Xa, thrombin, enterokinase, remin, collagenase, and tobacco etch virus (TEV) protease. Cleavage sites for these enzymes are well known in the art. Thus, for example, where factor Xa is to be used to cleave the carrier polypeptide from the cell wall, cell surface or secreted polypeptide, the fusion construct can be designed to comprise a linker sequence encoding a factor Xa-sensitive cleavage site, for example, the sequence IEGR (see, for example, Nagai and Thøgersen (1984) *Nature* 309:810-812, Nagai and Thøgersen (1987) *Meth. Enzymol.* 153:461-481; and Pryor and Leiting (1997) *Protein Expr. Purif.* 10(3):309-319, herein incorporated by reference). Where thrombin is to be used to cleave the carrier polypeptide from the cell wall, cell surface and secreted polypeptide, the fusion construct can be designed to comprise a linker sequence encoding a thrombin-sensitive cleavage site, for example the sequence LVPRGS or VIAGR (see, for example, Pryor and Leiting (1997) *Protein Expr. Purif.* 10(3):309-319, and Hong *et al.* (1997) *Chin. Med. Sci. J.* 12(3):143-147, respectively, herein incorporated by reference). Cleavage sites for TEV protease are known in the art. See, for example, the cleavage sites described in U.S. Patent No. 5,532,142, herein incorporated by reference in its entirety. See also the discussion in Ausubel *et al.*, eds. (1998) *Current Protocols in Molecular Biology* (John Wiley & Sons, Inc.), Chapter 16.

Fusion proteins of the invention can utilize all or part of the "cell wall, cell surface or secreted protein" to target foreign peptides and proteins to the cell wall, cell surface or for secretion. Targeting to the cell wall, cell surface or for secretion by the cell results from signal sequences, secretion signals, or LPXTG-like (SEQ ID NO:308) motifs in the cell wall, cell surface or secreted protein. The functional region which allows the

native cell wall, cell surface or secreted protein to be secreted or bound at the cell wall or cell surface can be fused as described below in such a way as to enable a non-cell wall, cell surface or secreted protein to be secreted or bound to the cell wall or cell surface of the same or a different organism.

5

Antibodies

An isolated polypeptide of the present invention can be used as an immunogen to generate antibodies that specifically bind cell wall, cell surface or secreted proteins, or stimulate production of antibodies in vivo. The full-length cell wall, cell surface or secreted protein can be used as an immunogen or, alternatively, antigenic peptide fragments of cell wall, cell surface or secreted proteins as described herein can be used. The antigenic peptide of a cell wall, cell surface or secreted protein comprises at least 8, preferably 10, 15, 20, or 30 amino acid residues of the amino acid sequence shown in any of even SEQ ID NOS:1-307, and encompasses an epitope of a cell wall, cell surface or secreted protein such that an antibody raised against the peptide forms a specific immune complex with the cell wall, cell surface or secreted protein. Preferred epitopes encompassed by the antigenic peptide are regions of a cell wall, cell surface or secreted protein that are located on the surface of the protein, e.g., hydrophilic regions.

20 Recombinant Expression Vectors and Host Cells

The nucleic acid molecules of the present invention may be included in vectors, preferably expression vectors. "Vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. Expression vectors include one or more regulatory sequences and direct the expression of genes to which they are operably linked. By "operably linked" is intended that the nucleotide sequence of interest is linked to the regulatory sequence(s) such that expression of the nucleotide sequence is allowed (e.g., in an in vitro transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include controllable transcriptional promoters, operators, enhancers, transcriptional terminators, and other expression control elements such as translational control sequences

30

(e.g., Shine-Dalgarno consensus sequence, initiation and termination codons). These regulatory sequences will differ, for example, depending on the host cell being used.

The vectors can be autonomously replicated in a host cell (episomal vectors), or may be integrated into the genome of a host cell, and replicated along with the host genome (non-episomal mammalian vectors). Integrating vectors typically contain at least one sequence homologous to the bacterial chromosome that allows for recombination to occur between homologous DNA in the vector and the bacterial chromosome. Integrating vectors may also comprise bacteriophage or transposon sequences. Episomal vectors, or plasmids are circular double-stranded DNA loops into which additional DNA segments can be ligated. Plasmids capable of stable maintenance in a host are generally the preferred form of expression vectors when using recombinant DNA techniques.

The expression constructs or vectors encompassed in the present invention comprise a nucleic acid construct of the invention in a form suitable for expression of the nucleic acid in a host cell. Expression in prokaryotic host cells is encompassed in the present invention. It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., cell wall, cell surface and secreted proteins, mutant forms of cell wall, cell surface and secreted proteins, fusion proteins, etc.).

Regulatory sequences include those that direct constitutive expression of a nucleotide sequence as well as those that direct inducible expression of the nucleotide sequence only under certain environmental conditions. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiation region, which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region typically includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, which may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative

regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if
5 present is usually proximal (5') to the RNA polymerase binding sequence.

An example of a gene activator protein is the catabolite activator protein (CAP), which helps initiate transcription of the lac operon in *Escherichia coli* (Raibaud *et al.* (1984) *Annu. Rev. Genet.* 18:173). Regulated expression may therefore be positive or negative, thereby either enhancing or reducing transcription. Other examples of positive
10 and negative regulatory elements are well known in the art. Various promoters that can be included in the protein expression system include, but are not limited to, a T7/LacO hybrid promoter, a trp promoter, a T7 promoter, a lac promoter, and a bacteriophage lambda promoter. Any suitable promoter can be used to carry out the present invention, including the native promoter or a heterologous promoter. Heterologous promoters may
15 be constitutively active or inducible. A non-limiting example of a heterologous promoter is given in US Patent No. 6,242,194.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (lac) (Chang *et al.* (1987) *Nature*
20 198:1056), and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (trp) (Goeddel *et al.* (1980) *Nucleic Acids Res.* 8:4057; Yelverton *et al.* (1981) *Nucleic Acids Res.* 9:731; U.S. Patent No. 4,738,921; EPO Publication Nos. 36,776 and 121,775). The beta-lactamase (bla) promoter system (Weissmann, (1981) "The Cloning of Interferon and Other Mistakes," in *Interferon 3* (ed.
25 I. Gresser); bacteriophage lambda PL (Shimatake *et al.* (1981) *Nature* 292:128); the arabinose-inducible araB promoter (U.S. Patent No. 5,028,530); and T5 (U.S. Pat. No. 4,689,406) promoter systems also provide useful promoter sequences. See also Balbas (2001) *Mol. Biotech.* 19:251-267, where *E. coli* expression systems are discussed.

In addition, synthetic promoters that do not occur in nature also function as
30 bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or

bacteriophage promoter, creating a synthetic hybrid promoter (U.S. Patent No. 4,551,433). For example, the tac (Amann *et al.* (1983) *Gene* 25:167; de Boer *et al.* (1983) *Proc. Natl. Acad. Sci.* 80:21) and trc (Brosius *et al.* (1985) *J. Biol. Chem.* 260:3539-3541) promoters are hybrid trp-lac promoters comprised of both trp promoter and lac
5 operon sequences that are regulated by the lac repressor. The tac promoter has the additional feature of being an inducible regulatory sequence. Thus, for example, expression of a coding sequence operably linked to the tac promoter can be induced in a cell culture by adding isopropyl-1-thio- β -D-galactoside (IPTG). Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the
10 ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system (Studier *et al.* (1986) *J. Mol. Biol.* 189:113; Tabor *et al.* (1985) *Proc. Natl. Acad. Sci.* 82:1074). In
15 addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO Publication No. 267,851).

The vector may additionally contain a gene encoding the repressor (or inducer) for that promoter. For example, an inducible vector of the present invention may regulate transcription from the Lac operator (LacO) by expressing the gene encoding the LacI
20 repressor protein. Other examples include the use of the *lexA* gene to regulate expression of pRecA, and the use of *trpO* to regulate *ptpr*. Alleles of such genes that increase the extent of repression (e.g., *lacIq*) or that modify the manner of induction (e.g., *.lambda.CI857*, rendering *.lambda.pL* thermo-inducible, or *.lambda.CI+*, rendering *.lambda.pL* chemo-inducible) may be employed.

25 In addition to a functioning promoter sequence, an efficient ribosome-binding site is also useful for the expression of the fusion construct. In prokaryotes, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon (Shine *et al.* (1975) *Nature* 254:34). The SD sequence is thought to
30 promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' end of bacterial 16S rRNA (Steitz *et al.* (1979) "Genetic Signals and

Nucleotide Sequences in Messenger RNA," in *Biological Regulation and Development: Gene Expression* (ed. R. F. Goldberger, Plenum Press, NY).

Cell wall and cell surface proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a protein comprising a signal peptide sequence
5 fragment that provides for secretion of the cell wall or cell surface polypeptides in bacteria (U.S. Patent No. 4,336,336). The signal sequence fragment typically encodes a signal peptide comprised of hydrophobic amino acids that direct the secretion of the protein from the cell. The protein is either secreted into the growth media (Gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of
10 the cell (Gram-negative bacteria). Preferably there are processing sites, which can be cleaved either *in vivo* or *in vitro*, encoded between the signal peptide fragment and the cell wall, cell surface and secreted protein.

DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (*ompA*) (Masui *et al.*
15 (1983) FEBS Lett. 151(1):159-164; Ghrayeb *et al.* (1984) *EMBO J.* 3:2437-2442) and the *E. coli* alkaline phosphatase signal sequence (*phoA*) (Oka *et al.* (1985) *Proc. Natl. Acad. Sci.* 82:7212). Other prokaryotic signals include, for example, the signal sequence from penicillinase, Ipp, or heat stable enterotoxin II leaders.

Bacteria such as *L. acidophilus* generally utilize the start codon ATG, which
20 specifies the amino acid methionine (which is modified to N-formylmethionine in prokaryotic organisms). Bacteria also recognize alternative start codons, such as the codons GTG and TTG, which code for valine and leucine, respectively. When they are used as the initiation codon, however, these codons direct the incorporation of methionine rather than of the amino acid they normally encode. *Lactobacillus acidophilus* NCFM
25 recognizes these alternative start sites and incorporates methionine as the first amino acid.

Typically, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon and thus, together with the promoter, flank the coding sequence. These sequences direct the transcription of an
30 mRNA that can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences (of about 50 nucleotides) that

are capable of forming stem loop structures that aid in terminating transcription. Examples include transcription termination sequences derived from genes with strong promoters, such as the *trp* gene in *E. coli* as well as other biosynthetic genes.

The expression vectors will have a plurality of restriction sites for insertion of the cell wall, cell surface or secreted protein sequence so that it is under transcriptional regulation of the regulatory regions. Selectable marker genes that ensure maintenance of the vector in the cell can also be included in the expression vector. Preferred selectable markers include those that confer resistance to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline (Davies *et al.* (1978) *Annu. Rev. Microbiol.* 32:469). Selectable markers may also allow a cell to grow on minimal medium, or in the presence of toxic metabolite and may include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

The regulatory regions may be native (homologous), or may be foreign (heterologous) to the host cell and/or the nucleotide sequence of the invention. The regulatory regions may also be natural or synthetic. Where the region is "foreign" or "heterologous" to the host cell, it is intended that the region is not found in the native cell into which the region is introduced. Where the region is "foreign" or "heterologous" to the cell wall, cell surface or secreted protein nucleotide sequence of the invention, it is intended that the region is not the native or naturally occurring region for the operably linked cell wall, cell surface or secreted protein nucleotide sequence of the invention. For example, the region may be derived from phage. While it may be preferable to express the sequences using heterologous regulatory regions, native regions may be used. Such constructs would be expected in some cases to alter expression levels of cell wall, cell surface or secreted proteins in the host cell. Thus, the phenotype of the host cell could be altered.

In preparing the expression cassette, the various DNA fragments may be manipulated, so as to provide for the DNA sequences in the proper orientation and, as appropriate, in the proper reading frame. Toward this end, adapters or linkers may be employed to join the DNA fragments or other manipulations may be involved to provide for convenient restriction sites, removal of superfluous DNA, removal of restriction sites,

or the like. For this purpose, *in vitro* mutagenesis, primer repair, restriction, annealing, resubstitutions, e.g., transitions and transversions, may be involved.

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operably linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to a cell wall, cell surface or secreted protein mRNA. Regulatory sequences operably linked to a nucleic acid cloned in the antisense orientation can be chosen to direct the continuous or inducible expression of the antisense RNA molecule. The antisense expression vector can be in the form of a recombinant plasmid or phagemid in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes *see* Weintraub *et al.* (1986) *Reviews - Trends in Genetics*, Vol. 1(1).

Alternatively, some of the above-described components can be put together in transformation vectors. Transformation vectors are typically comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Microbial or Bacterial Host Cells

The production of bacteria containing the nucleic acid sequences or proteins designated, the preparation of starter cultures of such bacteria, and methods of fermenting substrates, particularly food substrates such as milk, may be carried out in accordance with known techniques.

By "introducing" as it pertains to nucleic acid molecules is intended introduction into prokaryotic cells via conventional transformation or transfection techniques, or by phage-mediated infection. As used herein, the terms "transformation," "transduction," "conjugation," and "protoplast fusion" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated

transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook *et al.* (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York) and other laboratory manuals. By "introducing" as it pertains to polypeptides or
5 microorganisms of the invention, is intended introduction into a host by ingestion, topical application, nasal, suppository, urogenital, or oral application of the polypeptide or microorganism.

Bacterial cells used to produce the cell wall, cell surface and secreted polypeptides of this invention are cultured in suitable media, as described generally in
10 Sambrook *et al.* (1989) *Molecular Cloning, A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

Function and Assays

Assays to measure binding activity of proteins such as periplasmic solute binding
15 proteins (PFAM Accession PF01297) are well known in the art (see, for example, Hosie *et al.* (2001) *Mol. Microbiol.* 40: 1449-59; Hazlett *et al.* (2003) *J. Biol. Chem.* 278:20687-20694). Periplasmic solute binding proteins of the present invention include that in SEQ ID NO:2.

Glycosyl hydrolases, such as the O-Glycosyl hydrolases (EC 3.2.1.-) are a
20 widespread group of enzymes that hydrolyse the glycosidic bond between two or more carbohydrates, or between a carbohydrate and a non-carbohydrate moiety. Glycosyl hydrolase family 32 (PFAM Accession PF00251) comprises enzymes with several known activities; invertase (EC:3.2.1.26); inulinase (EC:3.2.1.7); levanase (EC:3.2.1.65); exo-inulinase (EC:3.2.1.80); sucrose:sucrose 1-fructosyltransferase (EC:2.4.1.99); and
25 fructan:fructan 1-fructosyltransferase (EC:2.4.1.100). Glycosyl hydrolase family 32 proteins of the present invention include that in SEQ ID NO:10.

Glycoside hydrolase family 31 (PFAM Accession PF01055) comprises enzymes with several known activities; -glucosidase (EC:3.2.1.20), -galactosidase (EC:3.2.1.22); glucoamylase (EC:3.2.1.3), sucrase-isomaltase (EC:3.2.1.48) (EC:3.2.1.10); -xylosidase
30 (EC:3.2.1); -glucan lyase (EC:4.2.2.13). Glycosyl hydrolase family 31 proteins of the present invention include those in SEQ ID NOS:262, 264, and 268.

Assays to measure hydrolase activity are well known in the art (see, for example, Avigad and Bauer (1966) *Methods Enzymol.* 8:621-628; Neumann and Lampen (1967) *Biochemistry* 6:468-475; Henry and Darbyshire (1980) *Phytochemistry* 19:1017-1020).

Alpha amylase (PFAM Accession PF00128) is classified as family 13 of the glycosyl hydrolases. The structure of the alpha amylases consists of an 8 stranded alpha/beta barrel containing the active site, interrupted by an about 70 amino acid calcium-binding domain protruding between beta strand 3 and alpha helix 3, and a carboxyl-terminal Greek key beta-barrel domain. Assays to measure alpha-amylase activity are well known in the art (see, for example, Das *et al.* (2004) *Biotechnol. Appl. Biochem.* Mar 25; Grzybowska *et al.* (2004) *Mol. Biotechnol.* 26:101-110). Alpha amylase proteins of the present invention include those in SEQ ID NOS:260, 266, 270, 272, 274, 276, and 278.

Enzymes containing the Alpha amylase, N-terminal ig-like domain belong to family 13 of the glycosyl hydrolases (PFAM Accession PF02903). The maltogenic - amylase is an enzyme which catalyses hydrolysis of (1-4)-D-glucosidic linkages in polysaccharides so as to remove successive maltose residues from the non-reducing ends of the chains in the conversion of starch to maltose. Other enzymes include neopullulanase, which hydrolyses pullulan to panose, and cyclomaltodextrinase, which hydrolyses cyclodextrins. Alpha amylase, N-terminal ig-like domain proteins of the present invention include that in SEQ ID NO:274.

Enzymes containing the Isoamylase N-terminal domain belong to family 13 of the glycosyl hydrolases (PFAM Accession PF02922). This domain is found in a range of enzymes that act on branched substrates, ie. isoamylase, pullulanase and branching enzyme. Isoamylase hydrolyses 1,6-D-glucosidic branch linkages in glycogen, amylopectin and dextrin; 1,4-glucan branching enzyme functions in the formation of 1,6-glucosidic linkages of glycogen; and pullulanase is a starch-debranching enzyme. Isoamylase N-terminal domain proteins of the present invention include that in SEQ ID NO:272.

Surface layer proteins, which are glycoproteins forming a layer on the outermost cell envelope component of bacteria, may function as attachment structures for extracellular enzymes, or as cell shape determinants. Assays for measuring structure-

function relationships of s-layer proteins are well known in the art (see, for example, Sleytr *et al.* (1997) *Trends Biotechnol.* 15:20-26; Olabarria *et al.* (1996) *J. Bacteriol.* 178:4765-4772). Surface layer proteins of the present invention include that in SEQ ID NO:62.

- 5 The N-acetylmuramoyl-L-alanine amidase family of proteins (PFAM Accession PF01510) includes zinc amidases that have N-acetylmuramoyl-L-alanine amidase activity (EC:3.5.1.28). This enzyme domain cleaves the amide bond between N-acetylmuramoyl and L-amino acids in bacterial cell walls (preferentially: D-lactyl-L-Ala). Methods to measure amidase activity are well known in the art (see, for example, Wang *et al.* (2003) *J. Biol. Chem.* 278:49044-52; Gelius *et al.* (2003) *Biochem Biophys Res Commun.* 306:988-94). N-acetylmuramoyl-L-alanine amidase proteins of the present invention include that in SEQ ID NO:82.

- Proteins such as FtsW, RodA, and SpoVE are integral membrane proteins involved in cell cycle processes (PFAM Accession PF01098). Methods to assay activity
15 of cell cycle proteins are well known in the art (see, for example, Vinella *et al.* (1993) *J. Bacteriol.* 175:6704-6710). Cell cycle proteins of the present invention include those in SEQ ID NOS:92 and 286.

- Mur ligase family proteins contain a number of related ligase enzymes which have EC numbers 6.3.2.-. This family includes: MurC, MurD, MurE, MurF, Mpl and
20 FolC. MurC, MurD, MurE and MurF catalyse consecutive steps in the synthesis of peptidoglycan. Peptidoglycan consists of a sheet of two sugar derivatives, with one of these N-acetylmuramic acid attaching to a small pentapeptide. The pentapeptide is made of L-alanine, D-glutamic acid, Meso-diaminopimelic acid and D-alanyl alanine. The peptide moiety is synthesized by successively adding these amino acids to UDP-N-
25 acetylmuramic acid. MurC transfers the L-alanine; MurD transfers the D-glutamate; MurE transfers the diaminopimelic acid; and MurF transfers the D-alanyl alanine. This family also includes Folylpolyglutamate synthase that transfers glutamate to folypolyglutamate. Assays to measure ligase enzyme activity are well known in the art (see, for example, Bouhss *et al.* (1997) *Biochemistry.* 36:11556-11563; Hesse *et al.* (2003) *J. Bacteriol.* 185:6507-6512). Mur ligase family proteins of the present invention
30 include those in SEQ ID NOS:94, 96, 98, 100, and 116.

Glycosyltransferases are enzymes that catalyse the transfer of sugar moieties from activated donor molecules to specific acceptor molecules, forming glycosidic bonds. The glycosyltransferase family 28 N-terminal domain (PFAM Accession PF03033) includes monogalactosyldiacylglycerol synthase (P93115, EC 2.4.1.46), 1,2-diacylglycerol 3-galactosyltransferase (EC:2.4.1.46), 1,2-diacylglycerol 3-glucosyltransferase (EC:2.4.1.157), and UDP-N-acetylglucosamine transferase (MURG_SYNY3, EC 2.4.1.-). The N-terminal domain contains the acceptor binding site and likely membrane association site. Glycosyltransferase family 28 N-terminal domain proteins of the present invention include that in SEQ ID NO:102.

The glycosyl transferases (PFAM Accession PF00953) are a family of UDP-GlcNAc/MurNAc:polyisoprenol-P GlcNAc/MurNAc-1-P transferases. Members of the family include eukaryotic N-acetylglucosamine-1-phosphate transferases, which catalyze the conversion of UDP-N-acetyl-D-glucosamine and dolichyl phosphate to UMP and N-acetyl-D-glucosaminyl-diphosphodolichol in the glycosylation pathway; and bacterial phospho-N-acetylmuramoyl-pentapeptide-transferases, which catalyze the first step of the lipid cycle reactions in the biosynthesis of cell wall peptidoglycan. Glycosyltransferase proteins (PFAM Accession PF00953) of the present invention include those in SEQ ID NOS:104 and 126.

The Glycosyl transferase family (PFAM Accession PF00535) is a diverse family of a variety of glycosyl transferases that transfer the sugar from UDP-glucose, UDP-N-acetyl-galactosamine, GDP-mannose or CDP-abequose, to a range of substrates including cellulose, dolichol phosphate and teichoic acids. Glycosyltransferase proteins (PFAM Accession PF00535) of the present invention include those in SEQ ID NOS:164, 170, 236, and 252.

Members of the Glycosyl transferases group 1 family (PFAM Accession PF00534) transfer activated sugars to a variety of substrates, including glycogen, fructose-6-phosphate and lipopolysaccharides. Members of this family transfer UDP, ADP, GDP or CMP linked sugars to a variety of substrates, including glycogen, fructose-6-phosphate and lipopolysaccharides. The bacterial enzymes are involved in various biosynthetic processes that include exopolysaccharide biosynthesis, lipopolysaccharide core biosynthesis and the biosynthesis of the slime polysaccharide colanic acid. Glycosyl

transferases group 1 family proteins of the present invention include those in SEQ ID NOS:242, 250, and 258.

Assays to measure glycosyltransferase activity are well known in the art (see, for example, Mengin-Lecreulx *et al.* (1991) *J. Bacteriol.* 173:4625-4636).

5 The mannosyl-glycoprotein endo-beta-N-acetylglucosamidase family includes enzymes in EC:3.2.1.96, which cause endohydrolysis of the di-N-acetylchitobiosyl unit in high-mannose glycopeptides and glycoproteins containing the -[Man(GlcNAc)₂]Asn- structure. Assays to measure amidase activity are well known in the art (see, for example, Pierce *et al.* (1980) *Biochem. J.* 185:261-264; Koide and Muramatsu (1974) *J. Biol. Chem.* 249:4897-4904). Mannosyl-glycoprotein endo-beta-N-acetylglucosamidase
10 proteins of the present invention include those in SEQ ID NOS:106 and 108.

The LysM domain is found in a variety of enzymes involved in bacterial cell wall degradation (Bateman and Bycroft (2000) *J. Mol. Biol.* 299:1113-1119). This domain may have a general peptidoglycan binding function. The structure of this domain is
15 known (Joris *et al.* (1992) *FEMS Microbiol. Lett.* 70:257-264). LysM domain proteins of the present invention include that in SEQ ID NO:110.

The D-ala D-ala ligase N terminus family (PFAM Accession PF01820) includes D-alanine-D-alanine ligase (EC:6.3.2.4), a bacterial enzyme involved in cell-wall biosynthesis. It participates in forming UDP-N-acetylmuramyl pentapeptide, the
20 peptidoglycan precursor. These enzymes are proteins of 300 to 360 amino acids containing many conserved regions. The N-terminal Gly-rich region could be involved in ATP-binding. Methods for measuring D-alanine-D-alanine ligase activity are well known in the art (see, for example, Ito and Strominger (1962) *J. Biol. Chem.* 237:2696-2703; Marshall *et al.* (1997) *Proc. Natl. Acad. Sci. U.S.A.* 94:6480-6483). D-ala D-ala
25 ligase N terminus proteins of the present invention include that in SEQ ID NO:112)

D-alanyl-D-alanine carboxypeptidases (PFAM Accession PF00768) are serine peptidases belonging to Merops peptidase family S11 (D-Ala-D-Ala carboxypeptidase A family, clan SE). D-Ala-D-Ala carboxypeptidase A is involved in the metabolism of cell components. There are three families of serine-type D-Ala-D-Ala peptidase, which are
30 also known as low molecular weight penicillin-binding proteins (S11, S12, S13). Family S11 contains only D-Ala-D-Ala peptidases, unlike families S12 and S13, which contain

other enzymes, such as class C -lactamases and D-amino-peptidases (Rawlings and Barrett (1994) *Methods Enzymol.* 244:19-61). Assays for measuring serine carboxypeptidase activity are well known in the art (see, for example, Chang *et al.* (1990) *Proc. Natl. Acad. Sci. U.S.A.* 87:2823-7). D-alanyl-D-alanine carboxypeptidase proteins of the present invention include that in SEQ ID NO:118.

EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase) (EC:2.5.1.19) catalyzes the sixth step in the biosynthesis from chorismate of the aromatic amino acids (the shikimate pathway) in bacteria (gene *aroA*), plants and fungi (where it is part of a multifunctional enzyme which catalyzes five consecutive steps in this pathway). The sequence of EPSP from various biological sources shows that the structure of the enzyme has been well conserved throughout evolution. Two strongly conserved regions are well defined. The first one corresponds to a region that is part of the active site and which is also important for the resistance to glyphosate. The second second one is located in the C-terminal part of the protein and contains a conserved lysine which seems to be important for the activity of the enzyme. Assays for measuring EPSP synthase activity are well known in the art (see, for example, Okunuki *et al.* (2003) *Shokuhin Eiseigaku Zasshi.* 44:77-82; Oliveira *et al.* (2001) *Protein Expr. Purif.* 22:430-435). EPSP synthase proteins of the present invention include that in SEQ ID NO:120.

The bacterial transferase hexapeptide (three repeats) family (PFAM Accession PF00132) contains a repeat structure composed of tandem repeats of a [LIV]-G-X(4) hexapeptide, which, in the tertiary structure of LpxA (UDP N-acetylglucosamine acyltransferase), has been shown to form a left-handed parallel helix (Raetz and Roderick (1995) *Science* 270:997-1000). Bacterial transferase hexapeptide proteins of the present invention include that in SEQ ID NO:122.

Members of the Putative undecaprenyl diphosphate synthase family (PFAM Accession PF01255) include Di-trans-poly-cis-decaprenylcistransferase (EC:2.5.1.31) (UPP synthetase), which generates undecaprenyl pyrophosphate (UPP) from isopentenyl pyrophosphate (IPP). Methods for measuring Upp synthetase activity are well known in the art (see, for example, Apfel *et al.* (1999) *J. Bacteriol.* 181:483-492). Undecaprenyl diphosphate synthase proteins of the present invention include that in SEQ ID NO:124.

The penicillin-binding proteins are bifunctional proteins consisting of transglycosylase and transpeptidase in the N- and C-terminus respectively. The transglycosylase domain catalyses the polymerisation of murein glycan chains (Lefevre *et al.* (1997) *J. Bacteriol.* 179:4761-4767). Members of the Transglycosylase family (PFAM Accession PF00912) include the bifunctional penicillin-binding proteins that have a transglycosylase (N-terminus) and transpeptidase (C-terminus) domain and the monofunctional biosynthetic peptidoglycan transglycosylases. Methods to measure the catalytic activity of these proteins are well known in the art (see, for example, Di Guilmi *et al.* (2003) *J. Bacteriol.* 185:4418-4423). Penicillin-binding transglycosylase proteins of the present invention include those in SEQ ID NOS:134 and 138.

Members of the Penicillin binding protein transpeptidase domain family (PFAM Accession PF00905) have an active site serine (residue 337 in PBPX_STRPN) that is conserved in all members of the family. These proteins are responsible for the final stages of peptidoglycan biosynthesis for cell wall formation. The proteins synthesize cross-linked peptidoglycan from lipid intermediates, and contain a penicillin-sensitive transpeptidase carboxy-terminal domain. Assays for measuring transpeptidase activity are well known in the art (see, for example, Zijderfeld *et al.* (1995) *J. Bacteriol.* 177:6290-6293). Penicillin-binding transpeptidase proteins of the present invention include those in SEQ ID NOS:132, 134, 138, and 146.

Members of the AMP-binding enzyme family (PFAM Accession PF00501) appear to act via an ATP-dependent covalent binding of AMP to their substrate, and share a region of sequence similarity. This region is a Ser/Thr/Gly-rich domain that is further characterised by a conserved Pro-Lys-Gly triplet. Assays for measuring the catalytic activity of these proteins are well known in the art (see, for example, Weimar *et al.* (2002) *J. Biol. Chem.* 277:29369-29376). AMP-binding proteins of the present invention include that in SEQ ID NO:148.

Many members of the Polysaccharide biosynthesis protein family (PFAM Accession PF01943) are implicated in production of polysaccharide. Assays for measuring polysaccharide biosynthesis are well known in the art (see, for example, Yao and Valvano (1994) *J. Bacteriol.* 176:4133-4143). Polysaccharide biosynthesis proteins of the present invention include those in SEQ ID NOS:156 and 238.

Members of the UDP-galactopyranose mutase family (PFAM Accession PF03275) (EC:5.4.99.9) are involved in the conversion of UDP-GALP into UDP-GALF through a 2-keto intermediate, and contain FAD as a cofactor. Assays for measuring UDP-galactopyranose mutase activity are well known in the art (see, for example, Lee *et al.* (1996) *Anal. Biochem.* 242:1-7). UDP-galactopyranose mutase proteins of the present invention include that in SEQ ID NO:158.

The Bacterial sugar transferase family (PFAM Accession PF02397) represents a conserved region from a number of different bacterial sugar transferases, involved in diverse biosynthesis pathways. Examples include galactosyl-P-P-undecaprenol synthetase (EC:2.7.8.6), which transfers galatose-1-phosphate to the lipid precursor undecaprenol phosphate in the first steps of O-polysaccharide biosynthesis; UDP-galactose-lipid carrier transferase, which is involved in the biosynthesis of amylovoran; and galactosyl transferase CpsD, which is essential for assembly of the group B Streptococci (GBS) type III capsular polysaccharide. Methods for assaying for transferase activity are well known in the art (see, for example, Osborn and Yuan Tze-Yuen (1968) *J. Biol. Chem.* 243:5145-5152; Wright *et al.* (1967) *Proc. Natl. Acad. Sci. USA* 57:1798-1803). Bacterial sugar transferase proteins of the present invention include that in SEQ ID NO:174.

The Chain length determinant protein family (PFAM Accession PF02706) includes proteins involved in lipopolysaccharide (LSP) biosynthesis. Methods for measuring lipopolysaccharide biosynthesis are well known in the art (see, for example, Franco *et al.* (1998) *J. Bacteriol.* 180:2670-5). Chain length determinant proteins of the present invention include that in SEQ ID NO:180.

NlpC/P60 (PFAM Accession PF00877) is a family containing cell-wall peptidases, some members of which are known to hydrolyze D-gamma-glutamyl-meso-diaminopimelate or N-acetylmuramate-L-alanine linkages (Anantharaman and Aravind (2003) *Genome Biol.* 4:R11). NlpC/P60 proteins of the present invention include those in SEQ ID NOS:190, 194, and 196.

Ribonucleotide reductase (EC:1.17.4.1) provides the precursors necessary for DNA synthesis. This enzyme catalyzes the reductive synthesis of deoxyribonucleotides from their corresponding ribonucleotides: 2'-deoxyribonucleoside diphosphate + oxidized thioredoxin + H₂O = ribonucleoside diphosphate + reduced thioredoxin.

Ribonucleotide reductase is an oligomeric enzyme composed of a large subunit (700 to 1000 residues) and a small subunit (300 to 400 residues) - class II RNRs are less complex, using the small molecule B12 in place of the small chain. The small chain binds two iron atoms (three Glu, one Asp, and two His are involved in metal binding) and contains an active site tyrosine radical. The regions of the sequence that contain the metal-binding residues and the active site tyrosine are conserved in ribonucleotide reductase small chain from prokaryotes, eukaryotes and viruses. Assays for measuring ribonucleoside-diphosphate reductase activity are well known in the art (see, for example, Nilsson *et al.* (1988) *Biochem. Soc. Trans.* 16:91-94; Reichard (1993) *Science* 260:1773-1777). Ribonucleotide reductase proteins of the present invention include that in SEQ ID NO:208.

ABC transporters (PFAM Accession PF00005) form a large family of proteins responsible for translocation of a variety of compounds across biological membranes. They are minimally composed of four domains, with two transmembrane domains (TMDs) responsible for allocrite binding and transport and two nucleotide-binding domains (NBDs) responsible for coupling the energy of ATP hydrolysis to conformational changes in the TMDs. Both NBDs are capable of ATP hydrolysis, and inhibition of hydrolysis at one NBD effectively abrogates hydrolysis at the other. The proteins belonging to this family also contain one or two copies of the 'A' consensus sequence (Walker *et al.* (1982) *EMBO J.* 1:945-951) or the 'P-loop' (Saraste *et al.* (1990) *Trends Biochem Sci.* 15:430-434). Methods for measuring ATP-binding and transport are well known in the art (see, for example, Hung *et al.* (1998) *Nature* 396:703-707; Higgins *et al.* (1990) *J. Bioenerg. Biomembr.* 22:571-592). ABC transporters proteins of the present invention include those in SEQ ID NOS:218 and 226.

Members of the UDP-N-acetylglucosamine 2-epimerase family (PFAM Accession PF02350) consist of UDP-N-acetylglucosamine 2-epimerases (EC:5.1.3.14). This enzyme catalyzes the production of UDP-ManNAc from UDP-GlcNAc. Assays to measure UDP-N-acetylglucosamine 2-epimerase activity are well known in the art (see, for example, Stasche *et al.* (1997) *J. Biol. Chem.* 272:24319-24324). UDP-N-acetylglucosamine 2-epimerase proteins of the present invention include those in SEQ ID NOS:244 and 246.

The tRNA (Guanine-1)-methyltransferase (PFAM Accession PF01746) family consists of tRNA (Guanine-1)-methyltransferases (EC:2.1.1.31). In *E.coli K12* this enzyme catalyses the conversion of a guanosine residue to N1-methylguanine in position 37, next to the anticodon, in tRNA (Hjalmarsson *et al.* (1983) *J. Biol. Chem* 258:1343-1351. tRNA (guanine-N1-)-methyltransferase catalyses the reaction: S-adenosyl-L-methionine + tRNA -> S-adenosyl-L-homocysteine + tRNA containing N1-methylguanine. In the process, guanosine(G) is methylated to N1-methylguanine (1-methylguanosine (m1G)) at position 37 of tRNAs that read CUN (leucine), CCN (proline), and CGG (arginine) codons. The presence of m1G improves the cellular growth rate and the polypeptide step time and also prevents the tRNA from shifting the reading frame (Hagervall *et al.* (1990) *Biochim. Biophys. Acta.* 1050:263-266). Assays for measuring tRNA methyltransferase activity are well known in the art (see, for example, Hjalmarsson *et al.* (1983) *J. Biol. Chem.* 258:1343-1351). tRNA (Guanine-1)-methyltransferase proteins of the present invention include that in SEQ ID NO:294.

The aminoacyl-tRNA synthetases (EC:6.1.1) catalyse the attachment of an amino acid to its cognate transfer RNA molecule in a highly specific two-step reaction. The 20 aminoacyl-tRNA synthetases are divided into two classes, I and II (PFAM Accession PF00587). Class I aminoacyl-tRNA synthetases contain a characteristic Rossman fold and are mostly monomeric, while class II aminoacyl-tRNA synthetases share an anti-parallel-sheet formation, flanked by α -helices (Perona *et al.* (1993) *Biochemistry* 32:8758-8771), and are mostly dimeric or multimeric. In reactions catalysed by the class I aminoacyl-tRNA synthetases, the aminoacyl group is coupled to the 2'-hydroxyl of the tRNA, while, in class II reactions, the 3'-hydroxyl site is preferred. The synthetases specific for arginine, cysteine, glutamic acid, glutamine, isoleucine, leucine, methionine, tyrosine, tryptophan and valine belong to class I synthetases. The synthetases specific for alanine, asparagine, aspartic acid, glycine, histidine, lysine, phenylalanine, proline, serine, and threonine belong to class-II synthetases. Assays to measure aminoacyl-tRNA synthetases activity are well known in the art (see, for example, Augustine and Francklyn (1997) *Biochemistry* 36:3473-3482). Aminoacyl-tRNA synthetase proteins of the present invention include that in SEQ ID NO:296.

The LuxS protein family (LuxS) (PFAM Accession PF02664) consists of the LuxS protein involved in autoinducer AI2 synthesis and its hypothetical relatives. In bacteria, the regulation of gene expression in response to changes in cell density is called quorum sensing. Quorum-sensing bacteria produce, release, and respond to hormone-like molecules (autoinducers) that accumulate in the external environment as the cell population grows. The LuxS protein is involved in quorum sensing and is a autoinducer-production protein (Surette *et al.* (1999) *Proc. Natl. Acad. Sci. U.S.A.* 96:1639-1644). Methods to detect quorum sensing are well known in the art (see, for example, Surette *et al.* (1999) *Proc. Natl. Acad. Sci. U.S.A.* 96:1639-1644). LuxS proteins of the present invention include that in SEQ ID NO:304.

Methods of Use

In one embodiment, polypeptides of the present invention, as well as microbes expressing them may alter the immune system of a host, including alteration of the humoral, cellular, and nonspecific immune responses, both locally and systemically. Immune system alteration by probiotic bacteria may occur, for example, by augmentation of non-specific or antigen-specific defenses against infection and tumors, by increased mucosal immunity, by providing an adjuvant effect in an antigen-specific immune response, or by regulation of Th1/Th2 cells and their cytokine production (See, for example, U.S. Application No. 2002/0159976). By "adjuvant" is intended a substance that increases the immune response to an antigen when introduced together with the antigen.

Humoral immunity may be augmented by increased IgA production and stimulation of B lymphocyte production after consumption of probiotic bacteria. Methods used to study the mucosal immune system, including assays to measure the type and concentration of immunoglobulins and assays to assess the number and type of immune cells, are well known in the art (see, for example; Erickson and Hubbard (2000) *J. Nutr.* 130:403S-409S). Modification of non-specific immunity may result in altered production of cytokines such as IL-1 β , IL-6, IL-10, TNF α , IL-12, IFN- γ , and IL-18, and enhanced phagocytic activity; assays to detect the type and amount of cytokines released from cells after stimulation with probiotic bacteria, and other assays to measure non-

specific immunity are known in the art (see, for example, Miettinen *et al.* (1996) *Infect. Immun.* 64:5403-5405; Marin *et al.* (1998) *J. Food Prot.* 61:859-864; Schiffrin *et al.* (1994) *J. Dairy Sci.* 78:491-497). Alteration of cellular immunity may result in the increased production of macrophages, or altered cytokine production. Proteases from probiotic supplements can degrade the casein in cow milk, generating peptides that suppress lymphocyte proliferation (Sutas *et al.* (1996) *J. Allergy Clin. Immunol.* 98:216-224). Assays to measure the cellular immune response, such as lymphocyte proliferation assays, are well known in the art (see, for example, Erickson and Hubbard (2000) *J. Nutr.* 130:403S-409S; De Simone *et al.* (1993) *J. Immunother.* 9:23-28; Perdigon *et al.* (1986) *Infect. Immun.* 53:404-410).

Probiotic bacteria may also enhance the immune response to oral vaccines (see Chin *et al.* (2000) *Immunol. Cell Biol.* 78:55-66; Isolauri *et al.* (1995) *Vaccine* 13:310-312), have anti-inflammatory properties (Pessi *et al.* (1999) *Appl. Environ. Microbiol.* 65:475-478; Isolauri *et al.* (2001) *Am. J. Clin. Nutr.* 73:444S-450S; Antonopoulou *et al.* (1996) *J. Agric. Food Chem.* 44:3047-3051), and stabilize intestinal permeability to macromolecules (Heyman (2000) *J. Am. College Nutr.* 19:137S-146S; Isolauri *et al.* (1993) *Ped. Res.* 33:548-553). This effect on intestinal permeability may result from the maintenance or repair of tight junctions between the mucosal epithelial cells. Assays to measure these properties are known in the art, and examples can be found in the references cited.

In another embodiment, polypeptides of the present invention as well as microbes expressing them may alter the expression of various host proteins or compounds. These proteins and compounds include, but are not limited to, cell surface proteins (i.e. cell adhesion molecules), proteins involved in mucin production (i.e., MUC1 and MUC2), cell signaling proteins (i.e., tyrosine kinases, protein kinase C, mitogen-activated protein kinases, and nuclear factor kappa B (NF- κ B)), proteins involved in host tolerance of commensal bacteria, and antimicrobial proteins or compounds (i.e., hydrogen peroxide (Hawes *et al.* (1996) *J. Infect. Dis* 174:1058-1063) or nitric oxide (Korhonen *et al.* (2002) *Inflammation* 26:207-214)). By "cell surface" as it relates to an altered host protein is intended a protein found in association with a cell membrane. By "mucin" is intended a protein secreted by mucous glands or mucous cells. By "cell signaling protein" is

intended a protein involved in cell signaling. By "host tolerance" is intended the decrease in, or loss of, the ability of an animal to produce an immune response upon the administration of a particular antigen. By "commensal bacteria" is intended a bacterium that exists in close physical association with another organism, where neither organism
5 benefits nor is harmed as a result of the association. By "antimicrobial" is intended a compound that prevents the growth of or kills a microorganism.

Altered expression of cell adhesion molecules, or regions/domains/fragments thereof, may enable a microorganism to have modified adherence properties. Alternatively, proteins involved in mucin production may prevent the ability of
10 pathogenic organisms to attach to intestinal epithelial cells (Mack *et al.* (1999) *Am. J. Physiol.* 276:G941-G950). The composition, quality and quantity of mucin production could be affected, leading to altered pathogen-mucin interactions. Assays to measure altered expression of host proteins or compounds are well known in the art, and include Northern blots and Western blots. See, for example, Sambrook *et al.* (1989) *Molecular*
15 *Cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, Plainview, New York).

In yet another embodiment, the polypeptides and microorganisms expressing them may be useful for the treatment or prevention of gastrointestinal disorders, including, but not limited to, inflammatory bowel disease, Crohn's disease, ulcerative
20 colitis, irritable bowel syndrome, diarrhea, antibiotic associated diarrhea, constipation, and small bowel bacterial overgrowth. By "treatment or prevention" is intended a reduction in or prevention of any of the symptoms associated with a disease that occurs following administration of a polypeptide or microorganism of the present invention. This reduction includes any decrease in intensity or duration of symptoms in the subject
25 receiving therapy. As used herein, an "effective amount" of a polypeptide or microorganism of the present invention will be sufficient to prevent, reduce, or lessen the clinical symptoms of the disease being treated.

Probiotic bacteria may be effective in treating or preventing gastrointestinal disorders by acting as an immunomodulator, as mentioned above, by influencing the gut-
30 associated lymphoid tissue, or may attach to the epithelium forming a protective layer, preventing invasion by pathogenic bacteria (Kasper (1998) *Int. J. Food Micro.* 41:127-

131). Probiotic bacteria have been administered to patients with Crohn's disease, a chronic inflammatory bowel disease, with resultant immunological improvement (Malin *et al.* (1996) *Ann. Nutr. Metab.* 40:137-145). Positive effects have also been seen when treating constipation (Kasper (1998) *Int. J. Food Micro.* 41:127-131), enteric rotavirus-associated infection in children (Isolauro *et al.* (1991) *Pediatrics* 88:90-97; Boudraa *et al.* (1990) *Gastroenterol. Nutr.* 11:509-512), travelers' diarrhea (Hilton *et al.* (1997) *J. Travel Med.* 4:41-43), small bowel bacterial overgrowth (Vanderhoof *et al.* (1998) *J. Pediatr. Gastroenterol. Nutr.* 27:155-160), and antibiotic associated diarrhea (Biller *et al.* (1995) *J. Pediatr. Gastr. Nutr.* 21:224-226). Assays to determine the clinical effectiveness of using probiotic bacteria to treat or prevent a gastrointestinal disorder are known in the art (see, for example, Guandalini *et al.* (2000) *J. Pediatr. Gastroenterol. Nutr.* 30:54-60; Saavedra *et al.* (1994) *Lancet* 344:1046-1049).

In yet another embodiment, a polypeptide or a microorganism expressing a polypeptide of the current invention may prevent or reduce the occurrence of an infection in a host. By "reduce the occurrence of" is intended a reduction in the probability of a subject becoming infected with an organism and subsequently exhibiting symptoms of a disease caused by that organism. Infections that can be prevented or treated by probiotic bacteria include, but are not limited to, those caused by a food-borne pathogen (i.e., enterotoxigenic *Escherichia coli* (ETEC), *Salmonella typhimurium*, *Listeria monocytogenes*, and *Vibrio cholerae*) (see Boris *et al.* (1998) *Infect. Immun.* 66:1985-1989; Silva *et al.* (2001) *J. Med. Microbiol.* 50:161-164; Strus *et al.* (2001) *Med. Dosw. Mikrobiol.* 53:133-142; Tannock (1999) *Probiotics: a critical review*. Horizon Scientific Press, 161pp; Salminen, S, and von Wright, A. 1998. *Lactic acid bacteria: microbiology and functional aspects*. Marcel Dekker, Inc. NY. 617pp.), infections caused by an opportunistic pathogen, infections caused by *Helicobacter pylori* (Cremonini *et al.* (2001) *Dig. Dis.* 19:144-147; Lorca *et al.* (2001) *Current Micro.* 42:39-44), urogenital diseases such as vaginosis or vaginitis (Reid *et al.* (2001) *FEMS Immunol. Med. Micro.* 30:49-52), and HIV infection (Hashemi *et al.* (2000) *J. Infect. Dis.* 181:1574-1580). Methods to determine whether probiotic bacteria are effective at treating or preventing infections are well known in the art, and examples may be found in the above references.

In another embodiment, the polypeptides may enable a microorganism to bind and remove detrimental compounds in the gastrointestinal tract, including toxins, mutagens, bile salts, fats, cholesterol, and currently unidentified proteins or compounds. The compounds may also be inactivated, sequestered, degraded, digested, cleaved or
5 modified. The compounds may be produced by the host, for instance as a result of the digestion of a food product with mutagenic compounds (i.e., heterocyclic amines formed during the cooking of meat), or may be produced by microorganisms that are present in the gastrointestinal tract (i.e., microbial metabolites that possess genotoxic, mutagenic or carcinogenic activity). Bacterial enzymes such as NAD(P)H dehydrogenase
10 (azoreductase), nitroreductase, β -glucuronidase, β -glucosidase, and 7- α -dehydroxylase may increase the carcinogenic effect of toxic compounds. Bacteria such as *lactobacilli* have lower activities of these xenobiotic-metabolizing enzymes, and administration of some strains decreased the activity of nitroreductase and β -glucuronidase (Goldin and Gorbach (1984) *Am. J. Clin. Nutr.* 39:756-761; Goldin *et al.* (1992) *Dig. Dis. Sci.* 37:121-
15 128; Benno and Mitsuoka (1992) *Microbiol. Immunol.* 36:683-694; Bouhnik *et al.* (1996) *Eur. J. Clin. Nutr.* 50:269-273).

The polypeptides themselves may also possess these activities. Thus, the proteins of the invention or probiotic bacteria expressing them may find use in the treatment or prevention of cancer, particularly colon cancer. Anticarcinogenic effects of probiotic
20 bacteria have been noted (Wollowski *et al.* (2001) *Am. J. Clin. Nutr.* 73:451S-455S; Hayatsu and Hayatsu (1993) *Cancer Lett.* 73:173-179), and the physical binding of various mutagenic compounds to lactic acid bacteria has been shown (Orrhage *et al.* (1994) *Mutation Res.* 311:239-248). Assays to measure various anticarcinogenic effects of probiotic bacteria are well known in the art (see, for example, Wollowski *et al.* (2001)
25 *Am. J. Clin. Nutr.* 73:451S-455S; Goldin and Gorbach (1980) *J. Natl. Cancer Inst.* 64:263-265; Goldin and Gorbach (1984) *J. Natl. Cancer Inst.* 73:689-695).

In addition to cancer prevention, polypeptides of the invention or microorganisms expressing them may lower serum cholesterol levels and aid in the prevention of heart disease. Lactic acid bacteria can remove cholesterol from culture medium (Klaver and
30 van der Meer (1993) *Appl. Environ. Microbiol.* 59:1120-1124) and some studies have shown a decrease in serum cholesterol in humans after consumption of probiotic bacteria

(Lin *et al.* (1989) *J Dairy Res.* 72:2885-2899; Khedkar *et al.* (1993) *J. Dairy Foods Home Sci.* 12:33-38). Cholesterol levels may be lowered by probiotic bacteria through the deconjugation of bile acids, since cholesterol is converted to bile acids to replace those lost by excretion (Sanders (2000) *J. Nutr.* 130:384S-390S).

5 In another embodiment, a polypeptide of the present invention, or a variant thereof, may enhance the stability of a microorganism. This enhanced stability may enable a microorganism to survive passage through the stomach, small intestine and/or gastrointestinal tract, to resist acid and bile in those areas, or to persist in the gastrointestinal tract after ingestion by a host. Enhanced stability might also allow the
10 microorganism to withstand stressful conditions that occur during production and processing of a fermented product, including storage of the microorganism. These stresses include, but are not limited to, oxidative stress, pH, pressure, osmotic stress, dehydration, carbon starvation, phosphate starvation, nitrogen starvation, amino acid starvation, mechanical manipulation such as centrifugation, heat or cold shock,
15 mutagenic stress, and the stresses associated with various storage conditions, including cell culture, freezing, lyophilization, and drying (see Girgis *et al.* (2002) *Stress adaptations of lactic acid bacteria. In Microbial adaptation to stress and safety of new-generation foods.* Yousef, A.E. and Juneja, V.K. (Eds.) Technomic Publishing Co. Inc.). A polypeptide of the invention could provide protection against one or more stresses.
20 Assays to measure the stability of microorganisms are well known in the art (for example, Klaenhammer and Kleeman (1981) *Appl. Environ. Microbiol.* 41:1461-1467; Wright and Klaenhammer (1983) *J. Food Sci.* 48:773-777). Sequences that may be useful in enhancing stability include, but are not limited to, those set forth in SEQ ID NOS:60, 62, 286, 270, 294, 300, 302, 304 and 306.

25 In another embodiment, a polypeptide of the current invention, or a variant thereof, may enable a microorganism to have modified adherence properties. These adherence properties could allow the microorganism to bind with an increased or decreased ability to a specific cell type, such as an intestinal epithelial cell or to another bacterial cell, or to a compound, such as a mucin (see, for example, Ouwehand *et al.*
30 (2000) *Lett. Appl. Microbiol.* 30:10-13; Tuomola *et al.* (1999) *FEMS Immunol. Med. Microbiol.* 26:137-142). An increased ability to adhere to other bacterial cells may result

in aggregation. Assays to measure bacterial adhesion are well known in the art (see, for example, Jin *et al.* (2000) *Appl. Environ. Microbiol.* 66:4200-4204; Coconnier *et al.* (1992) *Appl. Environ. Microbiol.* 58:2034-2039; Greene and Klaenhammer (1994) *Appl. Environ. Microbiol.* 60:4487-4494; Lorca *et al.* (2002) *FEMS Microbiol Lett* 206:31-37;
5 Antikainen *et al.* (2002) *Mol. Microbiol.* 46:381-94).

In another embodiment, a polypeptide of the invention may enable a microorganism to reduce the occurrence of dental caries after oral administration to a subject. Methods to assess the ability of probiotic bacteria to reduce dental caries are known in the art (see, for example, Nase *et al.* (2001) *Caries Res.* 35:412-420).

10 In another embodiment, a polypeptide of the invention may enable a microorganism to increase feed conversion in a production animal. Methods of measuring increased feed conversion in a production animal are known in the art (see, for example, Fuller (1998) *Priobiotics for farm animals*. In: *Probiotics: A Critical Review* (Tannock, G.W., ed.). Horizon Scientific Press, Wymondham, UK.

15 In another embodiment, the polynucleotides and polypeptides of the invention may enable a microorganism to antagonize or kill another microorganism, including a pathogen. By "antagonizing" is intended an interaction between two biologically active substances, such that one partially or completely inhibits an activity of the other. The polypeptides may enable a microorganism expressing them to bind to another
20 microorganism, to have antimicrobial activity towards another microorganism, or to lyse another microorganism. Expression of the polypeptide may result in the first microorganism competing with the second microorganism for essential binding sites or essential nutrients, for example in the gastrointestinal tract of a host that has ingested the microorganism (see, for example, Jin *et al.* (2000) *Appl. Environ. Microbiol.* 66:4200-
25 4204). In different embodiments, isolated polypeptides themselves may antagonize or kill microorganisms, by the same mechanisms as mentioned above. Assays to measure antimicrobial activity, including the lysis or death of a microorganism are known in the art (see *Methods for General and Molecular Bacteriology*. 1994. Gerhardt, P., Murray, R.G.E., Wood, W.A. Krieg, N.R. (Eds.) American Society for Microbiology, 791 pp.).
30 Assays to measure bacterial adhesion are well known in the art (see, for example, Jin *et al.*, above). Assays to measure competition for binding sites or nutrients are known in the

art (see, for example, Edelman *et al.* (2003) *Vet. Microbiol.* 91:41-56; Gan *et al.* (2002) *J. Infect. Dis.* 185:1369-1372; Horie *et al.* (2002) *J. Appl. Microbiol.* 92:396-403).

In another embodiment, the polypeptides may have antimicrobial activity and provide use in various applications, including food protection and wound treatment, such as for a topical treatment. Methods for detecting antimicrobial activity in a protein are well known in the art (Allison and Klaenhammer (1999) Genetics of bacteriocins produced by lactic acid bacteria and their use in novel industrial applications. pp789-808. In *Manual of Industrial Microbiology and Biotechnology*. A.L. DeMain and J.E. Davies. (eds.) ASM Press, Washington, D.C.).

In another embodiment, the polypeptides of the invention may modulate the antibiotic sensitivity of a microorganism, or the polypeptides may modulate the sensitivity of a microorganism to other compounds with antimicrobial activity. Methods for detecting the antibiotic sensitivity of a microorganism or the sensitivity of a microorganism to a compound with antimicrobial activity are well known in the art.

In another embodiment, a polypeptide may enable a microorganism to aggregate or form a biofilm, or enable a first microorganism to interfere with a second microorganisms' ability to form a biofilm. The polypeptides themselves may also interfere with a microorganisms' ability to form a biofilm. By "biofilm" is intended a microbially derived sessile community characterized by cells that are irreversibly attached to a substratum or interface or to each other, are embedded in a matrix of extracellular polymeric substances that they have produced, and exhibit an altered phenotype with respect to growth rate and gene transcription. Assays to measure biofilm formation are well known in the art (see, for example, O'Toole and Kolter (1998) *Mol. Microbiol.* 28:449-461; Yoshida and Kuramitsu (2002) *Appl Environ Microbiol* 68:6283-6291).

In another embodiment, a sorting signal sufficient for cell wall anchoring isolated from a polypeptide of the present invention may be fused to a heterologous protein (Schneewind *et al.* (1993) *EMBO J.* 12:4803-4811; Schneewind *et al.* (1992) *Cell* 70:267-281). The LPXTG (SEQ ID NO:308) motif has been identified as characteristic of surface proteins in Gram-positive bacteria (Navarre and Schneewind (1994) *Molecular Microbiology* 14:115-121; Fischetti *et al.* (1990) *Mol. Microbiol.* 4:1603-1605). Assays

to measure expression of heterologous proteins on the surface of a cell are well known in the art (see, for example, Steidler *et al.* (1998) *Appl. Env. Micro.* 64:342-345).

- The polypeptides of the invention may modulate the texture or other physical properties of a food product produced using a lactic acid bacteria. Exopolysaccharides may act as stabilizers, thickeners, gelling agents, viscosifying agents, and emulsifiers in various food products (De Vuyst and Degeest (1999) *FEMS Microbiol. Rev.* 153-177). The increased viscosity of foods containing exopolysaccharides may be beneficial for probiotic bacterial colonization in the gastrointestinal tract (German *et al.* (1999) *Trends Biotechnol.* 17:491-499; Jolly *et al.* (2002) *Antonie van Leeuwenhoek* 82:367-374).
- Methods for measuring texture of a food product are known in the art (see, for example, van den Berg *et al.* (1995) *Appl. Envir. Microbiol.* 61:2840-2844).

Table 1.

SEQ ID NO:	IDENTITY/FUNCTION
1, 2	ABC-type metal ion transport system, periplasmic component/surface adhesin
3, 4	lemA protein
5, 6	FmtB surface protein
7, 8	67 kDa Myosin-crossreactive streptococcal antigen
9, 10	Myosin-crossreactive antigen
11, 12	Sortase
13, 14	Mucus binding protein precursor
15, 16	Mucus binding protein precursor
17, 18	Mucus binding protein precursor (Mub)
19, 20	Mucus binding protein precursor (Mub)
21, 22	Mucus binding protein precursor (Mub)
23, 24	Mucus binding protein precursor

SEQ ID NO:	IDENTITY/FUNCTION
25, 26	Mucus binding protein
27, 28	Mucus binding protein
29, 30	Mucus binding protein
31, 32	Mucus binding protein
33, 34	Mucus binding protein
35, 36	Mucus binding protein precursor
37, 38	Mucus binding protein precursor
39, 40	Steroid binding protein
41, 42	Surface exclusion protein
43, 44	Tropomyosin-like protein
45, 46	Biofilm-associated surface protein
47, 48	Aggregation promoting protein
49, 50	Aggregation promoting protein
51, 52	Fibrinogen-binding protein
53, 54	Fibrinogen-binding protein
55, 56	Fibrinogen-binding protein
57, 58	Fibronectin-binding protein
59, 60	Surface layer protein
61, 62	Surface layer protein
63, 64	Surface layer Protein
65, 66	Surface layer protein
67, 68	Surface layer protein

SEQ ID NO:	IDENTITY/FUNCTION
69, 70	Surface layer protein
71, 72	Surface layer protein
73, 74	Surface layer protein
75, 76	Surface protein
77, 78	Surface protein
79, 80	Surface protein
81, 82	Autolysin; amidase
83, 84	Cell shape-determining protein (MreB)
85, 86	Cell shape-determining protein (MreB)
87, 88	Cell shape-determining protein (MreC)
89, 90	Cell shape-determining protein (MreD)
91, 92	Rod shape-determining protein (RodA)
93, 94	UDP-N-acetylmuramate-alanine ligase
95, 96	UDP-N-acetylmuramyl tripeptide synthetase
97, 98	UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-lysine ligase
99, 100	UDP-N-acetylmuramoylalanine-D-glutamate ligase
101, 102	p-N-acetylmuramoyl-pentapeptide-transferase
103, 104	p-N-acetylmuramoyl-pentapeptide-transferase
105, 106	N-acetylmuramidase
107, 108	N-acetylmuramidase
109, 110	N-acetylmuramidase
111, 112	d-alanine-d-alanine ligase

SEQ ID NO:	IDENTITY/FUNCTION
113, 114	Permease
115, 116	d-ala-d-ala adding enzyme
117, 118	d-alanyl-d-alanine carboxypeptidase
119, 120	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
121, 122	UDP-N-acetylglucosamine pyrophosphorylase
123, 124	Undecaprenyl pyrophosphate synthetase
125, 126	Undecaprenyl-phosphate N-acetyl-glucosaminyltransferase
127, 128	Penicillin binding protein
129, 130	Penicillin binding protein
131, 132	Penicillin binding protein
133, 134	Penicillin binding protein
135, 136	Penicillin binding protein
137, 138	Penicillin binding protein 1A
139, 140	Penicillin binding protein-related factor A
141, 142	Penicillin binding protein
143, 144	Penicillin binding protein
145, 146	Penicillin binding protein 2B
147, 148	DltA D-alanine-D-alanyl carrier protein ligase
149, 150	DltB basic membrane protein
151, 152	DltC D-alanyl carrier protein
153, 154	DltD extramembranal transfer protein
155, 156	Oligosaccharide repeat unit transporter (EpsI)

SEQ ID NO:	IDENTITY/FUNCTION
157, 158	UDP-galactopyranose mutase
159, 160	UDP-galactopyranose mutase
161, 162	Polysaccharide polymerase
163, 164	Glycosyltransferase
165, 166	Cell surface, cell membrane or secreted protein
167, 168	Cell surface, cell membrane or secreted protein
169, 170	Glycosyltransferase
171, 172	Galactosyl transferase
173, 174	Phospho-glucosyltransferase (EpsE)
175, 176	EpsD
177, 178	EpsC
179, 180	EpsB
181, 182	EpsA
183, 184	GTP-binding protein
185, 186	Cell surface, cell membrane or secreted protein
187, 188	Cell surface protein
189, 190	Cell wall-associated hydrolase
191, 192	Cell surface, cell membrane or secreted protein
193, 194	Cell wall-associated hydrolase
195, 196	Glycosidase
197, 198	Guanylate kinase
199, 200	Cell surface, cell membrane or secreted protein

SEQ ID NO:	IDENTITY/FUNCTION
201, 202	Membrane protein
203, 204	Cell surface, cell membrane or secreted protein
205, 206	Ribonucleotide reductase (NrdI)
207, 208	Ribonucleotide reductase
209, 210	Cell surface, cell membrane or secreted protein
211, 212	Cell surface, cell membrane or secreted protein
213, 214	Cell surface, cell membrane or secreted protein
215, 216	ABC transporter component
217, 218	ABC transporter
219, 220	Cell surface, cell membrane or secreted protein
221, 222	Membrane protein
223, 224	Membrane protein
225, 226	ATPase component of ABC transporter
227, 228	Cell surface, cell membrane or secreted protein
229, 230	Acetyltransferase
231, 232	Transcriptional regulator
233, 234	Polysaccharide transporter
235, 236	EpsV
237, 238	EpsU
239, 240	EpsA
241, 242	Capsular polysaccharide biosynthesis protein J (capJ)
243, 244	Cap5P

SEQ ID NO:	IDENTITY/FUNCTION
245, 246	Cap5P
247, 248	CpsIVN
249, 250	Lipopolysaccharide biosynthesis protein
251, 252	Cellulose synthase
253, 254	Sucrose phosphorylase
255, 256	Polysaccharide transporter
257, 258	LPS biosynthesis protein
259, 260	Oligo-1,6-glucosidase
261, 262	Alpha-glucosidase
263, 264	Alpha-glucosidase
265, 266	Glucan 1,6-alpha-glucosidase
267, 268	Alpha-glucosidase II
269, 270	Dextran glucosidase
271, 272	1,4-alpha-glucan branching enzyme
273, 274	Neopullulanase
275, 276	Pullulanase
277, 278	Amylopullulanase
279, 280	Cyclomaltodextrin transport membrane protein
281, 282	Cell surface, cell membrane or secreted protein
283, 284	Cell surface protein
285, 286	Cell surface protein (bacterial cell division membrane protein)
287, 288	Membrane protein

SEQ ID NO:	IDENTITY/FUNCTION
289, 290	Membrane protein
291, 292	DNA methylase
293, 294	tRNA (guanine-N1)-methyltransferase
295, 296	Theronyl-tRNA synthetase
297, 298	Surface protein
299, 300	Transport accessory protein
301, 302	Methionine synthase
303,304	Autoinducer-2 production protein (LuxS)
305, 306	Cell division protein (cdpA)
307	Biofilm-associated surface protein

The following examples are offered by way of illustration and not by way of limitation.

5 Example 1. Gapped BlastP Results for Amino Acid Sequences

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:2 (306 amino acids) has about 73% identity from amino acids 7-304 with a protein from *Lactobacillus gasseri* that is a ABC-type metal ion transport system, periplasmic component/surface adhesin (Accession No. ZP_00046648.1), about 71% identity from
10 amino acids 9-304 with a protein from *Lactobacillus johnsonii* that is an ABC transporter solute-binding component (Accession No. NP_965678.1), about 62% identity from amino acids 18-306 with a protein from *Lactobacillus gasseri* that is an ABC-type metal ion transport system, periplasmic component/surface adhesin (Accession No. ZP_00046208.1), about 62% identity from amino acids 26-306 with a hypothetical
15 protein from *Lactobacillus johnsonii* (Accession No. NP_964756.1), and about 45% identity from amino acids 18-306 with a protein from *Leuconostoc mesenteroides* subsp.

mesenteroides that is an ABC-type metal ion transport system, periplasmic component/surface adhesin (Accession No. ZP_00064315.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:4 (191 amino acids) has about 75% identity from amino acids 29-191 with an uncharacterized conserved protein from *Lactobacillus gasseri* (Accession No. ZP_00047066.1), about 76% identity from amino acids 29-191 with a protein from *Lactobacillus johnsonii* that is a LemA-like protein (Accession No. NP_964093.1), about 68% identity from amino acids 29-191 with an unknown protein from *Lactobacillus plantarum* (Accession No. NP_784295.1), about 65% identity from amino acids 29-191 with a protein from *Streptococcus mutans* that is a LemA-like protein (Accession No. NP_722235.1), and about 61% identity from amino acids 29-191 with a protein from *Streptococcus pneumoniae* that is a lemA protein (Accession No. NP_345748.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:6 (2539 amino acids) has about 41% identity from amino acids 1-2501 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964984.1), about 27% identity from amino acids 797-2209 with a protein from *Abiotrophia defectiva* that is an extracellular matrix binding protein (Accession No. pir||T31110), about 20% identity from amino acids 4-2521 with a protein from *Staphylococcus epidermidis* that is a FmtB protein (Accession No. NP_764984.1), about 21% identity from amino acids 1-2529 with a protein from *Staphylococcus aureus* subsp. *aureus* that is homologous to a streptococcal adhesin emb (Accession No. NP_374548.1), and about 20% identity from amino acids 1-2529 with a hypothetical protein from *Staphylococcus aureus* subsp. *aureus* (Accession No. NP_371958.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:8 (591 amino acids) has about 84% identity from amino acids 1-591 with a protein from *Lactobacillus gasseri* that is a myosin-crossreactive antigen (Accession No. ZP_00047333.1), about 83% identity from amino acids 1-591 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964681.1), about 70% identity from amino acids 1-591 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is a myosin-crossreactive antigen (Accession No. ZP_00063735.1), about 67% identity from amino acids 1-591 with a protein from *Streptococcus pyogenes* that is a 67

kDa myosin-crossreactive streptococcal antigen (Accession No. NP_268761.1), and about 67% identity from amino acids 1-591 with a protein from *Streptococcus pyogenes* that is a 67 kDa myosin-crossreactive *streptococcal* antigen (Accession No. NP_664136.1).

- 5 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:10 (590 amino acids) has about 79% identity from amino acids 1-590 with a protein from *Lactobacillus gasseri* that is a myosin-crossreactive antigen (Accession No. ZP_00046024.1), about 71% identity from amino acids 1-590 with a protein from *Streptococcus mutans* that is homologous to a 67 kDa myosin-crossreactive streptococcal
- 10 antigen (Accession No. NP_721921.1), about 60% identity from amino acids 1-590 with a protein from *Staphylococcus aureus* subsp. *aureus* that is homologous to a 67 kDa myosin-crossreactive *streptococcal* antigen (Accession No. NP_644896.1), about 59% identity from amino acids 1-590 with a protein from *Staphylococcus aureus* subsp. *aureus* that is homologous to a 67 kDa myosin-crossreactive *streptococcal* antigen
- 15 (Accession No. NP_370630.1), and about 58% identity from amino acids 1-590 with a protein from *Staphylococcus epidermidis* that is a 67 kDa myosin-crossreactive *streptococcal* antigen-like protein (Accession No. NP_764331.1).

- A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:12 (229 amino acids) has about 61% identity from amino acids 1-229 with a hypothetical
- 20 protein from *Lactobacillus johnsonii* (Accession No. NP_965278.1), about 65% identity from amino acids 31-229 with a protein from *Lactobacillus gasseri* that is a sortase (surface protein transpeptidase) (Accession No. ZP_00046569.1), about 38% identity from amino acids 31-229 with a protein from *Enterococcus faecalis* that is a sortase family protein (Accession No. NP_816668.1), about 37% identity from amino acids 31-
- 25 210 with a protein from *Lactobacillus plantarum* that is a sortase (Accession No. NP_784294.1), and about 36% identity from amino acids 31-229 with a hypothetical protein from *Lactococcus lactis* subsp. *lactis* (Accession No. NP_267269.1).

- A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:14 (643 amino acids) has about 34% identity from amino acids 1-643 with a hypothetical
- 30 protein from *Lactobacillus gasseri* (Accession No. ZP_00046128.1), about 38% identity from amino acids 2-456 with a hypothetical protein from *Lactobacillus gasseri*

(Accession No. ZP_00046781.1), about 38% identity from amino acids 2-456 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964064.1), about 34% identity from amino acids 124-602 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046133.1), and about 33% identity from amino acids 11-428 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964062.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:16 (1017 amino acids) has about 27% identity from amino acids 299-865 with a protein from *Lactobacillus gasseri* that is a large exoprotein involved in heme utilization or adhesion (Accession No. ZP_00046780.1), about 22% identity from amino acids 273-848 with a protein from *Lactobacillus fermentum* that is an Mlp protein (Accession No. gb|AAP41738.1), about 23% identity from amino acids 420-862 with a protein from *Lactobacillus reuteri* that is a mucus binding protein precursor (Mub) (Accession No. gb|AAF25576.1), about 25% identity from amino acids 487-859 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964063.1), and about 25% identity from amino acids 537-865 with a protein from *Lactobacillus plantarum* that is a cell surface protein precursor (Accession No. NP_786417.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:18 (4326 amino acids) has about 29% identity from amino acids 2234-4165 with a protein from *Lactobacillus gasseri* that is a large exoprotein involved in heme utilization or adhesion (Accession No. ZP_00046780.1), about 23% identity from amino acids 650-3974 with a protein from *Lactobacillus reuteri* that is a mucus binding protein precursor (Mub) (Accession No. gb|AAF25576.1), about 24% identity from amino acids 1778-4164 with a protein from *Lactobacillus fermentum* that is an Mlp protein (Accession No. gb|AAP41738.1), about 27% identity from amino acids 1673-2994 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046645.1), and about 25% identity from amino acids 1388-2974 with a protein from *Lactobacillus plantarum* that is a cell surface protein precursor (Accession No. NP_785232.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:20 (1208 amino acids) has about 64% identity from amino acids 725-1060 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964063.1), about

29% identity from amino acids 7-999 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046645.1), about 29% identity from amino acids 159-999 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965681.1), about 35% identity from amino acids 456-1060 with a protein from *Lactobacillus fermentum* that is an Mlp protein (Accession No. gb|AAP41738.1), and about 35% identity from amino acids 504-1060 with a protein from *Lactobacillus gasseri* that is a large exoprotein involved in heme utilization or adhesion (Accession No. ZP_00046780.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:22 (1174 amino acids) has about 30% identity from amino acids 662-1000 with a protein from *Lactobacillus plantarum* that is a cell surface protein precursor (Accession No. NP_784891.1), about 30% identity from amino acids 641-985 with a hypothetical protein from *Lactococcus lactis* subsp. *lactis* (Accession No. NP_268337.1), about 30% identity from amino acids 658-1000 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046308.1), about 26% identity from amino acids 672-1000 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965614.1), and about 29% identity from amino acids 636-974 with a protein from *Lactobacillus reuteri* that is a mucus binding protein precursor (Mub) (Accession No. gb|AAF25576.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:24 (697 amino acids) has about 25% identity from amino acids 135-649 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046316.1), about 24% identity from amino acids 185-681 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965614.1), about 23% identity from amino acids 86-697 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046645.1), about 22% identity from amino acids 185-615 with a protein from *Lactobacillus reuteri* that is a mucus binding protein precursor (Mub) (Accession No. gb|AAF25576.1), and about 22% identity from amino acids 190-630 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046308.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:26 (2319 amino acids) has about 53% identity from amino acids 10-2010 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964063.1), about 40% identity

from amino acids 10-1552 with a protein from *Lactobacillus gasseri* that is a large exoprotein involved in heme utilization or adhesion (Accession No. ZP_00046780.1), about 49% identity from amino acids 1154-2119 with a protein from *Lactobacillus fermentum* that is an Mlp protein (Accession No. gb|AAP41738.1), about 33% identity
5 from amino acids 1263-2118 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965818.1), and about 31% identity from amino acids 1270-2112 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046645.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:28 (2650 amino acids) has about 36% identity from amino acids 1-2373 with a protein from
10 *Lactobacillus gasseri* that is a large exoprotein involved in heme utilization or adhesion (Accession No. ZP_00046780.1), about 40% identity from amino acids 310-2086 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964063.1), about 42% identity from amino acids 1702-2463 with a protein from *Lactobacillus fermentum* that is an Mlp protein (Accession No. gb|AAP41738.1), about 30% identity from amino
15 acids 1504-2513 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965818.1), and about 32% identity from amino acids 1987-2513 with a protein from *Bos taurus* that is a bovine homologue of human Hr44 (Accession No. emb|CAC16354.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:30 (346 amino acids) has about 33% identity from amino acids 2-204 with a hypothetical
20 protein from *Lactobacillus gasseri* (Accession No. ZP_00046067.1), about 34% identity from amino acids 56-231 with a protein from *Lactobacillus reuteri* that is a mucus binding protein precursor (Mub) (Accession No. gb|AAF25576.1), about 26% identity from amino acids 1-346 with a hypothetical protein from *Lactobacillus johnsonii*
25 (Accession No. NP_964510.1), about 24% identity from amino acids 2-344 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964406.1), and about 29% identity from amino acids 2-182 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046945.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:32 (294 amino acids) has about 34% identity from amino acids 6-294 with a hypothetical
30 protein from *Lactobacillus gasseri* (Accession No. ZP_00046131.1), about 29% identity

from amino acids 6-293 with a protein from *Lactobacillus gasseri* that is an RTX toxin and related Ca²⁺-binding protein (Accession No. ZP_00046947.1), about 29% identity from amino acids 6-293 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046945.1), about 30% identity from amino acids 6-284 with a
5 hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046130.1), and about 30% identity from amino acids 3-279 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964510.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:34 (185 amino acids) has about 42% identity from amino acids 3-179 with a hypothetical
10 protein from *Lactobacillus johnsonii* (Accession No. NP_964510.1), about 33% identity from amino acids 10-176 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046067.1), about 30% identity from amino acids 10-177 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046946.1), about 30% identity from amino acids 10-177 with a protein from *Lactobacillus gasseri* that is
15 an RTX toxin and related Ca²⁺-binding protein (Accession No. ZP_00046947.1), and about 30% identity from amino acids 12-177 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046945.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:36 (508 amino acids) has about 30% identity from amino acids 4-474 with a hypothetical
20 protein from *Lactobacillus gasseri* (Accession No. ZP_00046128.1), about 31% identity from amino acids 9-409 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046781.1), about 30% identity from amino acids 9-362 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964064.), about 29% identity from amino acids 13-399 with a hypothetical protein from *Lactobacillus*
25 *gasseri* (Accession No. ZP_00046779.1), and about 31% identity from amino acids 13-385 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964062.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:38 (339 amino acids) has about 31% identity from amino acids 79-286 with a protein from
30 *Lactobacillus plantarum* that is a cell surface protein precursor (Accession No. NP_784891.1), about 32% identity from amino acids 86-285 with a hypothetical protein

from *Lactobacillus johnsonii* (Accession No. NP_965614.1), about 34% identity from amino acids 112-284 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046316.1), about 42% identity from amino acids 178-293 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046308.1), and about 29%
5 identity from amino acids 79-282 with a protein from *Lactobacillus fermentum* that is an Mlp protein (Accession No. gb|AAP41738.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:40 (76 amino acids) has about 47% identity from amino acids 4-75 with a protein from *Lactobacillus plantarum* (Accession No. NP_786269.1), about 43% identity from amino
10 acids 2-73 with a protein from *Clostridium acetobutylicum* that is a HypQ3 protein (Accession No. gb|AAK11585.1), about 43% identity from amino acids 2-73 with a protein from *Clostridium acetobutylicum* that is homologous to a steroid binding protein (Accession No. NP_149307.1), about 44% identity from amino acids 1-73 with a conserved hypothetical protein from *Methanosarcina acetivorans* (Accession No.
15 NP_618599.1), and about 42% identity from amino acids 1-73 with a hypothetical protein from *Clostridium perfringens* (Accession No. NP_563415.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:42 (355 amino acids) has about 26% identity from amino acids 99-340 with a protein from *Streptococcus pyogenes* that is homologous to a surface exclusion protein (Accession
20 Nos. NP_606538.1; NC_003485), about 26% identity from amino acids 99-340 with a protein from *Streptococcus pyogenes* that is homologous to a surface exclusion protein (Accession No. NP_664001.1), about 26% identity from amino acids 99-340 with a protein from *Streptococcus pyogenes* that is homologous to a surface exclusion protein (Accession Nos. NP_268623.1; NC_002737), about 23% identity from amino acids 116-
25 319 with a protein from *Enterococcus faecalis* that is a surface exclusion protein (seal) precursor (Accession No. pir|S22452), and about 23% identity from amino acids 116-319 with a protein from *Enterococcus faecalis* that is a surface exclusion protein (Seal) (Accession No. NP_816976.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:44
30 (111 amino acids) has about 27% identity from amino acids 1-107 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965479.1), about 27% identity

from amino acids 1-102 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046710.1), about 26% identity from amino acids 31-108 with a protein from *Salmo trutta* that is a cardiac tropomyosin (Accession No. emb|CAA91434.1), about 31% identity from amino acids 31-94 with a hypothetical
5 protein from *Homo sapiens* (Accession No. NP_653299.2), and about 25% identity from amino acids 33-108 with a protein from *Mus musculus* that is a testis-expressed gene 9 (Accession Nos. NP_033385.1; NM_009359).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:46 (66 amino acids) has about 58% identity from amino acids 15-62 with a hypothetical protein
10 from *Lactobacillus gasseri* (Accession No. ZP_00046645.1), about 58% identity from amino acids 12-60 with a protein from *Lactobacillus gasseri* that is a type V secretory pathway adhesin (AidA) (Accession No. ZP_00046948.1), about 61% identity from amino acids 15-53 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964984.1), about 58% identity from amino acids 16-54 with a hypothetical
15 protein from *Lactobacillus gasseri* (Accession No. ZP_00046307.1), and about 63% identity from amino acids 15-52 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965682.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:48 (231 amino acids) has about 44% identity from amino acids 66-231 with a protein from
20 *Lactobacillus gasseri* that is an Apf1 protein (Accession No. gb|AAO86515.1), about 44% identity from amino acids 66-231 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00047488.1), about 44% identity from amino acids 66-231 with a protein from *Lactobacillus johnsonii* that is an aggregation promoting factor (Accession No. gb|AAN78451.1), about 40% identity from amino acids 66-231 with a
25 protein from *Lactobacillus johnsonii* that is a surface protein, aggregation promoting factor (Accession No. NP_965551.1), and about 40% identity from amino acids 66-231 with a protein from *Lactobacillus johnsonii* that is a surface protein (Apf1) (Accession No. gb|AAN63951.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:50
30 (120 amino acids) has about 61% identity from amino acids 26-120 with a protein from *Lactobacillus plantarum* that is an extracellular protein (Accession No. NP_786365.1),

about 54% identity from amino acids 14-120 with a protein from *Lactobacillus plantarum* that is an extracellular protein (Accession No. NP_786209.1), about 52% identity from amino acids 24-120 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00047488.1), about 54% identity from amino acids 24-120 with a
 5 protein from *Lactobacillus johnsonii* that is an aggregation promoting factor (Accession No. gb|AAN78450.1), and about 55% identity from amino acids 26-120 with a protein from *Lactobacillus johnsonii* that is an aggregation promoting factor (Accession No. gb|AAN64914.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:52
 10 (264 amino acids) has about 27% identity from amino acids 1-94 with a protein from *Staphylococcus aureus* subsp. *aureus* that is a ser-asp rich fibrinogen-binding, bone sialoprotein-binding protein (Accession No. NP_373774.1), about 27% identity from amino acids 1-94 with a protein from *Staphylococcus aureus* subsp. *aureus* that is a ser-asp rich fibrinogen-binding, bone sialoprotein-binding protein (Accession No.
 15 NP_371087.1), and about 27% identity from amino acids 1-94 with a protein from *Staphylococcus aureus* that is homologous to a fibrinogen-binding protein (Accession No. pir|T28680).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:54
 (991 amino acids) has about 24% identity from amino acids 97-477 with a hypothetical
 20 protein from *Plasmodium falciparum* (Accession No. NP_701725.1), about 22% identity from amino acids 270-510 with a hypothetical protein from *Dictyostelium discoideum* (Accession No. gb|AAO51593.1), about 23% identity from amino acids 47-452 with a protein from *Plasmodium falciparum* that is a starp antigen (Accession No. NP_703988.1), about 19% identity from amino acids 13-401 with a hypothetical protein
 25 from *Plasmodium falciparum* (Accession No. NP_704588.1), and about 23% identity from amino acids 44-403 with a protein from *Fusobacterium nucleatum* subsp. *nucleatum* that is a hemolysin (Accession No. NP_602617.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:56
 (906 amino acids) has about 70% identity from amino acids 1-888 with a hypothetical
 30 protein from *Lactobacillus johnsonii* (Accession No. NP_964984.1), about 24% identity from amino acids 1-760 with a protein from *Lactobacillus gasseri* that is a large

exoprotein involved in heme utilization or adhesion (Accession No. ZP_00046780.1), about 23% identity from amino acids 1-645 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964063.1), about 29% identity from amino acids 1-248 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046645.1), and about 17% identity from amino acids 27-869 with a protein from *Staphylococcus epidermidis* that is a streptococcal hemagglutinin protein (Accession No. NP_765804.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:58 (566 amino acids) has about 69% identity from amino acids 4-564 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965038.1), about 66% identity from amino acids 4-564 with a protein from *Lactobacillus gasseri* that is a predicted RNA-binding protein homologous to a eukaryotic snRNP (Accession No. ZP_00045959.1), about 41% identity from amino acids 4-566 with a protein from *Enterococcus faecium* that is a predicted RNA-binding protein homologous to a eukaryotic snRNP (Accession No. ZP_00037499.1), about 41% identity from amino acids 4-566 with a protein from *Enterococcus faecalis* that is homologous to a fibronectin/fibrinogen-binding protein (Accession No. NP_814975.1), and about 41% identity from amino acids 4-557 with a protein from *Lactobacillus plantarum* that is an adherence protein (Accession No. NP_785358.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:60 (444 amino acids) has about 90% identity from amino acids 49-444 with a protein from *Lactobacillus acidophilus* that is an S-layer protein precursor (Accession No. sp|P35829|SLAP_LACAC), about 67% identity from amino acids 49-443 with a protein from *Lactobacillus helveticus* that is a surface layer protein (Accession No. emb|CAA62606.1), about 67% identity from amino acids 49-443 with a protein from *Lactobacillus helveticus* that is a surface layer protein (Accession Nos. emb|CAB46984.1; AJ388558), 66% identity from amino acids 49-443 with a protein from *Lactobacillus helveticus* that is a surface layer protein (Accession No. emb|CAB46985.1), and 66% identity from amino acids 49-443 with a protein from *Lactobacillus helveticus* that is a surface layer protein (Accession No. emb|CAB46986.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:62 (457 amino acids) has about 88% identity from amino acids 1-457 with a protein from *Lactobacillus acidophilus* that is an SB-protein (Accession Nos. CAA61561.1; X89376), about 51% identity from amino acids 1-457 with a protein from *Lactobacillus acidophilus* that is an s-layer protein precursor (Accession No. sp|P35829|SLAP_LACAC), about 44% identity from amino acids 1-456 with a protein from *Lactobacillus helveticus* that is a surface layer protein (Accession Nos. emb|CAB46985.1; AJ388559), about 44% identity from amino acids 1-456 with a protein from *Lactobacillus helveticus* that is a surface layer protein (Accession No. emb|CAA62606.1), and about 44% identity from amino acids 1-456 with a protein from *Lactobacillus helveticus* that is a surface layer protein (Accession No. emb|CAA63409.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:64 (567 amino acids) has about 35% identity from amino acids 163-311 with a protein from *Lactobacillus crispatus* that is a surface layer protein (Accession Nos. gb|AAB58734.1; AF001313), about 37% identity from amino acids 182-311 with a protein from *Lactobacillus acidophilus* that is an SB-protein (Accession Nos. emb|CAA61561.1; X89376), about 34% identity from amino acids 163-304 with a protein from *Lactobacillus helveticus* that is a proteinase (Accession Nos. dbj|BAB72065.1; AB061775), about 25% identity from amino acids 27-311 with a protein from *Lactobacillus acidophilus* that is a surface layer protein precursor (Accession No. sp|P35829|SLAP_LACAC), and about 34% identity from amino acids 44-104 with a protein from *Homo sapiens* that is a myomesin 1 (Accession Nos. NP_003794.1; NM_003803).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:66 (177 amino acids) has about 28% identity from amino acids 13-170 with a protein from *Lactobacillus crispatus* that is a surface layer protein (Accession No. gb|AAB58734.1), about 26% identity from amino acids 9-170 with a protein from *Lactobacillus crispatus* that is homologous to a silent surface layer protein (Accession No. gb|AAF68972.1), about 26% identity from amino acids 42-162 with a protein from *Clostridium acetobutylicum* that is homologous to an enterotoxin (Accession No. NP_347713.1),

about 26% identity from amino acids 62-166 with a protein from *Lactobacillus gasseri* that is a glycerophosphoryl diester phosphodiesterase (Accession No. ZP_00046260.1), and about 25% identity from amino acids 40-162 with a protein from *Chromobacterium violaceum* that is homologous to an rhs-related protein (Accession No. NP_900908.1).

5 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:68 (173 amino acids) has about 32% identity from amino acids 68-135 with a protein from *Lama glama* that is an immunoglobulin heavy chain variable region (Accession No. emb|CAD22470.1), about 33% identity from amino acids 107-171 with a protein from *Rattus norvegicus* that is homologous to an olfactory receptor-like protein F3 (Accession
10 No. XP_216832.2), about 27% identity from amino acids 71-165 with a protein from *Arabidopsis thaliana* (Accession No. NP_191860.1), about 29% identity from amino acids 71-160 with an environmental sequence (Accession No. gb|EAD49084.1), and about 26% identity from amino acids 80-157 with a protein from *Dictyostelium discoideum* (Accession No. gb|AAO51562.1).

15 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:70 (292 amino acids) has about 66% identity from amino acids 2-292 with a protein from *Lactobacillus acidophilus* that is a surface layer protein (Accession Nos. gb|AAF65561.1; AF250229), about 28% identity from amino acids 8-291 with a protein from
20 *Lactobacillus acidophilus* that is an S-layer protein precursor (Accession Nos. sp|P35829; SLAP_LACAC), about 42% identity from amino acids 178-291 with a protein from *Lactobacillus acidophilus* that is an SB-protein (Accession Nos. emb|CAA61561.1; X89376), about 37% identity from amino acids 137-291 with a protein from *Lactobacillus crispatus* that is a surface layer protein (Accession Nos. gb|AAB58734.1; AF001313), and about 32% identity from amino acids 90-291 with a protein from
25 *Lactobacillus crispatus* that is homologous to a silent surface layer protein (Accession Nos. gb|AAF68972.1; AF253044).

 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:72 (216 amino acids) has about 27% identity from amino acids 35-128 with a protein from *Lactobacillus crispatus* that is a surface layer protein (Accession Nos. gb|AAB58734.1;
30 AF001313), about 27% identity from amino acids 35-128 with a protein from *Lactobacillus crispatus* that is a silent surface layer protein (Accession No.

dbj|BAC76687.1), about 28% identity from amino acids 35-128 with a protein from *Lactobacillus crispatus* that is homologous to a silent surface layer protein (Accession No. gb|AAF68972.1), about 31% identity from amino acids 41-126 with an environmental sequence (Accession No. gb|EAG77017.1), and about 28% identity from amino acids 45-169 with an environmental sequence (Accession No. gb|EAC33545.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:74 (359 amino acids) has about 27% identity from amino acids 34-228 with a hypothetical protein from *Cytophaga hutchinsonii* (Accession No. ZP_00118765.1), about 28% identity from amino acids 3-160 with a protein from *Lactobacillus crispatus* that is a silent surface layer protein (Accession No. dbj|BAC76687.1), about 26% identity from amino acids 98-256 with a protein from *Lactobacillus delbrueckii* subsp. *bulgaricus* that is a lactocepin (EC 3.4.21.96) precursor (Accession No. pir|JC6032), about 27% identity from amino acids 4-160 with a protein from *Lactobacillus crispatus* that is a surface layer protein (Accession No. gb|AAB58734.1), and about 28% identity from amino acids 3-160 with a protein from *Lactobacillus crispatus* that is homologous to a silent surface layer protein (Accession No. gb|AAF68972.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:76 (1676 amino acids) has about 42% identity from amino acids 926-1528 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965634.1), about 40% identity from amino acids 839-1528 with a protein from *Streptococcus pyogenes* that is a surface protein R28 (Accession Nos. gb|AAD39085.1; AF091393), about 39% identity from amino acids 839-1528 with a protein from *Streptococcus agalactiae* that is a surface protein Rib (Accession No. NP_687467.1), about 39% identity from amino acids 839-1528 with a protein from *Streptococcus agalactiae* that is a rib protein (Accession No. pir|T28681), and about 33% identity from amino acids 752-1528 with a protein from *Enterococcus faecium* that is homologous to a surface protein precursor (Accession No. emb|CAD32315.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:78 (1924 amino acids) has about 44% identity from amino acids 921-1796 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965634.1), about 29% identity from amino acids 807-1923 with a protein from *Streptococcus pyogenes*

that is a surface protein R28 (Accession No. gb|AAD39085.1), about 30% identity from amino acids 807-1923 with a protein from *Streptococcus agalactiae* that is a surface protein Rib (Accession No. NP_687467.1), about 30% identity from amino acids 807-1923 with a protein from *Streptococcus agalactiae* that is a rib protein (Accession No. pir|T28681), and about 31% identity from amino acids 984-1812 with a protein from *Lactobacillus fermentum* that is an Rlp protein (Accession No. gb|AAP41737.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:80 (353 amino acids) has about 22% identity from amino acids 128-344 with a protein from *Haemophilus somnus* that is a large exoprotein involved in heme utilization or adhesion (Accession No. ZP_00133279.1), about 22% identity from amino acids 128-344 with a protein from *Haemophilus somnus* that is a large exoprotein involved in heme utilization or adhesion (Accession No. ZP_00133280.1), about 26% identity from amino acids 137-278 with an environmental sequence (Accession No. gb|EAC64082.1), and about 27% identity from amino acids 84-250 with an environmental sequence (Accession No. gb|EAJ12295.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:82 (364 amino acids) has about 46% identity from amino acids 33-222 with a protein from *Listeria innocua* that is an autolysin, amidase (Accession No. NP_472032.1), about 45% identity from amino acids 49-237 with a protein from *Listeria monocytogenes* that is an autolysin, amidase (Accession No. gb|AAC46384.1), about 45% identity from amino acids 49-237 with a protein from *Listeria monocytogenes* that is an autolysin, amidase (Accession No. NP_466081.1), about 45% identity from amino acids 49-237 with a protein from *Listeria monocytogenes* that is an AMI protein (Accession No. gb|AAC45605.1), and about 39% identity from amino acids 49-299 with a protein from *Listeria monocytogenes* that is an Ami 4b protein (Accession No. emb|CAC20640.1; AJ276390).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:84 (334 amino acids) has about 87% identity from amino acids 1-333 with a protein from *Lactobacillus johnsonii* that is a rod shape-determining protein (MreB) (Accession No. NP_964817.1), about 86% identity from amino acids 23-333 with a protein from *Lactobacillus gasseri* that is an actin-like ATPase involved in cell morphogenesis

(Accession No. ZP_00047434.1), about 75% identity from amino acids 1-331 with a protein from *Lactobacillus plantarum* that is a cell shape determining protein (MreB) (Accession No. NP_785793.1), about 66% identity from amino acids 2-331 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is an actin-like ATPase involved in cell morphogenesis (Accession No. ZP_00063690.1), and about 66% identity from amino acids 1-333 with a protein from *Listeria innocua* that is homologous to a cell-shape determining protein (MreB) (Accession No. NP_470919.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:86 (329 amino acids) has about 86% identity from amino acids 1-329 with a protein from *Lactobacillus johnsonii* that is an mreB-like protein (Accession No. NP_964798.1), about 86% identity from amino acids 1-329 with a protein from *Lactobacillus gasseri* that is an actin-like ATPase involved in cell morphogenesis (Accession No. ZP_00046248.1), about 65% identity from amino acids 1-325 with a protein from *Lactobacillus plantarum* that is a cell shape determining protein (MreB) (Accession No. NP_785826.1), about 65% identity from amino acids 1-328 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is an actin-like ATPase involved in cell morphogenesis (Accession No. ZP_00063606.1), and about 64% identity from amino acids 2-328 with a protein from *Bacillus anthracis* that is an mbl protein (Accession No. NP_847679.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:88 (283 amino acids) has about 64% identity from amino acids 1-281 with a protein from *Lactobacillus gasseri* that is a cell shape-determining protein (Accession No. ZP_00047435.1), about 63% identity from amino acids 1-281 with a protein from *Lactobacillus johnsonii* that is a rod shape-determining protein (MreC) (Accession No. NP_964818.1), about 42% identity from amino acids 1-279 with a protein from *Lactobacillus plantarum* that is a cell-shape determining protein (MreC) (Accession No. NP_785792.1), about 38% identity from amino acids 1-279 with a protein from *Enterococcus faecium* that is a cell shape-determining protein (Accession No. ZP_00037396.1), and about 41% identity from amino acids 33-281 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is a cell shape determining protein (Accession No. ZP_00063689.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:90 (179 amino acids) has about 42% identity from amino acids 1-171 with a protein from *Lactobacillus johnsonii* that is a rod-shape determining protein (MreD) (Accession No. NP_964819.1), about 39% identity from amino acids 15-171 with a protein from
5 *Lactobacillus gasseri* that is a cell shape determining protein (Accession No. ZP_00047436.1), about 26% identity from amino acids 6-159 with a protein from *Lactobacillus plantarum* that is a cell shape determining protein (MreD) (Accession No. NP_785791.1), about 28% identity from amino acids 3-122 with a protein from *Oceanobacillus iheyensis* that is a cell-shape determining protein (Accession No.
10 NP_692972.1), and about 29% identity from amino acids 11-132 with a protein from *Lactococcus lactis* subsp. *lactis* that is a cell shape determining protein (Accession No. NP_268387.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:92 (397 amino acids) has about 61% identity from amino acids 1-397 with a hypothetical
15 protein from *Lactobacillus johnsonii* (Accession No. NP_964801.1), about 60% identity from amino acids 1-397 with a protein from *Lactobacillus gasseri* that is a cell division membrane protein (Accession No. ZP_00046251.1), about 50% identity from amino acids 13-392 with a protein from *Lactobacillus plantarum* that is a rod shape-determining protein (Accession No. NP_785823.1), about 41% identity from amino acids 5-384 with
20 a protein from *Enterococcus faecalis* that is a cell division protein in the FtsW/RodA/SpoVE family (Accession Nos. NP_816148.1), and about 41% identity from amino acids 16-368 with a protein from *Lactobacillus plantarum* that is a rod-shape determining protein (Accession No. NP_785596.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:94
25 (437 amino acids) has about 91% identity from amino acids 1-437 with a protein from *Lactobacillus gasseri* that is a UDP-N-acetylmuramate-alanine ligase (Accession No. ZP_00046723.1), about 91% identity from amino acids 1-437 with a protein from *Lactobacillus johnsonii* that is a UDP-N-acetyl muramate-alanine ligase (Accession No. NP_965470.1), about 56% identity from amino acids 2-434 with a protein from
30 *Lactobacillus plantarum* that is a UDP-N-acetylmuramate-alanine ligase (Accession No. NP_785073.1), about 56% identity from amino acids 5-437 with a protein from

Leuconostoc mesenteroides subsp. *mesenteroides* that is a UDP-N-acetylmuramate-alanine ligase (Accession No. ZP_00064100.1), and about 51% identity from amino acids 4-437 with a protein from *Enterococcus faecalis* that is a UDP-N-acetylmuramate-alanine ligase (Accession No. NP_815590.1).

5 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:96 (452 amino acids) has about 87% identity from amino acids 3-452 with a protein from *Lactobacillus gasseri* that is a UDP-N-acetylmuramyl tripeptide synthase (Accession No. ZP_00046234.1), about 86% identity from amino acids 3-452 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964783.1), about 55% identity from
10 amino acids 3-452 with a protein from *Lactobacillus plantarum* that is homologous to a UDP-N-acetylmuramyl tripeptide synthase (Accession No. NP_785844.1), about 50% identity from amino acids 3-452 with a protein from *Enterococcus faecalis* that is a mur ligase family protein (Accession No. NP_816226.1), and about 51% identity from amino acids 3-451 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is
15 a UDP-N-acetylmuramyl tripeptide synthase (Accession No. ZP_00063654.1).

 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:98 (532 amino acids) has about 83% identity from amino acids 11-528 with a protein from *Lactobacillus johnsonii* that is a UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-lysine ligase (Accession No. NP_965690.1), about 83% identity from amino acids 11-528 with
20 a protein from *Lactobacillus gasseri* that is a UDP-N-acetylmuramyl tripeptide synthase (Accession No. ZP_00046637.1), about 44% identity from amino acids 10-524 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is a UDP-N-acetylmuramyl tripeptide synthase (Accession No. ZP_00062837.1), about 43% identity from amino acids 24-522 with a protein from *Enterococcus faecium* that is a UDP-N-
25 acetylmuramyl tripeptide synthase (Accession No. ZP_00036035.1), and about 42% identity from amino acids 10-522 with a protein from *Enterococcus faecalis* that is homologous to a UDP-N-acetylmuramoylalanine-D-glutamate-2,6-diaminopimelate ligase (Accession No. NP_814420.1).

 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:100
30 (459 amino acids) has about 78% identity from amino acids 1-459 with a protein from *Lactobacillus johnsonii* that is a UDP-N-acetylmuramoylalanine-D-glutamate ligase

(Accession No. NP_964826.1), about 80% identity from amino acids 89-459 with a protein from *Lactobacillus gasseri* that is a UDP-N-acetylmuramoylalanine-D-glutamate ligase (Accession No. ZP_00046265.1), about 49% identity from amino acids 1-456 with a protein from *Bacillus anthracis* that is a UDP-N-acetylmuramoylalanine-D-glutamate
 5 ligase (Accession No. NP_846291.1), about 49% identity from amino acids 1-456 with a protein from *Bacillus cereus* that is a UDP-N-acetylmuramoylalanine-D-glutamate ligase (Accession No. NP_980253.1), and about 49% identity from amino acids 1-456 with a protein from *Bacillus cereus* that is a UDP-N-acetylmuramoylalanine-D-glutamate ligase (Accession No. NP_833632.1).

10 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:102 (368 amino acids) has about 79% identity from amino acids 1-364 with a protein from *Lactobacillus gasseri* that is a UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase (Accession No. ZP_00046266.1), about 78% identity from amino acids 1-366 with a protein from *Lactobacillus johnsonii* that is a UDP-N-acetylglucosamine-N-
 15 acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (Accession No. NP_964827.1), about 49% identity from amino acids 1-366 with a protein from *Lactobacillus plantarum* that is a UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (Accession No. NP_785692.1), about 46% identity from amino acids 1-368
 20 with a protein from *Bacillus halodurans* that is a UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophos (Accession No. NP_243431.1), and about 47% identity from amino acids 1-366 with a protein from *Enterococcus hirae* that is a UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (Accession No. sp|O07670|MURG_ENTHR).

25 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:104 (322 amino acids) has about 67% identity from amino acids 4-322 with a protein from *Lactobacillus gasseri* that is a UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase (Accession No. ZP_00047442.1), about 67% identity from amino acids 4-322 with a protein from
 30 *Lactobacillus johnsonii* that is a phospho-N-acetylmuramoyl-pentapeptide-transferase (Accession No. NP_964825.1), about 49% identity from amino acids 11-319 with a

protein from *Lactobacillus plantarum* that is a phospho-N-acetylmuramoyl-pentapeptide-transferase (Accession No. NP_785694.1), about 47% identity from amino acids 9-320 with a protein from *Enterococcus faecium* that is a UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase (Accession No. ZP_00037828.1), and about 47% identity from amino acids 9-320 with a protein from *Enterococcus faecalis* that is a phospho-N-acetylmuramoyl-pentapeptide-transferase (Accession No. NP_814728.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:106 (215 amino acids) has about 54% identity from amino acids 15-214 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965527.1), about 54% identity from amino acids 15-214 with a protein from *Lactobacillus gasseri* that is a muramidase (flagellum-specific) (Accession No. ZP_00046365.1), about 42% identity from amino acids 1-215 with a protein from *Listeria monocytogenes* that is homologous to an N-acetylmuramoyl-L-alanine amidase (autolysin) (Accession No. NP_464740.1), about 42% identity from amino acids 1-215 with a protein from *Listeria innocua* that is homologous to an N-acetylmuramoyl-L-alanine amidase (autolysin) (Accession Nos. NP_470515.1; NC_003212), and about 53% identity from amino acids 71-215 with a protein from *Lactococcus lactis* subsp. *lactis* that is an N-acetylmuramidase (Accession No. NP_267521.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:108 (409 amino acids) has about 43% identity from amino acids 1-262 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964171.1), about 39% identity from amino acids 26-257 with a protein from *Listeria monocytogenes* that is homologous to an autolysin (EC 3.5.1.28) (N-acetylmuramoyl-L-alanine amidase) (Accession No. NP_464601.1), about 38% identity from amino acids 16-236 with a protein from *Listeria innocua* that is homologous to an autolysin, N-acetylmuramidase (Accession No. NP_472166.1), about 34% identity from amino acids 16-274 with a protein from *Listeria monocytogenes* that is homologous to an autolysin, N-acetylmuramidase (Accession No. NP_466213.1), and about 39% identity from amino acids 40-222 with a protein from *Enterococcus faecium* that is homologous to a glycosidase (GlyA) (Accession No. gb|AAK72496.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:110 (153 amino acids) has about 47% identity from amino acids 105-152 with a protein from *Oenococcus oeni* that is a muramidase (flagellum-specific) (Accession No. ZP_00069384.1), about 53% identity from amino acids 108-150 with a protein from *Bacillus subtilis* that is an N-acetylmuramoyl-L-alanine amidase (Accession Nos. NP_389164.1; NC_000964), about 48% identity from amino acids 104-150 with a hypothetical protein from *Chloroflexus aurantiacus* (Accession No. ZP_00019741.1), about 54% identity from amino acids 107-152 with a protein from *Deinococcus radiodurans* that is homologous to a cell wall protein (Accession No. NP_294634.1), and about 47% identity from amino acids 109-152 with a protein from *Lactococcus lactis* subsp. *lactis* that is an N-acetylmuramidase (Accession No. NP_266697.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:112 (360 amino acids) has about 71% identity from amino acids 1-360 with a protein from *Lactobacillus gasseri* that is a D-alanine-D-alanine ligase and related ATP-grasp enzyme (Accession No. ZP_00047036.1), about 71% identity from amino acids 1-360 with a protein from *Lactobacillus johnsonii* that is a D-alanine-D-alanine ligase (Accession No. NP_964124.1), about 41% identity from amino acids 3-348 with a protein from *Escherichia coli* that is a D-alanine-D-alanine ligase A (Accession No. NP_308458.1), about 41% identity from amino acids 3-348 with a protein from *Escherichia coli* that is a D-alanine-D-alanine ligase A (Accession Nos. NP_752421.1), and about 39% identity from amino acids 4-348 with a protein from *Oceanobacillus iheyensis* that is a D-alanine-D-alanine ligase A (Accession No. NP_692227.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:114 (327 amino acids) has about 41% identity from amino acids 29-326 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965730.1), about 43% identity from amino acids 79-326 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046598.1), about 43% identity from amino acids 58-165 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046597.1), and about 38% identity from amino acids 141-187 with a protein from *Clostridium perfringens* that is homologous to a cell division protein (Accession No. NP_561266.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:116 (455 amino acids) has about 77% identity from amino acids 1-454 with a protein from *Lactobacillus johnsonii* that is a UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase (Accession No. NP_964286.1), about 79% identity from amino acids 150-454 with a protein from *Lactobacillus gasseri* that is a UDP-N-acetylmuramyl pentapeptide synthase (Accession No. ZP_00047007.1), about 54% identity from amino acids 1-454 with a protein from *Lactobacillus plantarum* that is a UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanine ligase (Accession No. NP_784298.1), about 46% identity from amino acids 1-454 with a protein from *Enterococcus faecalis* that is a UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase (Accession No. NP_814587.1), and about 43% identity from amino acids 1-454 with a protein from *Streptococcus pyogenes* that is homologous to a D-Ala-D-Ala adding enzyme (Accession No. NP_269511.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:118 (432 amino acids) has about 40% identity from amino acids 1-426 with a protein from *Lactobacillus plantarum* that is a serine-type D-Ala-D-Ala carboxypeptidase (Accession No. NP_786467.1), about 51% identity from amino acids 37-317 with a protein from *Lactobacillus johnsonii* that is a D-alanyl-D-alanine carboxypeptidase (Accession No. NP_964537.1), about 49% identity from amino acids 37-317 with a protein from *Lactobacillus gasseri* that is a D-alanyl-D-alanine carboxypeptidase (Accession No. ZP_00047293.1), about 38% identity from amino acids 5-430 with a protein from *Bacillus subtilis* that is a D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5) (Accession No. NP_387891.1), and about 40% identity from amino acids 56-430 with a protein from *Bacillus subtilis* that is a penicillin binding protein 5 (Accession No. gb|AAA22375.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:120 (441 amino acids) has about 88% identity from amino acids 11-430 with a protein from *Lactobacillus johnsonii* that is a UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 (Accession No. NP_964240.1), about 90% identity from amino acids 11-382 with a protein from *Lactobacillus gasseri* that is a UDP-N-acetylglucosamine enolpyruvyl transferase (Accession No. ZP_00047072.1), about 64% identity from amino acids 11-

435 with a protein from *Lactobacillus plantarum* that is a UDP-N-acetylglucosamine 1-carboxyvinyltransferase (Accession No. NP_784290.1), about 62% identity from amino acids 11-429 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is a UDP-N-acetylglucosamine enolpyruvyl transferase (Accession No. ZP_00063218.1),
 5 and about 58% identity from amino acids 11-436 with a protein from *Enterococcus faecalis* that is a UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2 (Accession No. NP_814899.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:122 (459 amino acids) has about 82% identity from amino acids 1-459 with a protein from
 10 *Lactobacillus johnsonii* that is a UDP-N-acetylglucosamine-1-phosphate uridyltransferase (Accession No. NP_964224.1), about 81% identity from amino acids 1-459 with a protein from *Lactobacillus gasseri* that is an N-acetylglucosamine-1-phosphate uridyltransferase (Accession No. ZP_00047088.1), about 62% identity from amino acids 3-453 with a protein from *Lactobacillus plantarum* that is a UDP-N-
 15 acetylglucosamine pyrophosphorylase (Accession No. NP_784257.1), about 61% identity from amino acids 3-457 with a protein from *Enterococcus faecalis* that is a UDP-N-acetylglucosamine pyrophosphorylase (Accession No. NP_813869.1), and about 56% identity from amino acids 1-453 with a protein from *Streptococcus agalactiae* that is a UDP-N-acetylglucosamine pyrophosphorylase (Accession No. NP_688532.1).

20 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:124 (244 amino acids) has about 69% identity from amino acids 1-239 with a protein from *Lactobacillus johnsonii* that is an undecaprenyl pyrophosphate synthetase (Accession No. NP_965298.1), about 68% identity from amino acids 1-239 with a protein from *Lactobacillus gasseri* that is an undecaprenyl pyrophosphate synthase (Accession No.
 25 ZP_00046589.1), about 57% identity from amino acids 10-242 with a protein from *Oenococcus oeni* that is an undecaprenyl pyrophosphate synthase (Accession No. ZP_00070158.1), about 59% identity from amino acids 10-237 with a protein from *Listeria innocua* that is homologous to an undecaprenyl diphosphate synthase (Accession No. NP_470688.1), and about 56% identity from amino acids 10-242 with a protein from
 30 *Enterococcus faecalis* that is an undecaprenyl diphosphate synthase (Accession No. NP_816141.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:126 (389 amino acids) has about 72% identity from amino acids 1-377 with a protein from *Lactobacillus gasseri* that is a UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase (Accession No. ZP_00046896.1), about 72% identity from amino acids 1-377 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964696.1), about 72% identity from amino acids 1-375 with a protein from *Lactobacillus delbrueckii* that is an RgpG protein (Accession No. gb|AAK00329.1), about 54% identity from amino acids 2-355 with a protein from *Lactobacillus plantarum* that is an undecaprenyl-phosphate N-acetyl-glucosaminyl transferase (Accession No. NP_784485.1), and about 51% identity from amino acids 1-358 with a protein from *Enterococcus faecalis* that is a glycosyl transferase, group 4 family protein (Accession No. NP_815860.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:128 (313 amino acids) has about 38% identity from amino acids 51-311 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965759.1), about 38% identity from amino acids 51-311 with a protein from *Lactobacillus gasseri* that is in the beta-lactamase class C and other penicillin binding protein family (Accession No. ZP_00046847.1), about 31% identity from amino acids 30-296 with a protein from *Enterococcus faecalis* that is homologous to a penicillin-binding protein (Accession No. NP_814494.1), about 31% identity from amino acids 12-290 with a protein from *Lactobacillus plantarum* that is a serine-type D-Ala-D-Ala carboxypeptidase (Accession No. NP_785548.1), and about 33% identity from amino acids 38-289 with a protein from *Enterococcus faecium* that is in the beta-lactamase class C and other penicillin binding protein family (Accession No. ZP_00035472.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:130 (374 amino acids) has about 51% identity from amino acids 49-304 with a protein from *Lactobacillus delbrueckii* subsp. *bulgaricus* that is a conserved hypothetical penicillin-binding protein (Accession No. gb|AAM22482.1), about 30% identity from amino acids 67-362 with a protein from *Lactobacillus plantarum* that is a serine-type D-Ala-D-Ala carboxypeptidase (Accession No. NP_784838.1), about 24% identity from amino acids 46-371 with a protein from *Streptococcus agalactiae* (Accession No. NP_735091.1),

about 24% identity from amino acids 46-371 with a protein from *Streptococcus agalactiae* that is homologous to a lipoprotein (Accession No. NP_687676.1), and about 27% identity from amino acids 48-346 with a protein from *Enterococcus faecalis* that is homologous to a penicillin-binding protein (Accession No. NP_814494.1).

- 5 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:132 (702 amino acids) has about 69% identity from amino acids 1-699 with a protein from *Lactobacillus johnsonii* that is a penicillin-binding protein 2B (Accession No. NP_965426.1), about 71% identity from amino acids 22-699 with a protein from *Lactobacillus gasseri* that is a cell division protein FtsI/penicillin-binding protein 2
- 10 (Accession No. ZP_00046928.1), about 44% identity from amino acids 1-700 with a protein from *Lactobacillus plantarum* that is a penicillin binding protein 2B (Accession No. NP_785166.1), about 39% identity from amino acids 19-699 with a protein from *Enterococcus faecalis* that is a penicillin-binding protein 2B (Accession No. NP_816479.1), and about 37% identity from amino acids 12-702 with a protein from
- 15 *Leuconostoc mesenteroides* subsp. *mesenteroides* that is a cell division protein FtsI/penicillin-binding protein 2 (Accession No. ZP_00063639.1).

- A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:134 (704 amino acids) has about 75% identity from amino acids 34-704 with a protein from *Lactobacillus johnsonii* that is a penicillin-binding protein 1F (Accession No.
- 20 NP_965485.1), about 74% identity from amino acids 34-704 with a protein from *Lactobacillus gasseri* that is a membrane carboxypeptidase (penicillin-binding protein) (Accession No. ZP_00046704.1), about 53% identity from amino acids 34-703 with a protein from *Lactobacillus plantarum* that is a penicillin-binding protein 2a (Accession No. NP_785034.1), about 47% identity from amino acids 24-699 with a protein from
- 25 *Enterococcus faecalis* that is a penicillin-binding protein 2a (Accession No. NP_814430.1), and about 47% identity from amino acids 61-704 with a protein from *Listeria monocytogenes* that is homologous to a penicillin-binding protein (Accession No. NP_465753.1).

- A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:136
- 30 (343 amino acids) has about 68% identity from amino acids 26-337 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965496.1), about 67% identity

from amino acids 26-338 with a protein from *Lactobacillus gasseri* that is in the beta-lactamase class C and other penicillin binding protein family (Accession No. ZP_00046698.1), about 67% identity from amino acids 27-178 with a protein from *Lactobacillus reuteri* that is homologous to a penicillin-binding protein class C fnt-like protein (Accession No. gb|AAP97059.1), about 29% identity from amino acids 27-343 with a protein from *Streptococcus mutans* that is homologous to a penicillin-binding protein class C, fnt-like protein (Accession No. NP_721297.1), and about 30% identity from amino acids 39-323 with a protein from *Streptococcus agalactiae* that is homologous to a lipoprotein (Accession No. NP_687676.1).

10 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:138 (776 amino acids) has about 71% identity from amino acids 1-679 with a protein from *Lactobacillus gasseri* that is a membrane carboxypeptidase (penicillin-binding protein) (Accession No. ZP_00045945.1), about 71% identity from amino acids 1-680 with a protein from *Lactobacillus johnsonii* that is a penicillin binding protein 1A (Accession No. NP_965052.1), about 45% identity from amino acids 19-688 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is a membrane carboxypeptidase (penicillin-binding protein) (Accession No. ZP_00064357.1), about 45% identity from amino acids 1-688 with a protein from *Lactobacillus plantarum* that is a penicillin-binding protein 1a (Accession No. NP_785323.1), and about 45% identity from amino acids 20-651 with a protein from *Enterococcus faecium* that is a membrane carboxypeptidase (penicillin-binding protein) (Accession No. ZP_00035508.1).

25 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:140 (218 amino acids) has about 72% identity from amino acids 7-217 with a protein from *Lactobacillus gasseri* that is a penicillin-binding protein-related factor A that is homologous to a recombinase (Accession No. ZP_00045946.1), about 74% identity from amino acids 7-212 with a protein from *Lactobacillus johnsonii* that is a recombination protein (RecU) (Accession No. NP_965051.1), about 53% identity from amino acids 7-213 with a protein from *Enterococcus hirae* that is a penicillin binding protein-related factor A (Accession No. emb|CAC21567.1), about 57% identity from amino acids 7-212 with a protein from *Lactobacillus plantarum* that is a recombination protein (RecU) (Accession No. NP_785324.1), and about 52% identity from amino acids 7-213 with a

protein from *Enterococcus faecium* that is a penicillin-binding protein-related factor A that is homologous to a recombinase (Accession No. ZP_00035507.1).

5 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:142 (364 amino acids) has about 46% identity from amino acids 48-290 with a protein from *Lactobacillus* *delbrueckii* subsp. *bulgaricus* that is a conserved hypothetical penicillin binding protein (Accession No. gb|AAM22482.1), about 30% identity from amino acids 37-337 with a protein from *Lactobacillus plantarum* that is a serine-type D-Ala-D-Ala carboxypeptidase (Accession No. NP_784838.1), about 27% identity from amino acids
10 19-336 with a protein from *Enterococcus faecalis* that is homologous to a penicillin-binding protein (Accession No. NP_814494.1), about 31% identity from amino acids 78-299 with a protein from *Streptococcus mutans* that is homologous to a penicillin-binding protein class C, fnt-like protein (Accession No. NP_721297.1), and about 27% identity from amino acids 48-336 with a protein from *Lactobacillus plantarum* that is a serine-type D-Ala-D-Ala carboxypeptidase (Accession No. NP_785548.1).
15

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:144 (369 amino acids) has about 46% identity from amino acids 46-299 with a protein from *Lactobacillus delbrueckii* subsp. *bulgaricus* that is a conserved hypothetical penicillin binding protein (Accession No. gb|AAM22482.1), about 30% identity from amino acids
20 16-350 with a protein from *Lactobacillus plantarum* that is a serine-type D-Ala-D-Ala carboxypeptidase (Accession No. NP_784838.1), about 29% identity from amino acids 26-362 with a protein from *Staphylococcus aureus* subsp. *aureus* that is an autolysis and methicillin resistant-related protein (Accession No. NP_371581.1), about 28% identity from amino acids 22-304 with a protein from *Staphylococcus epidermidis* that is an
25 autolysis and methicillin resistant-related protein (Accession No. NP_764309.1), and about 28% identity from amino acids 16-341 with a protein from *Lactobacillus plantarum* that is a serine-type D-Ala-D-Ala carboxypeptidase (Accession No. NP_785548.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:146
30 (720 amino acids) has about 60% identity from amino acids 14-719 with a protein from *Lactobacillus gasseri* that is a cell division protein FtsI/penicillin-binding protein 2

- (Accession No. ZP_00047441.1), about 60% identity from amino acids 14-719 with a protein from *Lactobacillus johnsonii* that is a penicillin-binding protein 2B (Accession No. NP_964824.1), about 43% identity from amino acids 42-719 with a protein from *Lactobacillus plantarum* that is a penicillin-binding protein 2B (Accession No. NP_785695.1), about 39% identity from amino acids 42-718 with a protein from *Listeria innocua* that is homologous to a penicillin-binding protein 2B (Accession No. NP_471479.1), and about 38% identity from amino acids 42-718 with a protein from *Listeria monocytogenes* that is homologous to a penicillin-binding protein 2B (Accession No. NP_465563.1).
- 10 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:148 (504 amino acids) has about 74% identity from amino acids 1-503 with a protein from *Lactobacillus johnsonii* that is a D-alanine-activating enzyme (Accession No. NP_965763.1), about 73% identity from amino acids 1-503 with a protein from *Lactobacillus gasseri* that is in the non-ribosomal peptide synthetase module and related
- 15 protein family (Accession No. ZP_00046843.1), about 53% identity from amino acids 1-503 with a protein from *Lactobacillus plantarum* that is a D-alanine-activating enzyme (DltA) (Accession No. NP_785546.1), about 51% identity from amino acids 1-503 with a protein from *Lactobacillus rhamnosus* that is a D-alanine-poly (phosphoribitol) ligase subunit 1 (D-alanine-activating enzyme) (Accession No. sp|P35854|DLTA_LACRH),
- 20 and about 49% identity from amino acids 1-504 with a protein from *Streptococcus agalactiae* that is a D-alanine-activating enzyme (Accession No. NP_688780.1).
- A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:150 (412 amino acids) has about 70% identity from amino acids 6-412 with a protein from *Lactobacillus gasseri* that is a predicted membrane protein involved in D-alanine export
- 25 (Accession No. ZP_00046844.1), about 70% identity from amino acids 6-412 with a protein from *Lactobacillus johnsonii* that is a DltB protein (Accession No. NP_965762.1), about 58% identity from amino acids 6-410 with a protein from *Lactobacillus plantarum* that is a D-alanyl transfer protein (DltB) (Accession No. NP_785545.1), about 55% identity from amino acids 4-409 with a protein from
- 30 *Enterococcus faecalis* that is a basic membrane protein (DltB) (Accession No. NP_816377.1), and about 51% identity from amino acids 6-409 with a protein from

Leuconostoc mesenteroides subsp. *mesenteroides* that is a predicted membrane protein involved in D-alanine export (Accession No. ZP_00064054.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:152 (79 amino acids) has about 81% identity from amino acids 1-79 with a protein from
5 *Lactobacillus johnsonii* that is a D-alanyl carrier protein (Accession No. NP_965761.1), about 79% identity from amino acids 1-79 with a protein from *Lactobacillus gasseri* that is an acyl carrier protein (Accession No. ZP_00046845.1), about 63% identity from amino acids 1-73 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is an acyl carrier protein (Accession No. ZP_00064053.1), about 67% identity from
10 amino acids 2-77 with a protein from *Lactobacillus plantarum* that is a D-alanyl carrier protein (DltC) (Accession No. NP_785544.1), and about 64% identity from amino acids 2-77 with a protein from *Lactobacillus plantarum* that is a D-alanyl carrier protein (DltC) (Accession No. NP_785028.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:154
15 (428 amino acids) has about 58% identity from amino acids 1-428 with a protein from *Lactobacillus johnsonii* that is a DltD precursor (Accession No. NP_965760.1), about 58% identity from amino acids 1-428 with a protein from *Lactobacillus gasseri* that is a protein involved in D-alanine esterification of lipoteichoic acid and wall teichoic acid (D-alanine transfer protein) (Accession No. ZP_00046846.1), about 50% identity from
20 amino acids 1-409 with a protein from *Lactobacillus plantarum* that is a D-alanyl transfer protein DltD (Accession No. NP_785543.1), about 46% identity from amino acids 1-410 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is a protein involved in D-alanine esterification of lipoteichoic acid and wall teichoic acid (D-alanine transfer protein) (Accession No. ZP_00064052.1), and about 45% identity
25 from amino acids 5-408 with a protein from *Streptococcus mutans* that is homologous to an extramembranal protein (DltD) (Accession No. NP_722019.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:156 (477 amino acids) has about 74% identity from amino acids 1-473 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964890.1), about 74% identity
30 from amino acids 1-474 with a protein from *Lactobacillus gasseri* that is a membrane protein involved in the export of O-antigen and teichoic acid (Accession No.

ZP_00045854.1), about 46% identity from amino acids 1-470 with a protein from *Streptococcus thermophilus* that is a cpsU protein (Accession No. gb|AAM93406.1), about 46% identity from amino acids 1-470 with a protein from *Streptococcus thermophilus* that is an EpsI protein (Accession No. gb|AAK61904.1), and about 46% identity from amino acids 1-470 with a protein from *Streptococcus thermophilus* that is an EpsU protein (Accession No. emb|CAB52225.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:158 (174 amino acids) has about 83% identity from amino acids 1-174 with a protein from *Lactobacillus gasseri* that is a UDP-galactopyranose mutase (Accession No. ZP_00045853.1), about 83% identity from amino acids 1-172 with a protein from *Lactobacillus johnsonii* that is a UDP-galactopyranose mutase (Accession No. NP_964888.1), about 74% identity from amino acids 1-169 with a protein from *Lactobacillus plantarum* that is a UDP-galactopyranose mutase (Accession No. NP_784842.1), about 69% identity from amino acids 1-172 with a protein from *Lactobacillus plantarum* that is a UDP-galactopyranose mutase (Accession No. NP_784882.1), and about 63% identity from amino acids 1-172 with a protein from *Streptococcus thermophilus* that is an EpsJ protein (Accession No. gb|AAK61905.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:160 (133 amino acids) has about 88% identity from amino acids 2-133 with a protein from *Lactobacillus johnsonii* that is a UDP-galactopyranose mutase (Accession No. NP_964888.1), about 79% identity from amino acids 4-133 with a protein from *Lactobacillus plantarum* that is a UDP-galactopyranose mutase (Accession No. NP_784842.1), about 78% identity from amino acids 4-133 with a protein from *Lactobacillus plantarum* that is a UDP-galactopyranose mutase (Accession No. NP_784882.1), about 73% identity from amino acids 1-133 with a protein from *Streptococcus pneumoniae* that is a Glf-like protein (Accession No. gb|AAL68431.1), and about 70% identity from amino acids 1-133 with a protein from *Streptococcus thermophilus* that is an EpsJ protein (Accession No. gb|AAK61905.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:162 (431 amino acids) has about 22% identity from amino acids 1-375 with a protein from *Streptococcus pneumoniae* that is homologous to a polysaccharide polymerase

(Accession No. gb|AAC44966.1), about 22% identity from amino acids 1-368 with a protein from *Streptococcus pneumoniae* that is a polysaccharide polymerase (Cps19aI) (Accession No. gb|AAC78671.1), about 24% identity from amino acids 4-376 with a protein from *Streptococcus pneumoniae* that is a Wzy protein (Accession No. gb|AAK20689.1), about 24% identity from amino acids 4-376 with a protein from *Streptococcus pneumoniae* that is homologous to a polysaccharide polymerase (Cps6aI) (Accession No. gb|AAL68424.1), and about 24% identity from amino acids 4-376 with a protein from *Streptococcus pneumoniae* that is homologous to a polysaccharide polymerase (Cps6aI) (Accession No. gb|AAL82786.1).

10 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:164 (346 amino acids) has about 35% identity from amino acids 35-251 with a protein from *Streptococcus pneumoniae* that is a glycosyltransferase (Accession Nos. emb|CAA07401.1; AJ006986), about 32% identity from amino acids 36-305 with a protein from *Streptococcus pneumoniae* that is homologous to a glycosyltransferase
 15 (Accession Nos. emb|CAB59291.1; AJ131984), about 33% identity from amino acids 4-272 with a protein from *Clostridium acetobutylicum* that is a glycosyltransferase involved in cell wall biogenesis (Accession Nos. NP_348116.1; NC_003030), about 31% identity from amino acids 4-254 with a protein from *Bifidobacterium longum* that is homologous to a glycosyltransferase (Accession No. NP_695639.1), and about 31%
 20 identity from amino acids 4-254 with a protein from *Bifidobacterium longum* that is a glycosyltransferase involved in cell wall biogenesis (Accession No. ZP_00120907.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:166 (218 amino acids) has about 29% identity from amino acids 8-151 with an environmental sequence (Accession No. gb|EAF15712.1), about 26% identity from amino acids 38-139
 25 with a hypothetical protein from *Helicobacter hepaticus* (Accession No. NP_860377.1), about 24% identity from amino acids 13-166 with an environmental sequence (Accession No. gb|EAB88932.1), about 27% identity from amino acids 51-155 with an environmental sequence (Accession No. gb|EAD88260.1), and about 24% identity from amino acids 2-167 with an environmental sequence (Accession No. gb|EAF01752.1).

30 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:168 (173 amino acids) has about 29% identity from amino acids 30-108 with an

environmental sequence (Accession No. gb|EAJ18143.1), about 29% identity from amino acids 30-108 with an environmental sequence (Accession No. gb|EAK67508.1), about 23% identity from amino acids 8-134 with an environmental sequence (Accession No. gb|EAD63991.1), about 23% identity from amino acids 38-173 with a protein from

5 *Arabidopsis thaliana* that is an F-box family protein (Accession No. NP_178986.1), and about 25% identity from amino acids 47-155 with a protein from *Photorhabdus luminescens* subsp. *laumondii* that is a maltodextrin phosphorylase (Accession No. NP_927823.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:170

10 (293 amino acids) has about 39% identity from amino acids 3-293 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964886.1), about 38% identity from amino acids 5-293 with a protein from *Oenococcus oeni* that is homologous to a glycosyltransferase (Accession No. ZP_00069921.1), about 36% identity from amino acids 3-290 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is

15 homologous to a glycosyltransferase (Accession No. ZP_00064030.1), about 33% identity from amino acids 4-292 with a protein from *Thermoanaerobacterium thermosaccharolyticum* that is homologous to a glycosyltransferase (Accession No. gb|AAR85515.1), and about 32% identity from amino acids 4-265 with a hypothetical protein from *Pyrococcus horikoshii* (Accession No. NP_142407.1).

20 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:172 (257 amino acids) has about 75% identity from amino acids 1-257 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964882.1), about 49% identity from amino acids 1-257 with a protein from *Lactobacillus plantarum* that is a polysaccharide biosynthesis protein (Accession No. NP_784889.1), about 51% identity

25 from amino acids 1-249 with a protein from *Lactobacillus plantarum* that is a glycosyltransferase (Accession No. NP_784846.1), about 44% identity from amino acids 1-249 with a hypothetical protein from *Oenococcus oeni* (Accession No. ZP_00069922.1), and about 46% identity from amino acids 2-228 with a protein from *Streptococcus thermophilus* that is an EpsF protein (Accession No. gb|AAK61900.1).

30 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:174 (217 amino acids) has about 73% identity from amino acids 1-217 with a protein from

Lactobacillus gasseri that is a sugar transferase involved in lipopolysaccharide synthesis (Accession No. ZP_00045843.1), about 71% identity from amino acids 1-217 with a protein from *Lactobacillus johnsonii* that is an undecaprenyl-phosphate galactosephosphotransferase (Accession No. NP_964881.1), about 70% identity from amino acids 9-215 with a protein from *Lactobacillus delbrueckii* subsp. *bulgaricus* that is a phospho-glucosyltransferase (EpsE) (Accession No. gb|AAG44709.1), about 66% identity from amino acids 18-217 with a protein from *Lactobacillus rhamnosus* that is homologous to an undecaprenyl-phosphate glycosyl-1-phosphate transferase (Accession No. gb|AAK63832.1), and about 60% identity from amino acids 7-217 with a protein from *Lactobacillus plantarum* that is priming glycosyltransferase (Accession No. NP_784894.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:176 (256 amino acids) has about 68% identity from amino acids 1-255 with a protein from *Lactobacillus delbrueckii* subsp. *bulgaricus* that is an EpsD protein (Accession Nos. gb|AAG44708.1; AF267127), about 67% identity from amino acids 1-256 with a protein from *Lactobacillus gasseri* that is a capsular polysaccharide biosynthesis protein (Accession No. ZP_00045842.1), about 66% identity from amino acids 1-256 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964880.1), about 57% identity from amino acids 3-250 with a protein from *Lactobacillus rhamnosus* that is an EpsB protein (Accession No. gb|AAK64289.1), and about 45% identity from amino acids 3-256 with a protein from *Lactobacillus plantarum* that is an exopolysaccharide biosynthesis protein (Accession No. NP_784865.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:178 (260 amino acids) has about 66% identity from amino acids 5-225 with a protein from *Lactobacillus johnsonii* that is homologous to a tyrosine-protein kinase (Accession No. NP_964879.1), about 65% identity from amino acids 5-225 with a protein from *Lactobacillus gasseri* that is an ATPase involved in chromosome partitioning (Accession No. ZP_00045840.1), about 57% identity from amino acids 1-228 with a protein from *Lactobacillus delbrueckii* subsp. *bulgaricus* that is an EpsC protein (Accession No. gb|AAG44707.1), about 51% identity from amino acids 1-226 with a protein from *Leuconostoc mesenteroides* subsp.

mesenteroides that is an ATPase involved in chromosome partitioning (Accession No. ZP_00063784.1), and about 46% identity from amino acids 5-230 with a protein from *Oceanobacillus iheyensis* that is a capsular polysaccharide biosynthesis protein (Accession No. NP_693822.1).

- 5 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:180 (291 amino acids) has about 51% identity from amino acids 1-288 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964878.1), about 50% identity from amino acids 2-289 with a protein from *Lactobacillus delbrueckii* subsp. *bulgaricus* that is an EpsB protein (Accession No. gb|AAG44706.1), about 51% identity from amino
10 acids 74-291 with a protein from *Lactobacillus gasseri* that is a capsular polysaccharide biosynthesis protein (Accession No. ZP_00045839.1), about 35% identity from amino acids 9-279 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is a capsular polysaccharide biosynthesis protein (Accession No. ZP_00063785.1), and about 31% identity from amino acids 8-284 with a protein from *Lactobacillus*
15 *plantarum* that is an exopolysaccharide biosynthesis protein (Accession No. NP_784863.1).

- A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:182 (351 amino acids) has about 52% identity from amino acids 45-340 with a protein from *Lactobacillus delbrueckii* subsp. *bulgaricus* that is an EpsA protein (Accession Nos.
20 gb|AAG44705.1; AF267127), about 51% identity from amino acids 26-335 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964877.1), about 43% identity from amino acids 58-335 with a protein from *Lactobacillus plantarum* that is a transcription regulator (Accession No. NP_784704.1), about 37% identity from amino acids 59-335 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides*
25 that is a transcriptional regulator (Accession No. ZP_00063495.1), and about 37% identity from amino acids 26-335 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is a transcriptional regulator (Accession No. ZP_00063643.1).

- A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:184
30 (421 amino acids) has about 76% identity from amino acids 1-417 with a protein from *Lactobacillus gasseri* that is a GTPase (Accession No. ZP_00046671.1), about 76%

identity from amino acids 1-417 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965656.1), about 51% identity from amino acids 10-421 with a protein from *Listeria monocytogenes* that is homologous to an ATP/GTP-binding protein (Accession No. NP_464289.1), about 51% identity from amino acids 13-421 with a
5 protein from *Listeria innocua* that is homologous to an ATP/GTP-binding protein (Accession No. NP_470098.1), and about 48% identity from amino acids 4-421 with a protein from *Lactobacillus plantarum* that is a GTPase (Accession No. NP_784620.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:186 (336 amino acids) has about 41% identity from amino acids 25-331 with a hypothetical
10 protein from *Lactobacillus johnsonii* (Accession No. NP_964123.1), about 39% identity from amino acids 2-331 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00047037.1), about 20% identity from amino acids 6-310 with a hypothetical protein from *Clostridium thermocellum* (Accession No. ZP_00059706.1), about 45% identity from amino acids 162-194 with an environmental sequence
15 (Accession No. gb|EAD87497.1), and about 24% identity from amino acids 215-324 with an environmental sequence (Accession No. gb|EAB36127.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:188 (1382 amino acids) has about 24% identity from amino acids 132-1035 with a
hypothetical protein from *Enterococcus faecalis* (Accession No. NP_815907.1), about
20 27% identity from amino acids 456-931 with a protein from *Lactobacillus plantarum* that is homologous to a cell surface protein (Accession No. NP_786384.1), about 31% identity from amino acids 491-925 with a protein from *Vibrio vulnificus* that is a membrane associated lipoprotein precursor (Accession No. NP_935020.1), about 28% identity from amino acids 408-926 with a hypothetical protein from *Helicobacter*
25 *hepaticus* (Accession No. NP_859581.1), and about 23% identity from amino acids 24-795 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964510.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:190 (250 amino acids) has about 52% identity from amino acids 126-249 with a protein from
30 *Lactobacillus gasseri* that is a cell wall-associated hydrolase (invasion-associated protein) (Accession No. ZP_00046669.1), about 50% identity from amino acids 126-249

- with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965658.1), about 54% identity from amino acids 131-249 with a protein from *Clostridium acetobutylicum* that has an N-terminal domain intergin-like repeat and a c-terminal cell wall-associated hydrolase domain (Accession No. NP_349545.1), about 46% identity
- 5 from amino acids 126-250 with a protein from *Oenococcus oeni* that is a cell wall-associated hydrolase (invasion-associated protein) (Accession No. ZP_00070605.1), and about 33% identity from amino acids 72-246 with a protein from *Lactobacillus plantarum* that is homologous to an extracellular protein, gamma-D-glutamate-meso-diaminopimelate muropeptidase (Accession No. NP_785666.1).
- 10 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:194 (262 amino acids) has about 54% identity from amino acids 145-260 with a protein from *Lactobacillus gasseri* that is a cell wall-associated hydrolase (invasion-associated protein) (Accession No. ZP_00046669.1), about 51% identity from amino acids 145-260 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965658.1),
- 15 about 53% identity from amino acids 143-261 with a conserved hypothetical protein from *Clostridium perfringens* (Accession No. NP_561194.1), about 50% identity from amino acids 145-261 with a protein from *Oenococcus oeni* that is a cell wall-associated hydrolase (invasion-associated protein) (Accession No. ZP_00070605.1), and about 51% identity from amino acids 143-260 with a protein from *Clostridium acetobutylicum* that is
- 20 a cell wall-associated hydrolase (Accession No. NP_346949.1).
- A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:196 (184 amino acids) has about 43% identity from amino acids 48-182 with a protein from *Lactobacillus gasseri* that is a cell wall-associated hydrolase (invasion-associated protein) (Accession No. ZP_00046669.1), about 43% identity from amino acids 47-182
- 25 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965658.1), about 48% identity from amino acids 66-182 with a protein from *Enterococcus faecium* that is a surface antigen (Accession No. ZP_00036908.1), about 48% identity from amino acids 66-182 with a protein from *Enterococcus faecium* that is homologous to a glycosidase (GlyA) (Accession No. gb|AAK72496.1), and about 41% identity from
- 30 amino acids 46-171 with a hypothetical protein from *Lactococcus lactis* subsp. *lactis* (Accession No. NP_267092.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:198 (149 amino acids) has about 52% identity from amino acids 1-146 with a protein from *Lactobacillus gasseri* that is a guanylate kinase (Accession No. ZP_00046668.1), about 54% identity from amino acids 1-145 with a protein from *Lactobacillus johnsonii* that is a guanylate kinase (Accession No. NP_965659.1), about 43% identity from amino acids 1-148 with a protein from *Lactobacillus plantarum* that is a guanylate kinase (Accession No. NP_784598.1), about 40% identity from amino acids 1-145 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is a guanylate kinase (Accession No. ZP_00063506.1), and about 38% identity from amino acids 1-145 with a protein from *Oenococcus oeni* that is a guanylate kinase (Accession No. ZP_00070365.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:200 (99 amino acids) has about 71% identity from amino acids 1-80 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046667.1), about 70% identity from amino acids 1-80 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965660.1), about 40% identity from amino acids 8-69 with a hypothetical protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* (Accession No. ZP_00063600.1), about 33% identity from amino acids 5-75 with a protein from *Lactobacillus plantarum* (Accession No. NP_785013.1), and about 39% identity from amino acids 4-69 with a protein from *Lactobacillus plantarum* (Accession No. NP_786559.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:202 (503 amino acids) has about 40% identity from amino acids 1-497 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965661.1), about 40% identity from amino acids 214-502 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046666.1), about 22% identity from amino acids 105-477 with a protein from *Bacillus cereus* that is homologous to a membrane protein (Accession No. NP_977301.1), about 19% identity from amino acids 4-497 with a hypothetical protein from *Bacillus anthracis* (Accession No. NP_653890.1), and about 19% identity from amino acids 4-497 with a protein from *Bacillus anthracis* that is homologous to a membrane protein (Accession No. NP_847818.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:204 (206 amino acids) has about 43% identity from amino acids 4-205 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965662.1), about 42% identity from amino acids 4-205 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046665.1), about 33% identity from amino acids 41-203 with a protein from *Lactobacillus plantarum* (Accession No. NP_786135.1), about 26% identity from amino acids 71-177 with a hypothetical protein from *Plasmodium falciparum* (Accession No. NP_701622.1), and about 27% identity from amino acids 62-145 with an environmental sequence (Accession No. gb|EAH10085.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:206 (148 amino acids) has about 60% identity from amino acids 1-147 with a protein from *Lactobacillus johnsonii* that is an NrdI protein (Accession No. NP_965663.1), about 60% identity from amino acids 1-147 with a protein from *Lactobacillus gasseri* that is a protein involved in ribonucleotide reduction (Accession No. ZP_00046664.1), about 38% identity from amino acids 4-123 with a protein from *Enterococcus faecalis* that is a NrdI protein (Accession No. NP_814256.1), about 33% identity from amino acids 4-124 with a protein from *Lactococcus lactis* that is a NrdI protein (Accession No. sp|Q48709|NRDI_LACLC), and about 33% identity from amino acids 4-124 with a protein from *Lactococcus lactis* subsp. *lactis* that is a ribonucleotide reductase (Accession No. NP_267132.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:208 (311 amino acids) has about 53% identity from amino acids 3-310 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965664.1), about 53% identity from amino acids 3-311 with a protein from *Lactobacillus gasseri* that is a ribonucleotide reductase, beta subunit (Accession No. ZP_00046663.1), about 42% identity from amino acids 5-296 with a protein from *Streptococcus pyogenes* that is a ribonucleotide diphosphate reductase small subunit (Accession No. NP_607484.1), about 42% identity from amino acids 5-296 with a protein from *Streptococcus pyogenes* that is a ribonucleotide diphosphate reductase small subunit (Accession No. NP_269482.1), and about 42% identity from amino acids 5-296 with a protein from *Streptococcus agalactiae*

that is a ribonucleoside-diphosphate reductase 2, beta subunit (Accession No. NP_687833.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:210 (177 amino acids) has about 58% identity from amino acids 1-152 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046662.1), about 57% identity from amino acids 1-152 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965665.1), about 33% identity from amino acids 1-132 with a protein from *Lactobacillus plantarum* (Accession No. NP_786047.1), about 29% identity from amino acids 23-144 with a hypothetical protein from *Pyrococcus horikoshii* (Accession No. NP_142266.1), and about 33% identity from amino acids 1-67 with an environmental sequence (Accession No. gb|EAC37753.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:212 (240 amino acids) has about 63% identity from amino acids 7-240 with a protein from *Lactobacillus gasseri* (Accession No. ZP_00047171.1), about 66% identity from amino acids 20-240 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965638.1), about 41% identity from amino acids 7-239 with a protein from *Lactobacillus plantarum* (Accession No. NP_786183.1), about 44% identity from amino acids 51-239 with a protein from *Listeria monocytogenes* that is homologous to a YvpB protein (Accession No. NP_464251.1), and about 42% identity from amino acids 52-240 with a protein from *Bacillus subtilis* that is a YvpB protein (Accession No. NP_391374.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:214 (105 amino acids) has about 60% identity from amino acids 4-105 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964999.1), about 50% identity from amino acids 4-104 with a hypothetical protein from *Lactococcus lactis* subsp. *lactis* (Accession No. NP_267039.1), about 50% identity from amino acids 3-104 with a protein from *Enterococcus faecium* that is homologous to a metal-sulfur cluster biosynthetic enzyme (Accession No. ZP_00036555.1), about 46% identity from amino acids 4-104 with a conserved hypothetical protein from *Enterococcus faecalis* (Accession No. NP_815231.1), and about 56% identity from amino acids 16-105 with a protein from *Lactobacillus plantarum* (Accession No. NP_784773.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:216 (98 amino acids) has about 81% identity from amino acids 3-98 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964998.1), about 72% identity from amino acids 3-98 with a protein from *Lactobacillus plantarum* that is homologous to an ABC transporter component, iron regulated (Accession No. NP_785081.1), about 67% identity from amino acids 3-98 with a protein from *Oenococcus oeni* that is an ABC-type transport system involved in Fe-S cluster assembly, permease component (Accession No. ZP_00069298.1), about 64% identity from amino acids 4-98 with a conserved hypothetical protein from *Streptococcus pneumoniae* (Accession No. NP_358369.1), and about 64% identity from amino acids 4-98 with a conserved hypothetical intein-containing protein from *Streptococcus pneumoniae* (Accession No. NP_345358.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:218 (76 amino acids) has about 80% identity from amino acids 1-73 with a protein from *Lactobacillus johnsonii* that is an ABC transporter ATPase component (Accession No. NP_964994.1), about 73% identity from amino acids 1-73 with a protein from *Lactobacillus plantarum* that is an ABC transporter, ATP-binding protein (Accession No. NP_785077.1), about 71% identity from amino acids 1-73 with a protein from *Streptococcus mutans* that is homologous to an ABC transporter, ATP-binding protein (Accession No. NP_720711.1), about 65% identity from amino acids 1-73 with a protein from *Enterococcus faecium* that is an ABC-type transport system involved in Fe-S cluster assembly, ATPase component (Accession No. ZP_00037285.1), and about 69% identity from amino acids 1-72 with a protein from *Streptococcus pneumoniae* that is an ABC transporter, ATP-binding protein (Accession No. NP_345354.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:220 (52 amino acids) has about 32% identity from amino acids 5-47 with a hypothetical protein from *Plasmodium falciparum* (Accession No. NP_700844.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:222 (161 amino acids) has about 59% identity from amino acids 1-146 with a protein from *Lactobacillus gasseri* (Accession No. ZP_00046659.1), about 60% identity from amino

acids 1-146 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965668.1), about 44% identity from amino acids 7-151 with a protein from *Listeria innocua* (Accession No. NP_469929.1), about 39% identity from amino acids 7-161 with a protein from *Enterococcus faecalis* that is homologous to a membrane protein
5 (Accession No. NP_814929.1), and about 40% identity from amino acids 11-137 with a protein from *Lactobacillus plantarum* that is an integral membrane protein (Accession No. NP_784703.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:224 (256 amino acids) has about 64% identity from amino acids 12-235 with a protein from
10 *Lactobacillus gasseri* (Accession No. ZP_00046658.1), about 63% identity from amino acids 12-235 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965669.1), about 48% identity from amino acids 12-216 with a protein from *Lactobacillus sakei* that is a LabL protein (Accession No. gb|AAL00959.1), about 45% identity from amino acids 13-235 with a conserved membrane protein from *Listeria*
15 *innocua* (Accession No. NP_469930.1), and about 45% identity from amino acids 13-235 with a conserved membrane protein from *Listeria monocytogenes* (Accession No. NP_464106.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:226 (513 amino acids) has about 81% identity from amino acids 1-513 with a protein from
20 *Lactobacillus gasseri* that is an ATPase component of ABC transporters with duplicated ATPase domains (Accession No. ZP_00046657.1), about 81% identity from amino acids 1-513 with a protein from *Lactobacillus johnsonii* that is an ABC transporter ATPase component (Accession No. NP_965670.1), about 52% identity from amino acids 1-513 with a protein from *Lactobacillus plantarum* that is an ABC transporter, ATP-binding
25 protein (Accession No. NP_785961.1), about 52% identity from amino acids 1-512 with a protein from *Enterococcus faecalis* that is an ABC transporter, ATP-binding protein (Accession No. NP_815740.1), and about 49% identity from amino acids 1-513 with a protein from *Oenococcus oeni* that is an ATPase component of ABC transporters with duplicated ATPase domains (Accession No. ZP_00070366.1).

30 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:228 (124 amino acids) has about 50% identity from amino acids 3-124 with a hypothetical

protein from *Lactobacillus johnsonii* (Accession No. NP_965671.1), about 51% identity from amino acids 3-121 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00046656.1), and about 48% identity from amino acids 53-81 with a hypothetical protein from *Pyrococcus furiosus* (Accession No. NP_578913.1).

5 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:230 (73 amino acids) has about 39% identity from amino acids 8-58 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is an acetyltransferase (Accession No. ZP_00063180.1), about 36% identity from amino acids 7-58 with a protein from *Oenococcus oeni* that is an acetyltransferase (Accession No. ZP_00069032.1), about 36%
10 identity from amino acids 7-56 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965082.1), about 36% identity from amino acids 15-55 with an environmental sequence (Accession No. gb|EAI00330.1), and about 37% identity from amino acids 12-54 with a protein from *Bacillus anthracis* that is an acetyltransferase in the GNAT family (Accession No. NP_658716.1).

15 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:232 (424 amino acids) has about 58% identity from amino acids 8-375 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965673.1), about 58% identity from amino acids 8-375 with a protein from *Lactobacillus gasseri* that is a transcriptional regulator (Accession No. ZP_00046655.1), about 41% identity from amino acids 42-383
20 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964188.1), about 42% identity from amino acids 42-370 with a protein from *Lactobacillus gasseri* that is a transcriptional regulator (Accession No. ZP_00047236.1), and about 46% identity from amino acids 78-350 with a protein from *Lactobacillus plantarum* that is a transcription regulator (Accession No. NP_784105.1).

25 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:234 (538 amino acids) has about 30% identity from amino acids 5-527 with a protein from *Lactobacillus gasseri* that is a membrane protein involved in the export of O-antigen and teichoic acid (Accession No. ZP_00047298.1), about 29% identity from amino acids 5-527 with a protein from *Lactobacillus johnsonii* that is an export protein for
30 polysaccharides and teichoic acids (Accession No. NP_964533.1), about 31% identity from amino acids 1-457 with a protein from *Enterococcus faecalis* that is a

polysaccharide biosynthesis family protein (Accession No. NP_814328.1), about 33% identity from amino acids 3-450 with a protein from *Enterococcus faecalis* that is a polysaccharide biosynthesis family protein (Accession No. NP_814421.1), and 28% identity from amino acids 3-526 with a protein from *Streptococcus mutans* that is
5 homologous to a membrane protein (Accession No. NP_722009.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:236 (271 amino acids) has about 58% identity from amino acids 1-271 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964116.1), about 58% identity from amino acids 1-271 with a protein from *Lactobacillus gasseri* that is a
10 glycosyltransferase involved in cell wall biogenesis (Accession No. ZP_00047045.1), about 31% identity from amino acids 7-234 with a protein from *Bacillus cereus* that is a glycosyltransferase (Accession No. NP_834930.1), about 28% identity from amino acids 2-250 with a protein from *Streptococcus thermophilus* that is an EpsV protein (Accession No. emb|CAB52224.1), and 31% identity from amino acids 2-222 with a protein from
15 *Lactobacillus plantarum* that is a glycosyltransferase (Accession No. NP_786160.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:238 (476 amino acids) has about 75% identity from amino acids 1-475 with a protein from *Lactobacillus gasseri* that is a membrane protein involved in the export of O-antigen and teichoic acid (Accession No. ZP_00047223.1), about 74% identity from amino acids 1-
20 475 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965532.1), about 30% identity from amino acids 7-460 with a protein from *Streptococcus thermophilus* that is a cpsU protein (Accession No. gb|AAM93406.1), about 30% identity from amino acids 7-460 with a protein from *Streptococcus thermophilus* that is an EpsU protein (Accession No. emb|CAB52225.1), and 30%
25 identity from amino acids 7-460 with a protein from *Streptococcus thermophilus* that is an EpsI protein (Accession No. gb|AAK61904.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:240 (367 amino acids) has about 54% identity from amino acids 3-364 with a protein from *Lactobacillus gasseri* that is a transcriptional regulator (Accession No. ZP_00047236.1),
30 about 53% identity from amino acids 3-364 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964188.1), about 42% identity from amino

acids 22-360 with a protein from *Lactobacillus gasseri* that is a transcription regulator (Accession No. ZP_00046655.1), about 41% identity from amino acids 21-360 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965673.1), and 44% identity from amino acids 33-338 with a protein from *Lactobacillus plantarum* that
5 is a transcription regulator (Accession No. NP_784704.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:242 (246 amino acids) has about 46% identity from amino acids 1-242 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965126.1), about 37% identity from amino acids 77-234 with a protein from *Clostridium thermocellum* that is a
10 glycosyltransferase (Accession No. ZP_00060425.1), about 33% identity from amino acids 10-220 with a protein from *Helicobacter pylori* that is a type 1 capsular polysaccharide biosynthesis protein J (capJ) (Accession No. NP_207219.1), about 32% identity from amino acids 17-225 with a protein from *Bifidobacterium longum* that is a glycosyltransferase (Accession No. ZP_00120944.1), and 32% identity from amino acids
15 17-225 with a protein from *Bifidobacterium longum* that is homologous to a glycosyltransferase (Accession No. NP_696276.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:244 (380 amino acids) has about 88% identity from amino acids 1-380 with a protein from *Lactobacillus gasseri* that is a UDP-N-acetylglucosamine 2-epimerase (Accession No.
20 ZP_00046464.1), about 84% identity from amino acids 1-379 with a protein from *Lactobacillus johnsonii* that is homologous to a UDP-N-acetylglucosamine 2-epimerase (Accession No. NP_965402.1), about 70% identity from amino acids 1-379 with a protein from *Streptococcus mutans* that is homologous to a UDP-N-acetylglucosamine 2-epimerase (Accession No. NP_721794.1), about 68% identity from amino acids 4-364
25 with a protein from *Lactobacillus plantarum* that is a UDP-N-acetylglucosamine 2-epimerase (Accession No. NP_784839.1), and 64% identity from amino acids 1-379 with a protein from *Listeria innocua* that is homologous to a UDP-N-acetylglucosamine 2-epimerase (Accession No. NP_472010.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:246 (399 amino acids) has about 85% identity from amino acids 7-398 with a protein from
30 *Lactobacillus gasseri* that is a UDP-N-acetylglucosamine 2-epimerase (Accession No.

ZP_00046464.1), about 84% identity from amino acids 20-398 with a protein from *Lactobacillus johnsonii* that is homologous to a UDP-N-acetylglucosamine 2-epimerase (Accession No. NP_965402.1), about 70% identity from amino acids 20-398 with a protein from *Streptococcus mutans* that is homologous to a UDP-N-acetylglucosamine 2-epimerase (Accession No. NP_721794.1), about 68% identity from amino acids 23-383 with a protein from *Lactobacillus plantarum* that is a UDP-N-acetylglucosamine 2-epimerase (Accession No. NP_784839.1), and 64% identity from amino acids 20-398 with a protein from *Listeria innocua* that is homologous to a UDP-N-acetylglucosamine 2-epimerase (Accession No. NP_472010.1).

10 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:248 (232 amino acids) has about 74% identity from amino acids 1-232 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965530.1), about 74% identity from amino acids 1-232 with a protein from *Lactobacillus gasseri* that is in the mannosyltransferase OCH1 and related enzyme family (Accession No. ZP_00047224.1),
15 about 40% identity from amino acids 1-208 with a protein from *Clostridium thermocellum* that is in the mannosyltransferase OCH1 and related enzyme family (Accession No. ZP_00060271.1), about 35% identity from amino acids 2-213 with a protein from *Lactobacillus gasseri* that is in the mannosyltransferase OCH1 and related enzyme family (Accession No. ZP_00045846.1), and 38% identity from amino acids 1-
20 211 with a protein from *Lactococcus lactis* subsp. *cremoris* that is an EpsQ protein (Accession No. gb|AAP32730.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:250 (387 amino acids) has about 70% identity from amino acids 1-379 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965577.1), about 77% identity
25 from amino acids 1-315 with a protein from *Lactobacillus gasseri* that is a glycosyltransferase (Accession No. ZP_00047202.1), about 53% identity from amino acids 1-374 with a protein from *Lactobacillus plantarum* that is a glycosyltransferase (Accession No. NP_784929.1), about 49% identity from amino acids 1-386 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is a
30 glycosyltransferase (Accession No. ZP_00063751.1), and 48% identity from amino acids

1-374 with a protein from *Enterococcus faecium* that is a glycosyltransferase (Accession No. ZP_00036762.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:252 (156 amino acids) has about 62% identity from amino acids 26-152 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964097.1), about 52% identity from amino acids 1-152 with a protein from *Lactobacillus gasseri* that is a glycosyltransferase (Accession No. ZP_00047062.1), about 56% identity from amino acids 50-152 with a protein from *Streptococcus mutans* that is homologous to a glycosyltransferase (Accession No. NP_721791.1), about 40% identity from amino acids 36-149 with a protein from *Clostridium tetani* that is an N-acetylglucosaminyltransferase (Accession No. NP_781499.1), and 37% identity from amino acids 44-152 with a protein from *Bacillus subtilis* that is homologous to a cellulose synthase (Accession No. NP_388311.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:254 (490 amino acids) has about 100% identity from amino acids 11-490 with a protein from *Lactobacillus acidophilus* that is a sucrose phosphorylase (Accession No. gb|AAO21861.1), about 69% identity from amino acids 11-490 with a protein from *Lactobacillus acidophilus* that is a sucrose phosphorylase (Accession No. gb|AAO21868.1), about 68% identity from amino acids 11-490 with a protein from *Lactobacillus johnsonii* that is a sucrose phosphorylase (Accession No. NP_964279.1), about 63% identity from amino acids 11-490 with a protein from *Streptococcus mutans* that is a sucrose phosphorylase (EC 2.4.1.7) (Accession No. pir|A27626), and 63% identity from amino acids 11-489 with a protein from *Streptococcus mutans* that is a gtfA protein (Accession No. pir|BWSOGM).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:256 (548 amino acids) has about 69% identity from amino acids 8-546 with a protein from *Lactobacillus gasseri* that is a membrane protein involved in the export of O-antigen and teichoic acid (Accession No. ZP_00047298.1), about 67% identity from amino acids 8-546 with a protein from *Lactobacillus johnsonii* that is an export protein for polysaccharides and teichoic acids (Accession No. NP_964533.1), about 42% identity from amino acids 5-546 with a protein from *Enterococcus faecalis* that is a

polysaccharide biosynthesis family protein (Accession Nos. NP_814421.1), about 42% identity from amino acids 17-546 with a protein from *Lactobacillus plantarum* that is an integral membrane protein (Accession No. NP_784959.1), and 38% identity from amino acids 13-547 with a protein from *Streptococcus mutans* that is homologous to a
5 membrane protein (Accession No. NP_722009.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:258 (363 amino acids) has about 64% identity from amino acids 1-363 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965541.1), about 62% identity from amino acids 1-363 with a protein from *Lactobacillus gasseri* that is a
10 glycosyltransferase (Accession No. ZP_00047215.1), about 41% identity from amino acids 1-363 with a protein from *Bacillus anthracis* that is a glycosyltransferase, group 1 family protein (Accession No. NP_847817.1), about 40% identity from amino acids 1-363 with a protein from *Bacillus anthracis* that is a glycosyltransferase group 1 protein (Accession No. NP_653889.1), and 39% identity from amino acids 1-363 with a protein
15 from *Bacillus cereus* that is a glycosyltransferase (Accession No. NP_835081.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:260 (556 amino acids) has about 74% identity from amino acids 6-555 with a protein from *Lactobacillus gasseri* that is a glycosidase (Accession No. ZP_00047085.1), about 73% identity from amino acids 6-553 with a hypothetical protein from *Lactobacillus johnsonii*
20 (Accession No. NP_964227.1), about 50% identity from amino acids 8-553 with a protein from *Lactobacillus plantarum* that is an alpha-glucosidase (Accession No. NP_784006.1), about 35% identity from amino acids 7-556 with a protein from *Bacillus halodurans* that is an oligo-1,6-glucosidase (Accession No. NP_243769.1), and 34% identity from amino acids 9-553 with a protein from *Bacillus cereus* that is an oligo-1,6-
25 glucosidase (oligosaccharide alpha-1,6-glucosidase) (Accession No. sp|P21332|O16G_BACCE).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:262 (759 amino acids) has about 75% identity from amino acids 1-757 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964589.1), about 52% identity
30 from amino acids 1-732 with a protein from *Clostridium acetobutylicum* that is an alpha-glucosidase (Accession No. NP_347719.1), about 51% identity from amino acids 1-726

with a protein from *Thermotoga maritima* that is an alpha-xylosidase (Accession No. NP_228120.1), about 49% identity from amino acids 1-724 with a protein from *Bacillus halodurans* (Accession No. NP_242771.1), and 47% identity from amino acids 1-727 with a hypothetical protein from *Escherichia coli* (Accession No. NP_418113.1).

5 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:264 (767 amino acids) has about 69% identity from amino acids 3-766 with a protein from *Lactobacillus johnsonii* that is an alpha-glucosidase (Accession No. NP_965686.1), about 69% identity from amino acids 3-766 with a protein from *Lactobacillus gasseri* that is an alpha-glucosidase (Accession No. ZP_00046641.1), about 64% identity from amino acids
10 5-761 with a protein from *Lactobacillus plantarum* that is an alpha-glucosidase (Accession No. NP_786738.1), about 41% identity from amino acids 15-720 with a protein from *Thermoanaerobacter tengcongensis* that is an alpha-glucosidase (Accession No. NP_621719.1), and 40% identity from amino acids 20-717 with a protein from *Bacillus thermoamyloliquefaciens* that is an alpha-glucosidase II (Accession No.
15 sp|Q9F234|AGL2_BACTQ).

 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:266 (544 amino acids) has about 78% identity from amino acids 6-541 with a protein from *Lactobacillus gasseri* that is a glycosidase (Accession No. ZP_00047077.1), about 77% identity from amino acids 6-541 with a protein from *Lactobacillus johnsonii* that is a
20 glucan 1,6-alpha-glucosidase (Accession No. NP_964235.1), about 63% identity from amino acids 2-542 with a protein from *Enterococcus faecium* that is a glycosidase (Accession No. ZP_00037211.1), about 62% identity from amino acids 9-542 with a protein from *Enterococcus faecalis* that is homologous to a glucan 1,6-alpha-glucosidase (Accession No. NP_815069.1), and 61% identity from amino acids 9-543 with a protein
25 from *Streptococcus pneumoniae* that is a glucan 1,6-alpha-glucosidase (Accession No. NP_344876.1).

 A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:268 (1004 amino acids) has about 48% identity from amino acids 4-1003 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964131.1), about 48% identity
30 from amino acids 1-1003 with a protein from *Lactobacillus gasseri* that is an alpha-glucosidase (Accession No. ZP_00047030.1), about 32% identity from amino acids 12-

1001 with a protein from *Enterococcus faecalis* that is a glycosyl hydrolase (Accession No. NP_815521.1), about 30% identity from amino acids 98-1000 with a protein from *Bacteroides thetaiotaomicron* that is an alpha-xylosidase (Accession No. NP_812081.1), and 25% identity from amino acids 11-995 with a hypothetical protein from *Clostridium*
5 *perfringens* (Accession No. NP_561962.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:270 (570 amino acids) has about 77% identity from amino acids 17-568 with a protein from *Lactobacillus gasseri* that is a glycosidase (Accession No. ZP_00045981.1), about 77% identity from amino acids 17-568 with a protein from *Lactobacillus johnsonii* that is a
10 trehalose-6-phosphate hydrolase (Accession No. NP_964610.1), about 66% identity from amino acids 18-566 with a protein from *Lactobacillus plantarum* that is an alpha, alpha-phosphotrehalase (Accession No. NP_784081.1), about 57% identity from amino acids 23-568 with a protein from *Streptococcus pneumoniae* that is a dextran glucosidase (Accession No. NP_359290.1), and 57% identity from amino acids 23-568 with a protein
15 from *Streptococcus pneumoniae* that is homologous to a dextran glucosidase (DexS) (Accession No. NP_346315.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:272 (638 amino acids) has about 56% identity from amino acids 8-621 with a protein from *Streptococcus mutans* that is homologous to a 1,4-alpha-glucan branching enzyme
20 (Accession No. NP_721883.1), about 57% identity from amino acids 8-619 with a protein from *Streptococcus agalactiae* that is a 1,4-alpha-glucan branching enzyme (Accession No. sp|Q8E5V8|GLGB_STRA3), about 57% identity from amino acids 8-619 with a protein from *Streptococcus agalactiae* that is a 1,4-alpha-glucan branching enzyme (Accession No. NP_687868.1), about 56% identity from amino acids 8-621 with
25 a protein from *Streptococcus pneumoniae* that is a 1,4-alpha-glucan branching enzyme (Accession No. NP_345592.1), and 56% identity from amino acids 8-621 with a protein from *Streptococcus pneumoniae* that is a 1,4-alpha-glucan branching enzyme (Accession No. NP_358623.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:274
30 (573 amino acids) has about 76% identity from amino acids 1-572 with a protein from *Lactobacillus johnsonii* that is a maltogenic amylase or neopullulanase (Accession No.

NP_964228.1), about 75% identity from amino acids 1-572 with a protein from *Lactobacillus gasseri* that is a glycosidase (Accession No. ZP_00047084.1), about 54% identity from amino acids 56-571 with a protein from *Enterococcus faecium* that is a glycosidase (Accession No. ZP_00036988.1), about 49% identity from amino acids 1-570 with a protein from *Enterococcus faecalis* that is a glycosyl hydrolase (Accession No. NP_815068.1), and 50% identity from amino acids 1-540 with a protein from *Lactococcus lactis* subsp. *lactis* that is a neopullulanase (Accession No. NP_267838.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:276 (1185 amino acids) has about 39% identity from amino acids 284-1008 with a protein from *Bacillus cereus* that is a pullulanase (Accession No. NP_832487.1), about 40% identity from amino acids 284-1008 with a protein from *Bacillus cereus* that is homologous to a pullulanase (Accession No. NP_979065.1), about 40% identity from amino acids 284-1008 with a protein from *Bacillus anthracis* that is homologous to a pullulanase (Accession No. NP_845079.1), about 41% identity from amino acids 306-1008 with a protein from *Bacillus anthracis* that is an alpha-amylase (Accession No. NP_656611.1), and 38% identity from amino acids 284-976 with a protein from *Anaerobranca horikoshii* that is a pullulanase (Accession No. gb|AAP45012.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:278 (589 amino acids) has about 42% identity from amino acids 5-548 with a protein from *Lactococcus lactis* subsp. *lactis* that is an amylopullulanase (Accession Nos. NP_266857.1; NC_002662), about 41% identity from amino acids 1-546 with a protein from *Lactobacillus plantarum* that is an alpha-amylase (Accession No. NP_783889.1), about 38% identity from amino acids 3-558 with a protein from *Clostridium perfringens* that is an amylopullulanase (Accession No. NP_560982.1), about 70% identity from amino acids 198-441 with a protein from *Lactobacillus delbrueckii* subsp. *lactis* that is a glycosyl hydrolase (Accession No. gb|AAQ06973.1), and 37% identity from amino acids 73-547 with a protein from *Desulfitobacterium hafniense* that is a glycosidase (Accession No. ZP_00100175.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:280 (435 amino acids) has about 22% identity from amino acids 78-384 with an environmental sequence (Accession No. gb|EAH69409.1), about 23% identity from

amino acids 53-387 with a hypothetical protein from *Plasmodium falciparum* (Accession No. NP_701320.1), about 22% identity from amino acids 59-382 with a hypothetical protein from *Plasmodium falciparum* (Accession No. NP_701961.1), about 22% identity from amino acids 56-386 with a hypothetical protein from *Plasmodium falciparum* (Accession No. NP_473199.1), and about 24% identity from amino acids 61-336 with a protein from *Plasmodium yoelii yoelii* that is homologous to a CCAAT-box DNA binding protein subunit B (Accession No. gb|EAA22696.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:282 (382 amino acids) has about 54% identity from amino acids 1-382 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965524.1), about 60% identity from amino acids 115-382 with a protein from *Lactobacillus gasseri* that is a protein involved in sex pheromone biosynthesis (Accession No. ZP_00046368.1), about 41% identity from amino acids 1-382 with a protein from *Lactobacillus plantarum* that is a lipoprotein precursor (Accession No. NP_784816.1), about 38% identity from amino acids 53-374 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is a protein involved in sex pheromone biosynthesis (Accession No. ZP_00063694.1), and 35% identity from amino acids 1-379 with a protein from *Listeria innocua* (Accession No. NP_471203.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:284 (173 amino acids) has about 52% identity from amino acids 1-161 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964736.1), about 51% identity from amino acids 1-161 with a hypothetical protein from *Lactobacillus gasseri* (Accession No. ZP_00047405.1), about 25% identity from amino acids 21-159 with a hypothetical protein from *Oenococcus oeni* (Accession No. ZP_00070369.1), about 28% identity from amino acids 4-74 with an environmental sequence (Accession No. gb|EAF86579.1), and 24% identity from amino acids 63-160 with a protein from *Listeria innocua* that is homologous to a cell surface protein (Accession No. NP_471613.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:286 (414 amino acids) has about 65% identity from amino acids 21-404 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_964852.1), about 64% identity from amino acids 21-404 with a protein from *Lactobacillus gasseri* that is a bacterial cell

division membrane protein (Accession No. ZP_00046289.1), about 39% identity from amino acids 23-407 with a protein from *Lactobacillus plantarum* that is a cell division protein FtsW (Accession No. NP_785648.1), about 36% identity from amino acids 48-411 with a protein from *Enterococcus faecalis* that is a cell division protein in the FtsW/RodA/SpoVE family (Accession No. NP_816105.1), and 35% identity from amino acids 48-404 with a protein from *Enterococcus faecium* that is a bacterial cell division membrane protein (Accession No. ZP_00035664.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:288 (151 amino acids) has about 53% identity from amino acids 1-149 with a protein from *Lactobacillus plantarum* that is an integral membrane protein (Accession No. NP_785439.1), about 58% identity from amino acids 18-146 with a protein from *Listeria monocytogenes* (Accession No. NP_465093.1), about 58% identity from amino acids 18-146 with a protein from *Listeria innocua* (Accession No. NP_470939.1), about 48% identity from amino acids 1-149 with a protein from *Enterococcus faecium* that is homologous to a membrane protein (Accession No. ZP_00036546.1), and 49% identity from amino acids 1-147 with a protein from *Enterococcus faecalis* (Accession No. NP_814972.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:290 (451 amino acids) has about 62% identity from amino acids 13-450 with a hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965202.1), about 61% identity from amino acids 13-450 with a protein from *Lactobacillus gasseri* (Accession No. ZP_00046546.1), about 53% identity from amino acids 6-451 with a protein from *Lactobacillus plantarum* that is an integral membrane protein (Accession No. NP_783922.1), about 51% identity from amino acids 13-451 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* (Accession No. ZP_00062829.1), and 51% identity from amino acids 19-451 with a protein from *Oenococcus oeni* (Accession No. ZP_00070095.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:292 (374 amino acids) has about 75% identity from amino acids 1-374 with a protein from *Lactobacillus gasseri* that is homologous to a DNA methylase (Accession No. ZP_00045949.1), about 74% identity from amino acids 1-374 with a hypothetical protein

from *Lactobacillus johnsonii* (Accession No. NP_965048.1), about 53% identity from amino acids 1-373 with a protein from *Lactobacillus plantarum* (Accession No. NP_785327.1), about 52% identity from amino acids 2-373 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is homologous to a DNA methylase (Accession No. ZP_00062777.1), and 50% identity from amino acids 2-373 with a conserved hypothetical protein from *Enterococcus faecalis* (Accession No. NP_814882.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:294 (242 amino acids) has about 79% identity from amino acids 1-238 with a protein from *Lactobacillus johnsonii* that is a tRNA (guanine-N1)-methyltransferase (Accession No. NP_965315.1), about 52% identity from amino acids 1-241 with a protein from *Lactobacillus plantarum* that is a tRNA (guanine-N1)-methyltransferase (Accession No. NP_785229.1), about 46% identity from amino acids 1-238 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is a tRNA methyltransferase (Accession No. ZP_00064008.1), 51% identity from amino acids 1-238 with a protein from *Bacillus cereus* that is a tRNA (guanine-N1)-methyltransferase (Accession No. NP_833560.1), and 51% identity from amino acids 1-236 with a protein from *Bacillus anthracis* that is a tRNA (guanine-N1)-methyltransferase (Accession No. NP_657810.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:296 (667 amino acids) has about 83% identity from amino acids 24-666 with a protein from *Lactobacillus johnsonii* that is a threonyl-tRNA synthetase (Accession No. NP_965452.1), about 83% identity from amino acids 24-666 with a protein from *Lactobacillus gasseri* that is a threonyl-tRNA synthetase (Accession No. ZP_00046734.1), about 61% identity from amino acids 25-665 with a protein from *Lactobacillus plantarum* that is a threonine-tRNA ligase 1 (Accession No. NP_785120.1), about 57% identity from amino acids 28-665 with a protein from *Streptococcus mutans* that is homologous to a threonyl-tRNA synthetase (Accession No. NP_721923.1), and 56% identity from amino acids 28-665 with a protein from *Lactococcus lactis* subsp. *lactis* that is a threonyl-tRNA synthetase (Accession No. NP_268068.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:298 (706 amino acids) has about 24% identity from amino acids 123-511 with a protein from *Lactobacillus plantarum* that is a cell surface protein precursor (Accession No. NP_786268.1), about 29% identity from amino acids 220-510 with a protein from

5 *Enterococcus faecium* that is an autotransporter adhesin (Accession No. ZP_00035995.1), about 23% identity from amino acids 181-503 with a protein from *Fusobacterium nucleatum* subsp. *nucleatum* that is a hemolysin (Accession No. NP_603198.1), about 19% identity from amino acids 26-260 with a protein from *Staphylococcus aureus* subsp. *aureus* that is a fibrinogen-binding protein (Accession No. NP_645581.1), and 25%

10 identity from amino acids 383-509 with a hypothetical protein from *Microbulbifer degradans* (Accession No. ZP_00064879.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:300 (438 amino acids) has about 31% identity from amino acids 116-297 with a hypothetical protein from *Streptococcus mutans* (Accession No. NP_722210.1), about 50% identity

15 from amino acids 116-188 with a protein from *Lactobacillus salivarius* subsp. *salivarius* (Accession No. gb|AAM61773.1), about 29% identity from amino acids 126-220 with a protein from *Streptococcus agalactiae* that is homologous to a bacteriocin transport accessory protein (Accession No. NP_687482.1), 24% identity from amino acids 125-338 with a protein from *Bradyrhizobium japonicum* that is a thioredoxin (Accession No.

20 NP_767234.1), and 27% identity from amino acids 123-201 with a protein from *Bacillus anthracis* (Accession No. NP_052783.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:302 (372 amino acids) has about 55% identity from amino acids 11-371 with a protein from *Leuconostoc mesenteroides* subsp. *mesenteroides* that is a methionine synthase II

25 (cobalamin-independent) protein (Accession No. ZP_00064070.1), about 47% identity from amino acids 5-372 with a protein from *Lactobacillus gasseri* that is a methionine synthase II (cobalamin-independent) protein (Accession No. ZP_00046311.1), about 46% identity from amino acids 7-372 with a hypothetical protein from *Chlamydomonas pneumoniae* (Accession No. NP_224351.1), 44% identity from amino acids 4-372 with a

30 hypothetical protein from *Lactobacillus johnsonii* (Accession No. NP_965623.1), and 45% identity from amino acids 9-372 with a protein from *Oenococcus oeni* that is a

methionine synthase II (cobalamin-independent) protein (Accession No. ZP_00069898.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:304 (157 amino acids) has about 87% identity from amino acids 1-157 with a protein from *Lactobacillus johnsonii* that is an autoinducer-2 production protein LuxS (Accession No. NP_965624.1), about 87% identity from amino acids 1-157 with a protein from *Lactobacillus gasseri* that is a LuxS protein involved in autoinducer AI2 synthesis (Accession No. ZP_00046310.1), about 76% identity from amino acids 4-157 with a protein from *Streptococcus bovis* that is a LuxS autoinducer 2 synthase (Accession No. dbj|BAD06876.1), 77% identity from amino acids 1-157 with a protein from *Lactobacillus plantarum* that is an autoinducer production protein (Accession No. NP_784522.1), and 73% identity from amino acids 4-157 with a protein from *Streptococcus pyogenes* that is an autoinducer-2 production protein (Accession No. NP_269689.1).

A Gapped BlastP amino acid sequence alignment showed that SEQ ID NO:306 (599 amino acids) has about 37% identity from amino acids 225-343 with a protein from *Lactobacillus crispatus* that is an S-layer protein (Accession No. emb|CAA07708.1), about 34% identity from amino acids 225-343 with a protein from *Lactobacillus crispatus* that is a surface layer protein (Accession No. gb|AAB58734.1), about 33% identity from amino acids 225-343 with a protein from *Lactobacillus crispatus* that is a silent surface layer protein (Accession No. dbj|BAC76687.1), about 34% identity from amino acids 225-343 with a protein from *Lactobacillus crispatus* that is homologous to a silent surface layer protein (Accession No. gb|AAF68972.1), and about 30% identity from amino acids 137-284 with a protein from *Lactobacillus helveticus* that is an extracellular proteinase (EC 3.4.21.-) (prtY) (Accession No. pir|JC7306).

Example 2. PFAM Results for Amino Acid Sequences

SEQ ID NO:2 contains a predicted Lipoprotein_4 domain located from about amino acids 25 to 306, and is a member of the Periplasmic solute binding protein family (SBP_bac_9)(PFAM Accession PF01297).

SEQ ID NO:10 contains a predicted Glyco_hydro_32 domain located from about amino acids 24 to 409, and is a member of the Glycosyl hydrolases family 32 (Glyco_hydro_32)(PFAM Accession PF00251).

5 SEQ ID NO:62 contains a predicted SLAP domain located from about amino acids 1 to 456, and is a member of the Bacterial surface layer protein family (SLAP) (PFAM Accession PF03217).

SEQ ID NO:82 contains a predicted Amidase_2 domain located from about amino acids 59 to 208, and is a member of the N-acetylmuramoyl-L-alanine amidase (Amidase_2) family (PFAM Accession PF01510).

10 SEQ ID NO:92 contains a predicted FTSW_RODA_SPOVE domain located from about amino acids 15 to 388, and is a member of the Cell cycle protein family (FTSW_RODA_SPOVE) (PFAM Accession PF01098).

SEQ ID NO:94 contains a predicted Mur_ligase domain located from about amino acids 43 to 293, and a predicted Mur_ligase_C domain from about amino acids
15 301-390, and is a member of the Mur ligase, catalytic domain family (Mur_ligase) (PFAM Accession PF01225) and the Mur ligase, glutamate ligase domain family (Mur_ligase_C) (PFAM Accession PF02875).

SEQ ID NO:98 contains a predicted Mur_ligase_C domain located from about amino acids 365 to 454, and is a member of the Mur ligase, glutamate ligase domain
20 family (Mur_ligase_C) (PFAM Accession PF02875).

SEQ ID NO:100 contains a predicted Mur_ligase domain located from about amino acids 48 to 309, and a predicted Mur_ligase_C domain from about amino acids 317-394, and is a member of the Mur ligase, catalytic domain family (Mur_ligase) (PFAM Accession PF01225) and the Mur ligase, glutamate ligase domain family
25 (Mur_ligase_C) (PFAM Accession PF02875).

SEQ ID NO:102 contains a predicted Glyco_transf_28 domain located from about amino acids 2 to 287, and is a member of the Glycosyltransferase family 28 N-terminal domain (Glyco_transf_28) (PFAM Accession PF03033).

SEQ ID NO:104 contains a predicted Glycos_transf_4 domain located from about
30 amino acids 82 to 254, and is a member of the Glycosyl transferase family (Glycos_transf_4) (PFAM Accession PF00953).

SEQ ID NO:106 contains a predicted Amidase_4 domain located from about amino acids 63 to 212, and is a member of the Mannosyl-glycoprotein endo-beta-N-acetylglucosamidase family (Amidase_4) (PFAM Accession PF01832).

5 SEQ ID NO:108 contains a predicted Amidase_4 domain located from about amino acids 43 to 196, and is a member of the Mannosyl-glycoprotein endo-beta-N-acetylglucosamidase family (Amidase_4) (PFAM Accession PF01832).

SEQ ID NO:110 contains a predicted LysM domain located from about amino acids 110 to 153, and is a member of the LysM domain family (LysM) (PFAM Accession PF01476).

10 SEQ ID NO:112 contains a predicted Dala_Dala_ligas (Dala_Dala_lig_N) domain located from about amino acids 5 to 343, and is a member of the D-ala D-ala ligase N terminus family (Dala_Dala_lig_N) (PFAM Accession PF01820).

SEQ ID NO:116 contains a predicted Mur_ligase domain located from about amino acids 36 to 303, and is a member of the Mur ligase, catalytic domain family
15 (Mur_ligase) (PFAM Accession PF01225).

SEQ ID NO:118 contains a predicted Peptidase_S11 domain located from about amino acids 25 to 321, and is a member of the D-alanyl-D-alanine carboxypeptidase family (Peptidase_S11) (PFAM Accession PF00768).

SEQ ID NO:120 contains a predicted EPSP_synthase domain located from about
20 amino acids 16 to 419, and is a member of the EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase) family (EPSP_synthase) (PFAM Accession PF00275).

SEQ ID NO:122 contains a predicted NTP_transferase domain located from about amino acids 4 to 233, and is a member of the Bacterial transferase hexapeptide (three repeats) family (Hexapep) (PFAM Accession PF00132).

25 SEQ ID NO:124 contains a predicted Prenyltransf (UPP_synthetase) domain located from about amino acids 14 to 238, and is a member of the Putative undecaprenyl diphosphate synthase family (Prenyltransf) (PFAM Accession PF01255).

SEQ ID NO:126 contains a predicted Glycos_transf_4 domain located from about amino acids 74 to 240, and is a member of the Glycosyl transferase family
30 (Glycos_transf_4) (PFAM Accession PF00953).

SEQ ID NO:132 contains a predicted Transpeptidase domain located from about amino acids 331 to 693, and is a member of the Penicillin binding protein transpeptidase domain family (Transpeptidase) (PFAM Accession PF00905).

5 SEQ ID NO:134 contains a predicted Transglycosyl domain located from about amino acids 82 to 251, and a predicted Transpeptidase domain located from about amino acids 336 to 640, and is a member of the Transglycosylase family (Transgly)(Transglycosyl) (PFAM Accession PF00912), as well as the Penicillin binding protein transpeptidase domain family (Transpeptidase) (PFAM Accession PF00905).

10 SEQ ID NO:138 contains a predicted Transglycosyl domain located from about amino acids 70 to 242, and a predicted Transpeptidase domain located from about amino acids 324 to 629, and is a member of the Transglycosylase family (Transgly)(Transglycosyl) (PFAM Accession PF00912), as well as the Penicillin binding protein transpeptidase domain family (Transpeptidase) (PFAM Accession PF00905).

15 SEQ ID NO:146 contains a predicted Transpeptidase domain located from about amino acids 259 to 593, and is a member of the Penicillin binding protein transpeptidase domain family (Transpeptidase) (PFAM Accession PF00905).

SEQ ID NO:148 contains a predicted AMP-binding domain located from about amino acids 30 to 426, and is a member of the AMP-binding enzyme family (AMP-binding) (PFAM Accession PF00501).

20 SEQ ID NO:156 contains a predicted Polysacc_synt domain located from about amino acids 3 to 269, and is a member of the Polysaccharide biosynthesis protein family (Polysacc_synt) (PFAM Accession PF01943).

25 SEQ ID NO:158 contains a predicted GLF domain located from about amino acids 1 to 154, and is a member of the UDP-galactopyranose mutase family (GLF) (PFAM Accession PF03275).

SEQ ID NO:164 contains a predicted Glycos_transf_2 domain located from about amino acids 7 to 179, and is a member of the Glycosyl transferase family (Glycos_transf_2) (PFAM Accession PF00535).

30 SEQ ID NO:170 contains a predicted Glycos_transf_2 domain located from about amino acids 5 to 171, and is a member of the Glycosyl transferase family (Glycos_transf_2) (PFAM Accession PF00535).

SEQ ID NO:174 contains a predicted Bac_transf (Bact_transf) domain located from about amino acids 24 to 217, and is a member of the Bacterial sugar transferase family (Bac_transf) (Bact_transf) (PFAM Accession PF02397).

5 SEQ ID NO:180 contains a predicted Wzz domain located from about amino acids 9 to 186, and is a member of the Chain length determinant protein family (Wzz) (PFAM Accession PF02706).

SEQ ID NO:190 contains a predicted NLPC_P60 domain located from about amino acids 141 to 249, and is a member of the NlpC/P60 family (NLPC_P60) (PFAM Accession PF00877).

10 SEQ ID NO:194 contains a predicted NLPC_P60 domain located from about amino acids 152 to 260, and is a member of the NlpC/P60 family (NLPC_P60) (PFAM Accession PF00877).

SEQ ID NO:196 contains a predicted NLPC_P60 domain located from about amino acids 77 to 182, and is a member of the NlpC/P60 family (NLPC_P60) (PFAM
15 Accession PF00877).

SEQ ID NO:208 contains a predicted Ribonuc_red_sm domain located from about amino acids 1 to 283, and is a member of the Ribonucleotide reductase, small chain family (Ribonuc_red_sm) (PFAM Accession PF00268).

SEQ ID NO:214 contains a predicted DUF59 domain located from about amino
20 acids 9 to 83, and is a member of the Domain of unknown function DUF59 family (DUF59) (PFAM Accession PF01883).

SEQ ID NO:216 contains a predicted UPF0051 domain located from about amino acids 2 to 73, and is a member of the Uncharacterized protein family (UPF0051) (PFAM Accession PF01458).

25 SEQ ID NO:218 contains a predicted ABC_tran domain located from about amino acids 35 to 73, and is a member of the ABC transporter family (ABC_tran) (PFAM Accession PF00005).

SEQ ID NO:226 contains predicted ABC_tran domains located from about amino acids 29 to 232, and from about amino acids 347 to 512, and is a member of the ABC
30 transporter family (ABC_tran) (PFAM Accession PF00005).

SEQ ID NO:236 contains a predicted Glycos_transf_2 domain located from about amino acids 8 to 171, and is a member of the Glycosyl transferase family (Glycos_transf_2) (PFAM Accession PF00535).

5 SEQ ID NO:238 contains a predicted Polysacc_synt domain located from about amino acids 4 to 273, and is a member of the Polysaccharide biosynthesis protein family (Polysacc_synt) (PFAM Accession PF01943).

SEQ ID NO:242 contains a predicted Glycos_transf_1 domain located from about amino acids 57 to 233, and is a member of the Glycosyl transferases group 1 family (Glycos_transf_1) (PFAM Accession PF00534).

10 SEQ ID NO:244 contains a predicted Epimerase_2 domain located from about amino acids 45 to 365, and is a member of the UDP-N-acetylglucosamine 2-epimerase family (Epimerase_2) (PFAM Accession PF02350).

SEQ ID NO:246 contains a predicted Epimerase_2 domain located from about amino acids 64 to 384, and is a member of the UDP-N-acetylglucosamine 2-epimerase
15 family (Epimerase_2) (PFAM Accession PF02350).

SEQ ID NO:250 contains a predicted Glycos_transf_1 domain located from about amino acids 189 to 359, and is a member of the Glycosyl transferases group 1 family (Glycos_transf_1) (PFAM Accession PF00534).

SEQ ID NO:252 contains a predicted Glycos_transf_2 domain located from about
20 amino acids 51 to 152, and is a member of the Glycosyl transferase family (Glycos_transf_2) (PFAM Accession PF00535).

SEQ ID NO:258 contains a predicted Glycos_transf_1 domain located from about amino acids 174 to 341, and is a member of the Glycosyl transferases group 1 family (Glycos_transf_1) (PFAM Accession PF00534).

25 SEQ ID NO:260 contains a predicted Alpha-amylase domain located from about amino acids 18 to 412, and is a member of the Alpha amylase, catalytic domain family (Alpha-amylase) (PFAM Accession PF00128).

SEQ ID NO:262 contains a predicted Glyco_hydro_31 domain located from about amino acids 110 to 757, and is a member of the Glycosyl hydrolases family 31
30 (Glyco_hydro_31) (PFAM Accession PF01055).

SEQ ID NO:264 contains a predicted Glyco_hydro_31 domain located from about amino acids 83 to 757, and is a member of the Glycosyl hydrolases family 31 (Glyco_hydro_31) (PFAM Accession PF01055).

5 SEQ ID NO:266 contains a predicted Alpha-amylase domain located from about amino acids 18 to 410, and is a member of the Alpha amylase, catalytic domain family (Alpha-amylase) (PFAM Accession PF00128).

SEQ ID NO:268 contains a predicted Glyco_hydro_31 domain located from about amino acids 68 to 682, and is a member of the Glycosyl hydrolases family 31 (Glyco_hydro_31) (PFAM Accession PF01055).

10 SEQ ID NO:270 contains a predicted Alpha-amylase domain located from about amino acids 28 to 429, and is a member of the Alpha amylase, catalytic domain family (Alpha-amylase) (PFAM Accession PF00128).

SEQ ID NO:272 contains a predicted Isoamylase_N domain located from about amino acids 23 to 109, and an Alpha-amylase domain located from about amino acids
15 145 to 495, and is a member of the Isoamylase N-terminal domain family (Isoamylase_N) (PFAM Accession PF02922) and the Alpha amylase, catalytic domain family (Alpha-amylase) (PFAM Accession PF00128).

SEQ ID NO:274 contains a predicted Alpha-amylase_N domain located from about amino acids 1 to 121, and an Alpha-amylase domain located from about amino
20 acids 140 to 503, and is a member of the Alpha amylase, catalytic domain family (Alpha-amylase) (PFAM Accession PF00128) and the Alpha amylase, N-terminal ig-like domain family (Alpha-amylase_N) (PFAM Accession PF02903).

SEQ ID NO:276 contains a predicted Alpha-amylase domain located from about amino acids 548 to 926, and is a member of the Alpha amylase, catalytic domain family
25 (Alpha-amylase) (PFAM Accession PF00128).

SEQ ID NO:278 contains a predicted Alpha-amylase domain located from about amino acids 133 to 505, and is a member of the Alpha amylase, catalytic domain family (Alpha-amylase) (PFAM Accession PF00128).

SEQ ID NO:286 contains a predicted FTSW_RODA_SPOVE domain located
30 from about amino acids 29 to 405, and is a member of the Cell cycle protein family (FTSW_RODA_SPOVE) (PFAM Accession PF01098).

SEQ ID NO:292 contains a predicted UPF0020 domain located from about amino acids 163 to 368, and is a member of the Putative RNA methylase family UPF0020 (UPF0020) (PFAM Accession PF01170).

5 SEQ ID NO:294 contains a predicted tRNA_m1G_MT domain located from about amino acids 21 to 226, and is a member of the tRNA (Guanine-1)-methyltransferase (tRNA_m1G_MT) (PFAM Accession PF01746).

10 SEQ ID NO:296 contains a predicted TGS domain located from about amino acids 22 to 85, a predicted tRNA-synt_2b domain located from about amino acids 283 to 438, and a predicted HGTP_anticodon domain located from about amino acids 562 to 659, and is a member of the tRNA synthetase class II core domain family (G, H, P, S and T) (tRNA-synt_2b) (PFAM Accession PF00587), the Anticodon binding domain family (HGTP_anticodon) (PFAM Accession PF03129), and the TGS domain family (TGS) (PFAM Accession PF02824).

15 SEQ ID NO:304 contains a predicted LuxS domain located from about amino acids 2 to 155, and is a member of the LuxS protein family (LuxS) (PFAM Accession PF02664).

Example 3. Identification of Sequences Involved in Cell Adhesion

20 The ability of microorganisms to adhere to mucosal surfaces can provide a distinct advantage when establishing residence in the gastrointestinal tract. Lactobacilli are normal components of the intestinal microbiota, although the molecular mechanisms by which these organisms attach to the epithelium have not yet been fully characterized. In order to identify genes potentially involved with adhesion in *L. acidophilus* NCFM, the complete genomic sequence was analyzed and open reading frames (ORFs) similar to
25 genes previously shown to be involved with adhesion were selected, including two streptococcal R28 homologs (SEQ ID NO:76 and SEQ ID NO:78, designated as ORF 1633 and ORF 1634, respectively in Figure 1), a fibronectin binding protein (FpbA)(SEQ ID NO:58), and a mucin binding protein (Mub) (SEQ ID NO:18). To determine their
30 impact on adhesion, these genes were targeted for insertional inactivation using the integration tools and strategy described by (Russell and Klaenhammer (2001) *Appl. Environ. Microbiol.* 67:4361-4364). Due to the interactive nature of bacterial surface

components with adhesion, a strain containing an inactivated surface layer protein (SlpA) (SEQ ID NO:60) was also evaluated for adhesive properties. All mutants were assessed for their adhesive properties on Caco-2 cells in comparison to *L. acidophilus* NCFM LacL⁻ which was used as an antibiotic control and designated as wild type. Caco-2 cells
5 express many of the markers associated with normal small intestine villus cells and are commonly used to study bacterial adherence.

The two R28 homolog mutants, SEQ ID NO:76 and SEQ ID NO:78, did not show reproducible decreases in adhesion (see Figure 1). SlpA (SEQ ID NO:60), the surface layer mutant, showed the highest decrease in adhesion while the fibronectin (SEQ ID
10 NO:58) and mucin binding (SEQ ID NO:18) mutants both had significant decreases in adhesion when compared to the wild type. These data suggest that fibronectin binding protein, surface layer protein, and mucin binding protein contribute to attachment or adherence processes.

15 *Adhesion Assays*

Caco-2 cells were grown on cell-culture treated coverslips for 15 days to achieve proper differentiation and expression of intestinal markers. The monolayers were then treated with a bacterial suspension at a concentration of about 4×10^8 bacteria/ml. Middle log-phase bacterial populations were used grown in MRS with 2.5 µg/ml Em to
20 maintain selection. Bacteria were incubated on the monolayers for 1.5 hr at 37°C in a mixture of MRS and cell line culture medium (Minimum Essential Medium supplemented with 20% Fetal Bovine Serum). Following incubation, the monolayers were washed five times with phosphate-buffered saline (PBS), fixed in methanol, and Gram-stained. The coverslips were then transferred to a microscope slide where the cells
25 were enumerated. For statistical purposes, 17 fields were enumerated in a fixed grid for each coverslip; duplicate coverslips were counted for each experiment. Total counts for each coverslip were used and adhesion was expressed as percent (%) of the control. *L. acidophilus*, NCFM::lacL, harboring pOR128 integrated into the β-galactosidase gene. Integration into lacL was not found to influence adhesion and the control could be
30 propagated under the same antibiotic selection conditions as all the other integrants.

All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and
5 individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

10

THAT WHICH IS CLAIMED:

1. An isolated nucleic acid molecule selected from the group consisting of:
 - a) a nucleic acid molecule comprising the nucleotide sequence of
SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43,
5 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95,
97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131,
133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167,
169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203,
205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239,
10 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275,
277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;
 - b) a nucleic acid molecule comprising a nucleotide sequence having
at least 80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11,
13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59,
15 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107,
109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143,
145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179,
181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215,
217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251,
20 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287,
289, 291, 293, 295, 297, 299, 301, 303, 305 or 307, wherein said nucleotide sequence
encodes a polypeptide that retains activity;
 - c) a nucleic acid molecule that encodes a polypeptide comprising the
amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30,
25 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82,
84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122,
124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158,
160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194,
196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230,
30 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266,

268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306; and,

- d) a nucleic acid molecule that encodes a polypeptide comprising an amino acid sequence having at least 80% sequence identity to the amino acid sequence of
- 5 SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204,
- 10 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, wherein said nucleotide sequence encodes a polypeptide that retains activity; and,
- e) a complement of any of a)-d).

15

2. A vector comprising the nucleic acid molecule of claim 1.

3. The vector of claim 2, further comprising a nucleic acid molecule encoding a heterologous polypeptide.

20

4. A host cell that contains the vector of claim 2.

5. The host cell of claim 4 that is a bacterial host cell.

25

6. An isolated polypeptide selected from the group consisting of:

- a) a polypeptide comprising the amino acid sequence of SEQ ID
- NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134,
- 30 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206,

208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;

b) a polypeptide encoded by the nucleotide sequence of SEQ ID

5 NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 10 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;

c) a polypeptide comprising an amino acid sequence having at least

80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 15 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 20 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and,

d) a polypeptide that is encoded by a nucleotide sequence that is at

least 80% identical to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 25 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 30 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255,

257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

7. The polypeptide of claim 6 further comprising a heterologous amino
5 acid sequence.

8. An antibody that selectively binds to the polypeptide of claim 6.

9. A method for producing a polypeptide comprising culturing the host cell
10 of claim 4 under conditions in which a nucleic acid molecule encoding the polypeptide is expressed, said polypeptide being selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID
NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48,
50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98,
15 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134,
136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170,
172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206,
208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242,
244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278,
20 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;

b) a polypeptide encoded by the nucleotide sequence of SEQ ID
NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47,
49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99,
101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135,
25 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171,
173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207,
209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243,
245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279,
281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;

30 c) a polypeptide comprising an amino acid sequence having at least
80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14,

- 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and,
- d) a polypeptide encoded by a nucleotide sequence having at least
- 80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

10. A method for detecting the presence of a polypeptide in a sample comprising contacting the sample with a compound that selectively binds to a polypeptide and determining whether the compound binds to the polypeptide in the sample; wherein said polypeptide is selected from the group consisting of:

- a) a polypeptide comprising the amino acid sequence of SEQ ID
- NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242,

244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;

b) a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;

c) a polypeptide comprising an amino acid sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and,

d) a polypeptide encoded by a nucleotide sequence having at least 80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

11. The method of claim 10, wherein the compound that binds to the polypeptide is an antibody.

5 12. A method for detecting the presence of a nucleic acid molecule of claim 1 in a sample, comprising the steps of:

- a) contacting the sample with a nucleic acid probe or primer that selectively hybridizes to the nucleic acid molecule; and,
 - b) determining whether the nucleic acid probe or primer binds to a
- 10 nucleic acid molecule in the sample.

13. The method of claim 12, wherein the sample comprises mRNA molecules and is contacted with a nucleic acid probe.

15 14. A method for modulating the immune system of a host, comprising introducing into said host a polypeptide selected from the group consisting of:

- a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;
- 25

- b) a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207,
- 30

209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;

- c) a polypeptide comprising an amino acid sequence having at least
 5 80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182,
 10 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and,
- d) a polypeptide encoded by a nucleotide sequence having at least
 15 80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183,
 20 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

25 15. The method of claim 14, wherein the modulation of said immune system comprises altering the production of host cytokines.

16. The method of claim 15, wherein the modulation of said immune system comprises altering the anti-inflammatory activity.

30

17. A method for modulating the immune system of a host, comprising introducing into said host a microorganism that expresses a polypeptide selected from the group consisting of:

- a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;
- b) a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;
- c) a polypeptide comprising an amino acid sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and,

- d) a polypeptide encoded by a nucleotide sequence having at least 80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

18. A method for altering the expression of a host protein or compound, comprising introducing into said host a polypeptide selected from the group consisting of:

- a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;
- b) a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;

- c) a polypeptide comprising an amino acid sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and,
- d) a polypeptide encoded by a nucleotide sequence having at least 80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

19. The method of claim 18, wherein the host protein to be altered is selected from the group consisting of a cell surface protein, a protein involved in mucin production, a protein involved in cell-cell signaling, a protein involved in host tolerance of commensal bacteria, and a protein that has antimicrobial activity.

20. A method for altering the expression of a host protein or compound, comprising introducing into said host a microorganism that expresses a polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48,

50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98,
 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134,
 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170,
 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206,
 5 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242,
 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278,
 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;

b) a polypeptide encoded by the nucleotide sequence of SEQ ID
 NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, .
 10 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99,
 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135,
 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171,
 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207,
 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243,
 15 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279,
 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;

c) a polypeptide comprising an amino acid sequence having at least
 80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14,
 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62,
 20 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110,
 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146,
 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182,
 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218,
 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254,
 25 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290,
 292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and,

d) a polypeptide encoded by a nucleotide sequence having at least
 80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15,
 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63,
 30 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111,
 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147,

- 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 5 293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

21. A method for treating a gastrointestinal disorder in a subject, comprising introducing into said subject a microorganism comprising a polypeptide selected from the group consisting of:

- 10 a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 15 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;
- b) a polypeptide encoded by the nucleotide sequence of SEQ ID 20 NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 25 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;
- c) a polypeptide comprising an amino acid sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 30 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110,

112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 5 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and,

d) a polypeptide encoded by a nucleotide sequence having at least 80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 10 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 15 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

22. The method of claim 21, wherein the gastrointestinal disorder is selected from the group consisting of inflammatory bowel disease, Crohn's disease, ulcerative colitis, irritable bowel syndrome, diarrhea, antibiotic associated diarrhea, constipation, 20 and small bowel bacterial overgrowth.

23. A method for treating a gastrointestinal disorder in a subject comprising introducing into said subject a polypeptide selected from the group consisting of:

25 a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 30 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242,

244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;

b) a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;

c) a polypeptide comprising an amino acid sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and,

d) a polypeptide encoded by a nucleotide sequence having at least 80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

24. A method for preventing or reducing the occurrence of an infection in a host, comprising introducing into said subject a polypeptide selected from the group consisting of:

- 5 a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 10 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;
- b) a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 15 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 20 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;
- c) a polypeptide comprising an amino acid sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 25 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 30 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254,

256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and,

d) a polypeptide encoded by a nucleotide sequence having at least 80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

25. The method of claim 24, wherein the infection is caused by a pathogen selected from the group consisting of a food-borne pathogen, an opportunistic pathogen, and *Helicobacter pylori*.

26. The method of claim 24, wherein the infection is selected from the group consisting of vaginosis, a yeast infection, and an HIV infection.

27. The method for preventing or reducing the occurrence of an infection in a host, comprising introducing into said subject a microorganism expressing a polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242,

244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;

b) a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;

c) a polypeptide comprising an amino acid sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and,

d) a polypeptide encoded by a nucleotide sequence having at least 80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291,

293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

28. A method for removing a detrimental compound from the gastrointestinal tract of a subject, comprising introducing into said subject a polypeptide selected from the group consisting of:

- a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;
- b) a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;
- c) a polypeptide comprising an amino acid sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254,

256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and,

- d) a polypeptide encoded by a nucleotide sequence having at least 80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

29. The method of claim 28, wherein said compound is selected from the group consisting of a toxin, a mutagen, a bile salt, a fat, and a cholesterol.

30. A method for removing a detrimental compound from the gastrointestinal tract of a subject, comprising introducing into said subject a microorganism expressing a polypeptide selected from the group consisting of:

- a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;
- b) a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99,

101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135,
137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171,
173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207,
209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243,
5 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279,
281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;

c) a polypeptide comprising an amino acid sequence having at least
80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14,
16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62,
10 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110,
112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146,
148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182,
184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218,
220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254,
15 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290,
292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and

d) a polypeptide encoded by a nucleotide sequence having at least
80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15,
17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63,
20 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111,
113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147,
149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183,
185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219,
221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255,
25 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291,
293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

31. The method of claim 30, wherein the compound is selected from the group
consisting of a toxin, a mutagen, a bile salt, a fat, and a cholesterol.

30

32. A method for enhancing the stability of a microorganism comprising introducing a vector into said organism, wherein the vector comprises at least one nucleotide sequence selected from the group consisting of:

- a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;
- b) a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;
- c) a polypeptide comprising an amino acid sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and,

d) a polypeptide encoded by a nucleotide sequence having at least 80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

33. The method of claim 32, wherein said enhanced stability allows said microorganism an increased ability to survive passage through the stomach, small intestine, and/or gastrointestinal tract.

34. The method of claim 32, wherein said enhanced stability allows said microorganism to resist acid and bile in the stomach, small intestine, and/or gastrointestinal tract.

35. The method of claim 32, wherein said enhanced stability allows said microorganism to persist in the gastrointestinal tract.

36. The method of claim 32, wherein said enhanced stability allows said microorganism to withstand stressful conditions that occur during storage.

37. The method of claim 36, wherein said conditions are selected from the group consisting of culturing, freezing, lyophilizing, and drying.

38. The method of claim 36, wherein said enhanced stability allows said microorganism to withstand stressful conditions that occur during production and processing.

39. The method of claim 38, wherein said conditions are selected from the group consisting of changes in temperature, changes in pH, changes in osmolarity, changes in oxidation state, desiccation, mechanical manipulation, and changes in
 5 pressure.

40. A method for enabling a microorganism to possess modified adherence properties, comprising introducing into said microorganism a polypeptide selected from the group consisting of:

10 a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170,
 15 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;

b) a polypeptide encoded by the nucleotide sequence of SEQ ID
 20 NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207,
 25 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;

c) a polypeptide comprising an amino acid sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14,
 30 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110,

112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146,
148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182,
184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218,
220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254,
5 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290,
292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and,

d) a polypeptide encoded by a nucleotide sequence having at least
80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15,
17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63,
10 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111,
113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147,
149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183,
185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219,
221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255,
15 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291,
293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

41. The method of claim 40, wherein said microorganism is able to adhere to
an epithelial cell.

20

42. A method for protecting food from contamination by a microorganism,
comprising contacting said food with a polypeptide selected from the group consisting of:

a) a polypeptide comprising the amino acid sequence of SEQ ID
NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48,
25 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98,
100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134,
136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170,
172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206,
208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242,
30 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278,
280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306;

- b) a polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307;
- 10 c) a polypeptide comprising an amino acid sequence having at least 80% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 15 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, wherein said polypeptide retains activity; and,
- 20 d) a polypeptide encoded by a nucleotide sequence having at least 80% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 25 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307, wherein said polypeptide retains activity.

30

43. A method for modifying the texture of a food product produced by a lactic acid bacteria, comprising introducing into said lactic acid bacteria a vector comprising a nucleic acid sequence selected from the group consisting of:

a) the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17,
5 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65,
67, 69, 71, 73, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111,
113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147,
149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183,
185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219,
10 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255,
257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291,
293, 295, 297, 299, 301, 303, 305 or 307;

b) a nucleotide sequence having at least 80% sequence identity to the
nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31,
15 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 79, 81, 83,
85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123,
125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159,
161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195,
197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231,
20 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267,
269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303,
305 or 307, wherein said polypeptide retains activity;

c) a nucleotide sequence encoding a polypeptide comprising the
amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30,
25 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82,
84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122,
124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158,
160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194,
196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230,
30 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266,

268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306; and,

d) a nucleotide sequence encoding a polypeptide comprising an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306.

44. The method of claim 43, wherein said modifying of said texture comprises viscosifying, thickening, emulsifying, or gelling.

45. A *Lactobacillus acidophilus* bacterial strain with a modified ability for modulating the immune system of a host, as compared to a wild-type *Lactobacillus acidophilus*, wherein said modified ability is due to expression of at least one polypeptide as found in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306.

46. A *Lactobacillus acidophilus* bacterial strain with a modified ability for altering the expression of a host protein or compound, as compared to a wild-type

Lactobacillus acidophilus, wherein said modified ability is due to expression of at least one polypeptide as found in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306.

47. A *Lactobacillus acidophilus* bacterial strain with a modified ability for treating a gastrointestinal disorder in a subject, as compared to a wild-type *Lactobacillus acidophilus*, wherein said modified ability is due to expression of at least one polypeptide as found in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306.

48. A *Lactobacillus acidophilus* bacterial strain with a modified ability for preventing or reducing the occurrence of an infection in a host, as compared to a wild-type *Lactobacillus acidophilus*, wherein said modified ability is due to expression of at least one polypeptide as found in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154,

156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190,
192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226,
228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262,
264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298,
5 300, 302, 304 or 306.

49. A *Lactobacillus acidophilus* bacterial strain with a modified ability for removing a detrimental compound from the gastrointestinal tract of a subject, as compared to a wild-type *Lactobacillus acidophilus*, wherein said modified ability is due
10 to expression of at least one polypeptide as found in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182,
15 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306.

20 50. A *Lactobacillus acidophilus* bacterial strain with a modified ability for enhancing the stability of a microorganism, as compared to a wild-type *Lactobacillus acidophilus*, wherein said modified ability is due to expression of at least one polypeptide as found in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88,
25 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270,
30 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306.

51. A *Lactobacillus acidophilus* bacterial strain with modified adherence properties, as compared to a wild-type *Lactobacillus acidophilus*, wherein said modified ability is due to expression of at least one polypeptide as found in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306.

52. A *Lactobacillus acidophilus* bacterial strain with a modified ability for protecting food from contamination by a microorganism, as compared to a wild-type *Lactobacillus acidophilus*, wherein said modified ability is due to expression of at least one polypeptide as found in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306.

53. A *Lactobacillus acidophilus* bacterial strain with a modified ability for modifying the texture of a food product produced by a lactic acid bacteria, as compared to a wild-type *Lactobacillus acidophilus*, wherein said modified ability is due to expression of at least one polypeptide as found in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64,

66, 68, 70, 72, 74, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110,
112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146,
148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182,
184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218,
5 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254,
256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290,
292, 294, 296, 298, 300, 302, 304 or 306.

1/1

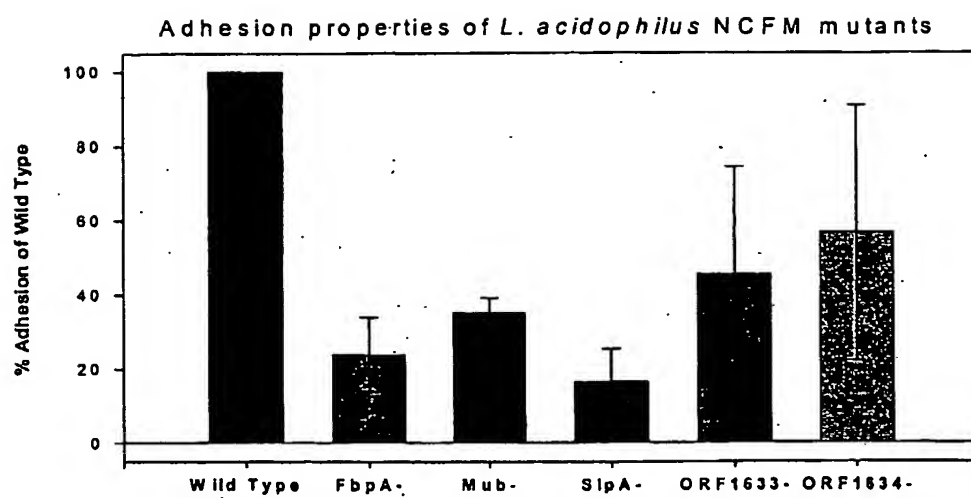


Fig. 1

SEQUENCE LISTING

<110> Klaenhammer, Todd R.
 Russell, William M.
 Alterman, Eric
 Cano, Raul J.
 Hamrick, Alice

<120> Lactobacillus Acidophilus Nucleic Acid
 Sequences Encoding Cell Surface Homologues and Uses
 Therefore

<130> 5051.690

<160> 308

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 918

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1773 - psaA adhesin

<220>

<221> CDS

<222> (1)...(918)

<400> 1

atg ctt ttt tta tgg agg aaa att atg caa aat tgg aaa act aga att	48
Met Leu Phe Leu Trp Arg Lys Ile Met Gln Asn Trp Lys Thr Arg Ile	
1 5 10 15	
aca aaa tta tct ttt ctc ata ggt att gtg gga aca atc atg ctt ttt	96
Thr Lys Leu Ser Phe Leu Ile Gly Ile Val Gly Thr Ile Met Leu Phe	
20 25 30	
gtt tct gct tgt tca aat aat aaa caa tct tca act aat gat ggt aag	144
Val Ser Ala Cys Ser Asn Asn Lys Gln Ser Ser Thr Asn Asp Gly Lys	
35 40 45	
att tcg atc gtt acc tca act aat gtt tat gca gat att gct aag aat	192
Ile Ser Ile Val Thr Ser Thr Asn Val Tyr Ala Asp Ile Ala Lys Asn	
50 55 60	
ata gtt ggt aag tac ggc agt gct aag gca att att aaa aat agt gct	240
Ile Val Gly Lys Tyr Gly Ser Ala Lys Ala Ile Ile Lys Asn Ser Ala	
65 70 75 80	
act gat ccg cat gac ttt gaa cca act act caa gac gct aag gaa tta	288
Thr Asp Pro His Asp Phe Glu Pro Thr Thr Gln Asp Ala Lys Glu Leu	

	85	90	95	
tct ³ agt acc aat att att gta gct aac ggt tta ggc tat gat agc tgg				336
Ser Ser Thr Asn Ile Ile Val Ala Asn Gly Leu Gly Tyr Asp Ser Trp				
	100	105	110	
atg aac aag tta gct agc tca gtt gat aag aag cca gtt tta gtt ggt				384
Met Asn Lys Leu Ala Ser Ser Val Asp Lys Lys Pro Val Leu Val Gly				
	115	120	125	
gaa gag cta atg aag tta aag aaa ggg gct aac cct cat att tgg tac				432
Glu Glu Leu Met Lys Leu Lys Lys Gly Ala Asn Pro His Ile Trp Tyr				
	130	135	140	
agt tta agt atg cca act gag tat gtt gat tat tta gtg aaa cgt tta				480
Ser Leu Ser Met Pro Thr Glu Tyr Val Asp Tyr Leu Val Lys Arg Leu				
	145	150	155	160
tca aaa atc gat tcc aag cac aaa gca tac ttt gaa gct aat ggt aaa				528
Ser Lys Ile Asp Ser Lys His Lys Ala Tyr Phe Glu Ala Asn Gly Lys				
	165	170	175	
aaa tat tta gct aag att aat cag gta aag gct ctt gct aaa aat agt				576
Lys Tyr Leu Ala Lys Ile Asn Gln Val Lys Ala Leu Ala Lys Asn Ser				
	180	185	190	
aaa aag acc gat aag atg gtt ttt gtt agt gaa ccc gtc ttt gat tac				624
Lys Lys Thr Asp Lys Met Val Phe Val Ser Glu Pro Val Phe Asp Tyr				
	195	200	205	
gcc tta gct gaa gct ggt tac aag att ggt gac aag gac ttt gaa aaa				672
Ala Leu Ala Glu Ala Gly Tyr Lys Ile Gly Asp Lys Asp Phe Glu Lys				
	210	215	220	
gct gta gaa aac aac aca gat cca agt cct aaa act att aac aga atg				720
Ala Val Glu Asn Asn Thr Asp Pro Ser Pro Lys Thr Ile Asn Arg Met				
	225	230	235	240
aca aat gat att aag aat aag aag atc gca ttc ttt gtt aac aat act				768
Thr Asn Asp Ile Lys Asn Lys Lys Ile Ala Phe Phe Val Asn Asn Thr				
	245	250	255	
caa tca agt agt tca act gta aag aca ttt gtt aaa ttg gca aaa caa				816
Gln Ser Ser Ser Ser Thr Val Lys Thr Phe Val Lys Leu Ala Lys Gln				
	260	265	270	
aat aat att cca gta ttg aac gtg cgc gaa act att cct aat cac aca				864
Asn Asn Ile Pro Val Leu Asn Val Arg Glu Thr Ile Pro Asn His Thr				
	275	280	285	
act tac tta aat tgg atg aag gaa aat tat caa aat tta gct aat att				912
Thr Tyr Leu Asn Trp Met Lys Glu Asn Tyr Gln Asn Leu Ala Asn Ile				
	290	295	300	
agt aag				918
Ser Lys				
305				

<210> 2
 <211> 306
 <212> PRT
 <213> *Lactobacillus acidophilus*

<400> 2
 Met Leu Phe Leu Trp Arg Lys Ile Met Gln Asn Trp Lys Thr Arg Ile
 1 5 10 15
 Thr Lys Leu Ser Phe Leu Ile Gly Ile Val Gly Thr Ile Met Leu Phe
 20 25 30
 Val Ser Ala Cys Ser Asn Asn Lys Gln Ser Ser Thr Asn Asp Gly Lys
 35 40 45
 Ile Ser Ile Val Thr Ser Thr Asn Val Tyr Ala Asp Ile Ala Lys Asn
 50 55 60
 Ile Val Gly Lys Tyr Gly Ser Ala Lys Ala Ile Ile Lys Asn Ser Ala
 65 70 75 80
 Thr Asp Pro His Asp Phe Glu Pro Thr Thr Gln Asp Ala Lys Glu Leu
 85 90 95
 Ser Ser Thr Asn Ile Ile Val Ala Asn Gly Leu Gly Tyr Asp Ser Trp
 100 105 110
 Met Asn Lys Leu Ala Ser Ser Val Asp Lys Lys Pro Val Leu Val Gly
 115 120 125
 Glu Glu Leu Met Lys Leu Lys Lys Gly Ala Asn Pro His Ile Trp Tyr
 130 135 140
 Ser Leu Ser Met Pro Thr Glu Tyr Val Asp Tyr Leu Val Lys Arg Leu
 145 150 155 160
 Ser Lys Ile Asp Ser Lys His Lys Ala Tyr Phe Glu Ala Asn Gly Lys
 165 170 175
 Lys Tyr Leu Ala Lys Ile Asn Gln Val Lys Ala Leu Ala Lys Asn Ser
 180 185 190
 Lys Lys Thr Asp Lys Met Val Phe Val Ser Glu Pro Val Phe Asp Tyr
 195 200 205
 Ala Leu Ala Glu Ala Gly Tyr Lys Ile Gly Asp Lys Asp Phe Glu Lys
 210 215 220
 Ala Val Glu Asn Asn Thr Asp Pro Ser Pro Lys Thr Ile Asn Arg Met
 225 230 235 240
 Thr Asn Asp Ile Lys Asn Lys Lys Ile Ala Phe Phe Val Asn Asn Thr
 245 250 255
 Gln Ser Ser Ser Thr Val Lys Thr Phe Val Lys Leu Ala Lys Gln
 260 265 270
 Asn Asn Ile Pro Val Leu Asn Val Arg Glu Thr Ile Pro Asn His Thr
 275 280 285
 Thr Tyr Leu Asn Trp Met Lys Glu Asn Tyr Gln Asn Leu Ala Asn Ile
 290 295 300
 Ser Lys
 305

<210> 3
 <211> 573
 <212> DNA
 <213> *Lactobacillus acidophilus*

<220>
 <221> misc_feature

<222> (0)...(0)

<223> ORF 97 - lemA protein

<220>

<221> CDS

<222> (1)...(573)

<400> 3

atg gag gat tct atc atg tca cca tta ctt tgg ata att tta att atc	48
Met Glu Asp Ser Ile Met Ser Pro Leu Leu Trp Ile Ile Leu Ile Ile	
1 5 10 15	
att gtt tta ata gta gct atc tat atc act act tat aac ggt tta caa	96
Ile Val Leu Ile Val Ala Ile Tyr Ile Thr Thr Tyr Asn Gly Leu Gln	
20 25 30	
aga tct cgt gta tat gta gac gaa gca tgg agc caa att gac gtt caa	144
Arg Ser Arg Val Tyr Val Asp Glu Ala Trp Ser Gln Ile Asp Val Gln	
35 40 45	
tta aaa cga cgt aat gac tta att cct aac tta gtt gaa act acc aaa	192
Leu Lys Arg Arg Asn Asp Leu Ile Pro Asn Leu Val Glu Thr Thr Lys	
50 55 60	
ggt tat gca caa cac gaa aaa tct act ttt gag agt ata gtt aaa ctt	240
Gly Tyr Ala Gln His Glu Lys Ser Thr Phe Glu Ser Ile Val Lys Leu	
65 70 75 80	
aga gat gaa tta act caa gtt cca caa ggt aac cat gaa gaa gca atg	288
Arg Asp Glu Leu Thr Gln Val Pro Gln Gly Asn His Glu Glu Ala Met	
85 90 95	
aag cta tct aat cag ctt acc gat tcc ttg aag tcc atc ttt gct tta	336
Lys Leu Ser Asn Gln Leu Thr Asp Ser Leu Lys Ser Ile Phe Ala Leu	
100 105 110	
gca gag gca tac cct gac ctt aaa gca aat caa aac ttc tta aaa ctt	384
Ala Glu Ala Tyr Pro Asp Leu Lys Ala Asn Gln Asn Phe Leu Lys Leu	
115 120 125	
caa gag gaa ttg act aat act gaa aat aaa att gct tat tct cgt cag	432
Gln Glu Glu Leu Thr Asn Thr Glu Asn Lys Ile Ala Tyr Ser Arg Gln	
130 135 140	
ctt tat aac tca tca gtt gct aca tac gat caa aaa tta tta act ttc	480
Leu Tyr Asn Ser Ser Val Ala Thr Tyr Asp Gln Lys Leu Leu Thr Phe	
145 150 155 160	
ccc tca aac tta att gct aaa att cac ggc ttt act aag gtt aac tac	528
Pro Ser Asn Leu Ile Ala Lys Ile His Gly Phe Thr Lys Val Asn Tyr	
165 170 175	
ttg gaa act cct gca gaa gaa aag aat gta cct aaa gtt aaa ttt	573
Leu Glu Thr Pro Ala Glu Glu Lys Asn Val Pro Lys Val Lys Phe	
180 185 190	

<210> 4
 <211> 191
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 4
 Met Glu Asp Ser Ile Met Ser Pro Leu Leu Trp Ile Ile Leu Ile Ile
 1 5 10 15
 Ile Val Leu Ile Val Ala Ile Tyr Ile Thr Thr Tyr Asn Gly Leu Gln
 20 25 30
 Arg Ser Arg Val Tyr Val Asp Glu Ala Trp Ser Gln Ile Asp Val Gln
 35 40 45
 Leu Lys Arg Arg Asn Asp Leu Ile Pro Asn Leu Val Glu Thr Thr Lys
 50 55 60
 Gly Tyr Ala Gln His Glu Lys Ser Thr Phe Glu Ser Ile Val Lys Leu
 65 70 75 80
 Arg Asp Glu Leu Thr Gln Val Pro Gln Gly Asn His Glu Glu Ala Met
 85 90 95
 Lys Leu Ser Asn Gln Leu Thr Asp Ser Leu Lys Ser Ile Phe Ala Leu
 100 105 110
 Ala Glu Ala Tyr Pro Asp Leu Lys Ala Asn Gln Asn Phe Leu Lys Leu
 115 120 125
 Gln Glu Glu Leu Thr Asn Thr Glu Asn Lys Ile Ala Tyr Ser Arg Gln
 130 135 140
 Leu Tyr Asn Ser Ser Val Ala Thr Tyr Asp Gln Lys Leu Leu Thr Phe
 145 150 155 160
 Pro Ser Asn Leu Ile Ala Lys Ile His Gly Phe Thr Lys Val Asn Tyr
 165 170 175
 Leu Glu Thr Pro Ala Glu Glu Lys Asn Val Pro Lys Val Lys Phe
 180 185 190

<210> 5
 <211> 7617
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF - 1611 FmtB surface protein

<220>
 <221> CDS
 <222> (1)...(7617)

<400> 5
 ttg act acc att aat aat gca aaa gat gct tta aat ggg gat gtt aag 48
 Met Thr Thr Ile Asn Asn Ala Lys Asp Ala Leu Asn Gly Asp Val Lys
 1 5 10 15
 aaa gca gca agt aag gaa gct ctt caa aaa gca gtt gat gaa gca cct 96
 Lys Ala Ala Ser Lys Glu Ala Leu Gln Lys Ala Val Asp Glu Ala Pro
 20 25 30

act gta aaa tca gat gat gcg gca tac tac aat ggt tct gat gaa gct	144
Thr Val Lys Ser Asp Asp Ala Ala Tyr Tyr Asn Gly Ser Asp Glu Ala	
35 40 45	
aag gct gct tat gat aag gca atc agt gcc ggt caa aca gtt tta aat	192
Lys Ala Ala Tyr Asp Lys Ala Ile Ser Ala Gly Gln Thr Val Leu Asn	
50 55 60	
aat cca gat gca acc gct act caa att act gat gct tta aat gcc att	240
Asn Pro Asp Ala Thr Ala Thr Gln Ile Thr Asp Ala Leu Asn Ala Ile	
65 70 75 80	
aat act gct aag ggt gac ttt gat ggt aaa act acc gat aaa tca gca	288
Asn Thr Ala Lys Gly Asp Phe Asp Gly Lys Thr Thr Asp Lys Ser Ala	
85 90 95	
ctt gaa act gca att aat aat tct aaa act gta aaa gac agc aac aac	336
Leu Glu Thr Ala Ile Asn Asn Ser Lys Thr Val Lys Asp Ser Asn Asn	
100 105 110	
tat act aat gca gac gaa act caa aag act gca tat gat agt gca gta	384
Tyr Thr Asn Ala Asp Glu Thr Gln Lys Thr Ala Tyr Asp Ser Ala Val	
115 120 125	
aca tct gca caa ata gtt tta gat aaa act aat gca act caa gca gaa	432
Thr Ser Ala Gln Ile Val Leu Asp Lys Thr Asn Ala Thr Gln Ala Glu	
130 135 140	
gtg aac caa gct ctt caa gat ctt gaa act gca aat aat aac cta aat	480
Val Asn Gln Ala Leu Gln Asp Leu Glu Thr Ala Asn Asn Asn Leu Asn	
145 150 155 160	
ggg gat gct aag act gaa gct gca aac aag gct gcc tta gaa gct gcc	528
Gly Asp Ala Lys Thr Glu Ala Ala Asn Lys Ala Ala Leu Glu Ala Ala	
165 170 175	
gtt aag gat gcg cca aat gta aga aat acg cct gca tac tac aac ggt	576
Val Lys Asp Ala Pro Asn Val Arg Asn Thr Pro Ala Tyr Tyr Asn Gly	
180 185 190	
act aac gaa gct caa aca aca tat aat aat gca att aat gct ggg caa	624
Thr Asn Glu Ala Gln Thr Thr Tyr Asn Asn Ala Ile Asn Ala Gly Gln	
195 200 205	
gca gtt tta gat cag gca aat cca tct gca aat gac gtt aag tct gct	672
Ala Val Leu Asp Gln Ala Asn Pro Ser Ala Asn Asp Val Lys Ser Ala	
210 215 220	
tta gat gca att aat gca gca aaa gct aac ctt aaa ggt gaa gct act	720
Leu Asp Ala Ile Asn Ala Ala Lys Ala Asn Leu Lys Gly Glu Ala Thr	
225 230 235 240	
aat act aca tct ttg gaa aca gct tta acc aat gct aat aat gtt aag	768
Asn Thr Thr Ser Leu Glu Thr Ala Leu Asn Ala Asn Asn Val Lys	
245 250 255	

aac act ggt aac tac act aat gct gat caa gca aaa caa gaa gct ctt	816
Asn Thr Gly Asn Tyr Thr Asn Ala Asp Gln Ala Lys Gln Glu Ala Leu	
260 265 270	
aat aat aca att att gct ggt caa gat ctt tta aag aat act aat gca	864
Asn Asn Thr Ile Ile Ala Gly Gln Asp Leu Leu Lys Asn Thr Asn Ala	
275 280 285	
act cag gca gaa gta gac aat gca gca aag gct att act aat gca att	912
Thr Gln Ala Glu Val Asp Asn Ala Ala Lys Ala Ile Thr Asn Ala Ile	
290 295 300	
aat ggc ttg aat ggg gat act aac ctt aca aat gct aag aat gct gct	960
Asn Gly Leu Asn Gly Asp Thr Asn Leu Thr Asn Ala Lys Asn Ala Ala	
305 310 315 320	
act gaa gat att caa aag gca tta gat agt aag act acc gaa atc act	1008
Thr Glu Asp Ile Gln Lys Ala Leu Asp Ser Lys Thr Thr Glu Ile Thr	
325 330 335	
gac gct act aat att gat caa gct act aag gat caa tta att gcg gat	1056
Asp Ala Thr Asn Ile Asp Gln Ala Thr Lys Asp Gln Leu Ile Ala Asp	
340 345 350	
gct aaa aag gca gca gaa gat gct aat act gct att aat caa gca acc	1104
Ala Lys Lys Ala Ala Glu Asp Ala Asn Thr Ala Ile Asn Gln Ala Thr	
355 360 365	
aat gcc gat gca gtt aat act gct aaa act gaa gga att gct aat atc	1152
Asn Ala Asp Ala Val Asn Thr Ala Lys Thr Glu Gly Ile Ala Asn Ile	
370 375 380	
aat aag gtg aca gtt cca agt tta gat gat gct aaa act aag gca gcc	1200
Asn Lys Val Thr Val Pro Ser Leu Asp Asp Ala Lys Thr Lys Ala Ala	
385 390 395 400	
aaa gaa att gat caa gca tta act gat aag acc aag gaa atc act gat	1248
Lys Glu Ile Asp Gln Ala Leu Thr Asp Lys Thr Lys Glu Ile Thr Asp	
405 410 415	
gct gaa aat att gat caa aca act aaa gat cag tta att aaa gaa gca	1296
Ala Glu Asn Ile Asp Gln Thr Thr Lys Asp Gln Leu Ile Lys Glu Ala	
420 425 430	
act gat gca gca aat aca gca aaa gat act att gaa aaa tct aca act	1344
Thr Asp Ala Ala Asn Thr Ala Lys Asp Thr Ile Glu Lys Ser Thr Thr	
435 440 445	
aac gac gaa gca act aaa gca ggc caa gat ggt gta gat gca gtt aac	1392
Asn Asp Glu Ala Thr Lys Ala Gly Gln Asp Gly Val Asp Ala Val Asn	
450 455 460	
aat gta aag gta cca agc gtt act gat agt caa aat gcg gca aaa gat	1440
Asn Val Lys Val Pro Ser Val Thr Asp Ser Gln Asn Ala Ala Lys Asp	
465 470 475 480	
gct att gat gat gcc ctt aac gct aag act aag gaa atc aac gat gct	1488

Ala Ile Asp Asp	Ala Leu Asn Ala Lys Thr Lys Glu Ile Asn Asp Ala	485	490	495	
aac aat att gat	caa aca act aag gat caa tta atc aaa gaa gca acc	1536			
Asn Asn Ile Asp	Gln Thr Thr Lys Asp Gln Leu Ile Lys Glu Ala Thr	500	505	510	
gat gca gct aat	aat gct aaa gaa gcc att gat aaa gca acc aca gct	1584			
Asp Ala Ala Asn	Asn Ala Lys Glu Ala Ile Asp Lys Ala Thr Thr Ala	515	520	525	
gat gca att aag	act gca caa gat gaa gga acc act aac atc aac aat	1632			
Asp Ala Ile Lys	Thr Ala Gln Asp Glu Gly Thr Thr Asn Ile Asn Asn	530	535	540	
gtt act gtt cca	agc tta gag gat gcc aag aag gca gca act aaa gca	1680			
Val Thr Val Pro	Ser Leu Glu Asp Ala Lys Lys Ala Ala Thr Lys Ala	545	550	555	560
gta gat gat gct	ctt act gct caa act gaa gta att aat aaa gct gat	1728			
Val Asp Asp Ala	Leu Thr Ala Gln Thr Glu Val Ile Asn Lys Ala Asp	565	570	575	
aat ctt agt gat	gca gaa aag aaa gat ctg att gat caa gca act act	1776			
Asn Leu Ser Asp	Ala Glu Lys Lys Asp Leu Ile Asp Gln Ala Thr Thr	580	585	590	
gaa gcc aat aag	gct aaa gaa agt att gaa act gct acg aca aac aat	1824			
Glu Ala Asn Lys	Ala Lys Glu Ser Ile Glu Thr Ala Thr Thr Asn Asn	595	600	605	
gaa gca gct caa	gca ggc aaa gat ggt gtg gat gca att aat aag att	1872			
Glu Ala Ala Gln	Ala Gly Lys Asp Gly Val Asp Ala Ile Asn Lys Ile	610	615	620	
gtt cca aca agc	tta gat act gtg aaa tct gat gca aat aaa gca att	1920			
Val Pro Thr Ser	Leu Asp Thr Val Lys Ser Asp Ala Asn Lys Ala Ile	625	630	635	640
gat gat gct tta	act aag aaa tta gaa gag att aat tca gct aat gct	1968			
Asp Asp Ala Leu	Thr Lys Lys Leu Glu Glu Ile Asn Ser Ala Asn Ala	645	650	655	
tta act act gat	gaa aag acc gcg tta aca caa gaa gcc aat aca gct	2016			
Leu Thr Thr Asp	Glu Lys Thr Ala Leu Thr Gln Glu Ala Asn Thr Ala	660	665	670	
gca gct aag gca	aaa gaa aaa att act aat gca aca act aat gat gca	2064			
Ala Ala Lys Ala	Lys Glu Lys Ile Thr Asn Ala Thr Thr Asn Asp Ala	675	680	685	
gta att gaa gca	caa aat aat ggt gtt act gca att gat gga att aaa	2112			
Val Ile Glu Ala	Gln Asn Asn Gly Val Thr Ala Ile Asp Gly Ile Lys	690	695	700	
gtt ccg act gaa	tca gca gtc aaa gaa gca gct aag aag gca gta gcc	2160			
Val Pro Thr Glu	Ser Ala Val Lys Glu Ala Ala Lys Lys Ala Val Ala				

705	710	715	720	
gaa gca gca aca gca aag act aat gca att gat tct tca aac tta aca Glu Ala Ala Thr Ala Lys Thr Asn Ala Ile Asp Ser Ser Asn Leu Thr	725	730	735	2208
gct gaa gaa aaa gcg gca ttg aag caa gaa gtt act gaa gct caa aca Ala Glu Glu Lys Ala Ala Leu Lys Gln Glu Val Thr Glu Ala Gln Thr	740	745	750	2256
gct gct aat act gca att gat aat gca act aca aac gca gac gta act Ala Ala Asn Thr Ala Ile Asp Asn Ala Thr Thr Asn Ala Asp Val Thr	755	760	765	2304
gaa gct aaa gac aaa ggt att aag gca att aat ggt att gaa gta cca Glu Ala Lys Asp Lys Gly Ile Lys Ala Ile Asn Gly Ile Glu Val Pro	770	775	780	2352
aat aaa tca gat act aag gga aag gca atc act gat ctt aac aac gaa Asn Lys Ser Asp Thr Lys Gly Lys Ala Ile Thr Asp Leu Asn Asn Glu	785	790	795	2400
gtt gaa aat gct aag aaa gca att gat caa gat agc aac tta act gat Val Glu Asn Ala Lys Lys Ala Ile Asp Gln Asp Ser Asn Leu Thr Asp	805	810	815	2448
gaa gag aag caa gca gct aaa gac caa att gac tct gat gct aag act Glu Glu Lys Gln Ala Ala Lys Asp Gln Ile Asp Ser Asp Ala Lys Thr	820	825	830	2496
gct caa gat gct att aac aat gca aag act aat gat gat gtt aag aat Ala Gln Asp Ala Ile Asn Asn Ala Lys Thr Asn Asp Asp Val Lys Asn	835	840	845	2544
gca gtt gct gct ggt aca tta gca att gat aag gat gtt gct aat gca Ala Val Ala Ala Gly Thr Leu Ala Ile Asp Lys Asp Val Ala Asn Ala	850	855	860	2592
gcc att gat aat gca gct gct ggt aag ctt aaa gaa atc aaa gat ccg Ala Ile Asp Asn Ala Ala Ala Gly Lys Leu Lys Glu Ile Lys Asp Pro	865	870	875	2640
tta act agt gaa gag aaa caa act tac aca gat tta att aat tct gag Leu Thr Ser Glu Glu Lys Gln Thr Tyr Thr Asp Leu Ile Asn Ser Glu	885	890	895	2688
gta aat aac gca aaa caa aat att gct aat gca acg act gtt gaa gaa Val Asn Asn Ala Lys Gln Asn Ile Ala Asn Ala Thr Thr Val Glu Glu	900	905	910	2736
gta act act gca caa aca aac ggt gta aat gaa att act aat acc aaa Val Thr Thr Ala Gln Thr Asn Gly Val Asn Glu Ile Thr Asn Thr Lys	915	920	925	2784
att cca acc act tct tca gcc aaa gat aag gca att gct gct atc aat Ile Pro Thr Thr Ser Ser Ala Lys Asp Lys Ala Ile Ala Ala Ile Asn	930	935	940	2832

gat gct ctt caa aag aag tct gac gaa atc aac aat gcc tct aac atc Asp Ala Leu Gln Lys Lys Ser Asp Glu Ile Asn Asn Ala Ser Asn Ile 945 950 955 960	2880
aac act caa gaa aag act gat tta att aag caa gca act gaa gca gcc Asn Thr Gln Glu Lys Thr Asp Leu Ile Lys Gln Ala Thr Glu Ala Ala 965 970 975	2928
aat act gct aag gat aat atc aac aat gcc act act aac gcg gat gtt Asn Thr Ala Lys Asp Asn Ile Asn Asn Ala Thr Thr Asn Ala Asp Val 980 985 990	2976
aag act gcg caa act aat ggt gaa aaa gca att gct gat gta aca gtt Lys Thr Gln Thr Asn Gly Glu Lys Ala Ile Ala Asp Val Thr Val 995 1000 1005	3024
cca aac ttg tct gat gtt aag aag gaa aac att gat ctc att aac aag Pro Asn Leu Ser Asp Val Lys Lys Glu Asn Ile Asp Leu Ile Asn Lys 1010 1015 1020	3072
gcg tta gat gcc aag aca gac gaa atc aac aat gct tct aac ctt tct Ala Leu Asp Ala Lys Thr Asp Glu Ile Asn Asn Ala Ser Asn Leu Ser 1025 1030 1035 1040	3120
caa gat gaa aag caa agt ttg atc aat gat gca act aat atc gca act Gln Asp Glu Lys Gln Ser Leu Ile Asn Asp Ala Thr Asn Ile Ala Thr 1045 1050 1055	3168
gaa gca att aac aac gtc aac caa tct caa aca aat gac gat gct aaa Glu Ala Ile Asn Asn Val Asn Gln Ser Gln Thr Asn Asp Asp Ala Lys 1060 1065 1070	3216
gct gct gca act att ggt gtt caa aat atc gag aat gtt act att cca Ala Ala Ala Thr Ile Gly Val Gln Asn Ile Glu Asn Val Thr Ile Pro 1075 1080 1085	3264
act ctt gat gat gct aag aag aac gct aac caa gct att gat gct gca Thr Leu Asp Asp Ala Lys Lys Asn Ala Asn Gln Ala Ile Asp Ala Ala 1090 1095 1100	3312
ttg aat tct aaa gta aat gag att aat aat gct tct aac ttg aat gac Leu Asn Ser Lys Val Asn Glu Ile Asn Asn Ala Ser Asn Leu Asn Asp 1105 1110 1115 1120	3360
act gaa aag caa aaa tta gtt gat cag gca aat gat gca gca act act Thr Glu Lys Gln Lys Leu Val Asp Gln Ala Asn Asp Ala Ala Thr Thr 1125 1130 1135	3408
gca aag aat aat gtt gaa aat gcc act acc aat gat gct gct cgc gat Ala Lys Asn Asn Val Glu Asn Ala Thr Thr Asn Asp Ala Ala Arg Asp 1140 1145 1150	3456
gca gct aat gct gga att aat aac att aaa ggt att acc ttt act tca Ala Ala Asn Ala Gly Ile Asn Asn Ile Lys Gly Ile Thr Phe Thr Ser 1155 1160 1165	3504

cta gaa gat gct aaa aat gca gca aac act gca att gac aat gct ttt	3552
Leu Glu Asp Ala Lys Asn Ala Ala Asn Thr Ala Ile Asp Asn Ala Phe	
1170 1175 1180	
caa gtt aag aca gat gaa att aat aat gca tct aac tta agt act gaa	3600
Gln Val Lys Thr Asp Glu Ile Asn Asn Ala Ser Asn Leu Ser Thr Glu	
1185 1190 1195 1200	
gaa aag caa gac tta atc aat caa gca agt gaa gca gct aaa aat gca	3648
Glu Lys Gln Asp Leu Ile Asn Gln Ala Ser Glu Ala Ala Lys Asn Ala	
1205 1210 1215	
aaa gac aat atc aac aat gcc act acc aat gat gct gtg act gac gca	3696
Lys Asp Asn Ile Asn Asn Ala Thr Thr Asn Asp Ala Val Thr Asp Ala	
1220 1225 1230	
cag aat aag ggt att gca gat att gct aat gtg act gtt cca agc tta	3744
Gln Asn Lys Gly Ile Ala Asp Ile Ala Asn Val Thr Val Pro Ser Leu	
1235 1240 1245	
gat caa gtt aaa caa gat gca att aat gca att aag caa gtt caa gat	3792
Asp Gln Val Lys Gln Asp Ala Ile Asn Ala Ile Lys Gln Val Gln Asp	
1250 1255 1260	
gct aag aat aag caa att tct aat gca tct aac cta agt gct gaa gag	3840
Ala Lys Asn Lys Gln Ile Ser Asn Ala Ser Asn Leu Ser Ala Glu Glu	
1265 1270 1275 1280	
caa aaa gaa tta act gat caa gta gat aaa att gct aac gat gca att	3888
Gln Lys Glu Leu Thr Asp Gln Val Asp Lys Ile Ala Asn Asp Ala Ile	
1285 1290 1295	
gct aag att aat gat gca gca act act acc aat gat gca gtt act gca	3936
Ala Lys Ile Asn Asp Ala Ala Thr Thr Thr Asn Asp Ala Val Thr Ala	
1300 1305 1310	
acc tgc gat gaa gca atc aag caa att act gat cta ttt att cca act	3984
Thr Cys Asp Glu Ala Ile Lys Gln Ile Thr Asp Leu Phe Ile Pro Thr	
1315 1320 1325	
cta gac ggt gcg cag aca gat gct ctt aat gca att gaa agt gct aag	4032
Leu Asp Gly Ala Gln Thr Asp Ala Leu Asn Ala Ile Glu Ser Ala Lys	
1330 1335 1340	
aat gct aag ctg aat gac att aac aat gct gct cac tta act gat caa	4080
Asn Ala Lys Leu Asn Asp Ile Asn Asn Ala Ala His Leu Thr Asp Gln	
1345 1350 1355 1360	
gaa aag cag gct ttg gtt gat caa aca aat aaa gct gcc gat gat gca	4128
Glu Lys Gln Ala Leu Val Asp Gln Thr Asn Lys Ala Ala Asp Asp Ala	
1365 1370 1375	
act aag gaa att aag ggc gct caa act aat gat gca gtc aag agt gca	4176
Thr Lys Glu Ile Lys Gly Ala Gln Thr Asn Asp Ala Val Lys Ser Ala	
1380 1385 1390	
gaa aca gcc ggt tta gat aat att aat aaa gtt act att cca acc tta	4224

Glu Thr Ala Gly Leu Asp Asn Ile Asn Lys Val Thr Ile Pro Thr Leu	
1395 1400 1405	
ggt cag aag caa caa gaa gct att gga gaa ttg aat gta gca cgt gat	4272
Val Gln Lys Gln Gln Glu Ala Ile Gly Glu Leu Asn Val Ala Arg Asp	
1410 1415 1420	
gct aag aat agg gca att gat gat gct act gat tta act act gat gaa	4320
Ala Lys Asn Arg Ala Ile Asp Asp Ala Thr Asp Leu Thr Thr Asp Glu	
1425 1430 1435 1440	
aag aac agc ttg aaa gat aaa gtt caa gca gaa tac agt aac gca gta	4368
Lys Asn Ser Leu Lys Asp Lys Val Gln Ala Glu Tyr Ser Asn Ala Val	
1445 1450 1455	
tca aat atc acc agt gca aca act gat gaa gca gta aca acc gct aaa	4416
Ser Asn Ile Thr Ser Ala Thr Thr Asp Glu Ala Val Thr Thr Ala Lys	
1460 1465 1470	
gaa aac ggc atc aat gca att aaa gac att gaa atc cca act aag tca	4464
Glu Asn Gly Ile Asn Ala Ile Lys Asp Ile Glu Ile Pro Thr Lys Ser	
1475 1480 1485	
gct acg aag gac cag gca acc aca gac ctt aag act gcc gtt gac gaa	4512
Ala Thr Lys Asp Gln Ala Thr Thr Asp Leu Lys Thr Ala Val Asp Glu	
1490 1495 1500	
gct aag aag gca att gat caa gat aac aac ttg aac aat gag caa aag	4560
Ala Lys Lys Ala Ile Asp Gln Asp Asn Asn Leu Asn Asn Glu Gln Lys	
1505 1510 1515 1520	
caa gca gct aaa gat caa att gat tct gat gct aag aaa gct caa gaa	4608
Gln Ala Ala Lys Asp Gln Ile Asp Ser Asp Ala Lys Lys Ala Gln Glu	
1525 1530 1535	
gcc atc gat aat gcg aag act gat gat gag gta aac agt gcc gtt gat	4656
Ala Ile Asp Asn Ala Lys Thr Asp Asp Glu Val Asn Ser Ala Val Asp	
1540 1545 1550	
aat ggt aag ctt gct att gat aaa gat att gct aat gcc gcc atc gac	4704
Asn Gly Lys Leu Ala Ile Asp Lys Asp Ile Ala Asn Ala Ala Ile Asp	
1555 1560 1565	
aat gca gtt gct ggt aag aag gac gaa att gct aaa tca cca tta act	4752
Asn Ala Val Ala Gly Lys Lys Asp Glu Ile Ala Lys Ser Pro Leu Thr	
1570 1575 1580	
gat gaa gaa aag act gcg tta aat aat gaa gtc gat caa aag gct caa	4800
Asp Glu Glu Lys Thr Ala Leu Asn Asn Glu Val Asp Gln Lys Ala Gln	
1585 1590 1595 1600	
gat gct aaa gaa gca atc aat aat gcc act acc cca gaa gct gta acc	4848
Asp Ala Lys Glu Ala Ile Asn Asn Ala Thr Thr Pro Glu Ala Val Thr	
1605 1610 1615	
act gcg caa gac aat ggt gtt aag aat atc aat gat act gaa gtg cca	4896
Thr Ala Gln Asp Asn Gly Val Lys Asn Ile Asn Asp Thr Glu Val Pro	

1620	1625	1630	
act gag tca aca gct aaa gaa gca gct aag aaa gct att gca gaa gca			4944
Thr Glu Ser Thr Ala Lys Glu Ala Ala Lys Lys Ala Ile Ala Glu Ala			
1635	1640	1645	
gcc gaa gct aag aac aat gca atc gat tct tca aac tta acg gac gaa			4992
Ala Glu Ala Lys Asn Asn Ala Ile Asp Ser Ser Asn Leu Thr Asp Glu			
1650	1655	1660	
gaa aaa act gca ttg aag cag gaa gtt act gat gcc caa aac gct gcc			5040
Glu Lys Thr Ala Leu Lys Gln Glu Val Thr Asp Ala Gln Asn Ala Ala			
1665	1670	1675	1680
aat act gca att gat aac gca act acc aat gcc gca gta acc gaa gca			5088
Asn Thr Ala Ile Asp Asn Ala Thr Thr Asn Ala Ala Val Thr Glu Ala			
1685	1690	1695	
gaa gac aat ggt att aaa gct att aat ggt att gga atc cca act aag			5136
Glu Asp Asn Gly Ile Lys Ala Ile Asn Gly Ile Gly Ile Pro Thr Lys			
1700	1705	1710	
tca cca gct aag gac caa gca atc act gac ctt aat gat gcc gtt gac			5184
Ser Pro Ala Lys Asp Gln Ala Ile Thr Asp Leu Asn Asp Ala Val Asp			
1715	1720	1725	
gag gct aag aag gca att gac caa gat aac aac ttg act gat gcc gaa			5232
Glu Ala Lys Lys Ala Ile Asp Gln Asp Asn Asn Leu Thr Asp Ala Glu			
1730	1735	1740	
aag caa gca gcg aag gat caa atc gat tcc gat gct aag aag gcc caa			5280
Lys Gln Ala Ala Lys Asp Gln Ile Asp Ser Asp Ala Lys Lys Ala Gln			
1745	1750	1755	1760
gaa gcc atc gat aat gcg aag act gac gat gag gtt aag act gcc gtt			5328
Glu Ala Ile Asp Asn Ala Lys Thr Asp Asp Glu Val Lys Thr Ala Val			
1765	1770	1775	
gac aat ggt cag ctt gcc att gat aaa gat gtt gct aat gcc gcc atc			5376
Asp Asn Gly Gln Leu Ala Ile Asp Lys Asp Val Ala Asn Ala Ala Ile			
1780	1785	1790	
gac aat gca gtt gct ggt aag aag gct gaa att gca aag gca cca tta			5424
Asp Asn Ala Val Ala Gly Lys Lys Ala Glu Ile Ala Lys Ala Pro Leu			
1795	1800	1805	
acc acc gat gaa gct aag gac ttg aat gac tta gtt gac caa gaa gca			5472
Thr Thr Asp Glu Ala Lys Asp Leu Asn Asp Leu Val Asp Gln Glu Ala			
1810	1815	1820	
aag gcc gct aag aag gca att gat tca gct act act att cca gcg gtt			5520
Lys Ala Ala Lys Lys Ala Ile Asp Ser Ala Thr Thr Ile Pro Ala Val			
1825	1830	1835	1840
gac gat gct aag aat acc gga gtt gct gca atc aac aat att gca gtt			5568
Asp Asp Ala Lys Asn Thr Gly Val Ala Ala Ile Asn Asn Ile Ala Val			
1845	1850	1855	

cca aca act tca tca acc aag gat caa gct aac caa aca att gat gat	5616
Pro Thr Thr Ser Ser Thr Lys Asp Gln Ala Asn Gln Thr Ile Asp Asp	
1860 1865 1870	
gct tta gct aac aag act aaa gaa atc aat gat gca acc aac tta tct	5664
Ala Leu Ala Asn Lys Thr Lys Glu Ile Asn Asp Ala Thr Asn Leu Ser	
1875 1880 1885	
gat aag caa aag caa gac ttg att gat caa gcc aac gag gaa gca gca	5712
Asp Lys Gln Lys Gln Asp Leu Ile Asp Gln Ala Asn Glu Glu Ala Ala	
1890 1895 1900	
aag gct aag gaa aac att aag aat gcc act agc aat gaa gca gtc aac	5760
Lys Ala Lys Glu Asn Ile Lys Asn Ala Thr Ser Asn Glu Ala Val Asn	
1905 1910 1915 1920	
aaa gct act aca gat ggt gta gat gct att gca aat gtc act gtc cca	5808
Lys Ala Thr Thr Asp Gly Val Asp Ala Ile Ala Asn Val Thr Val Pro	
1925 1930 1935	
agt ctt gat gat gcg aag aaa gat gct agt caa tta att gac gac gtt	5856
Ser Leu Asp Asp Ala Lys Lys Asp Ala Ser Gln Leu Ile Asp Asp Val	
1940 1945 1950	
ctt aag caa aaa gaa gat gag atc aat aat gct tcc cac ttg act gat	5904
Leu Lys Gln Lys Glu Asp Glu Ile Asn Asn Ala Ser His Leu Thr Asp	
1955 1960 1965	
caa gag aag caa gac ctc att gac caa gca caa aac gcc gct gac gaa	5952
Gln Glu Lys Gln Asp Leu Ile Asp Gln Ala Gln Asn Ala Ala Asp Glu	
1970 1975 1980	
gcc aaa gac aag atc aac caa gcg aca act aat gac gat gta gct acg	6000
Ala Lys Asp Lys Ile Asn Gln Ala Thr Thr Asn Asp Asp Val Ala Thr	
1985 1990 1995 2000	
gaa aga gat gcg ggc gca gaa aag att gcc aat att gtt gtt ccg agt	6048
Glu Arg Asp Ala Gly Ala Glu Lys Ile Ala Asn Ile Val Val Pro Ser	
2005 2010 2015	
ctt gaa gat gct aag gat aaa gcc acg aag gca ata gat aac gct tta	6096
Leu Glu Asp Ala Lys Asp Lys Ala Thr Lys Ala Ile Asp Asn Ala Leu	
2020 2025 2030	
gca gat aag acg aag gaa att aat gat caa acc aac tta tct gat caa	6144
Ala Asp Lys Thr Lys Glu Ile Asn Asp Gln Thr Asn Leu Ser Asp Gln	
2035 2040 2045	
gaa aag aat gat ctt atc aac caa att act gat att gct gat aag gca	6192
Glu Lys Asn Asp Leu Ile Asn Gln Ile Thr Asp Ile Ala Asp Lys Ala	
2050 2055 2060	
aag gat aag atc aat aat gct gct act gat gca gat att gct aag aat	6240
Lys Asp Lys Ile Asn Asn Ala Ala Thr Asp Ala Asp Ile Ala Lys Asn	
2065 2070 2075 2080	

gaa aaa gat ggt att gat gca att gtt gat act aag att cct ggc tta	6288
Glu Lys Asp Gly Ile Asp Ala Ile Val Asp Thr Lys Ile Pro Gly Leu	
2085 2090 2095	
gaa gat cat aaa aag aat gca att aat tct tta gat gaa gct aaa tct	6336
Glu Asp His Lys Lys Asn Ala Ile Asn Ser Leu Asp Glu Ala Lys Ser	
2100 2105 2110	
act aag ctt gcc caa att gat gga gca act cat cta act gca aat gaa	6384
Thr Lys Leu Ala Gln Ile Asp Gly Ala Thr His Leu Thr Ala Asn Glu	
2115 2120 2125	
aag acc gac tta act caa caa gtt gat gca gaa tac aat aag gca ctt	6432
Lys Thr Asp Leu Thr Gln Val Asp Ala Glu Tyr Asn Lys Ala Leu	
2130 2135 2140	
gat gag atc aat aaa gct aca acc aat gat gat gca gat aaa gct agt	6480
Asp Glu Ile Asn Lys Ala Thr Thr Asn Asp Asp Ala Asp Lys Ala Ser	
2145 2150 2155 2160	
gct gat ggt gtg gaa gct atc ctt aat att aaa gtt ccg agc ctt aat	6528
Ala Asp Gly Val Glu Ala Ile Leu Asn Ile Lys Val Pro Ser Leu Asn	
2165 2170 2175	
gaa aag aaa caa gat agt ata aat gct ctt aat gaa gtg cgt gat gct	6576
Glu Lys Lys Gln Asp Ser Ile Asn Ala Leu Asn Glu Val Arg Asp Ala	
2180 2185 2190	
aag aag gat gaa atc aat aag gca act aat tta aac caa aat gaa aag	6624
Lys Lys Asp Glu Ile Asn Lys Ala Thr Asn Leu Asn Gln Asn Glu Lys	
2195 2200 2205	
gac gag ctg aac aaa caa gtt gat caa att gct gat aaa gct att aat	6672
Asp Glu Leu Asn Lys Gln Val Asp Gln Ile Ala Asp Lys Ala Ile Asn	
2210 2215 2220	
gcg atc aat gaa gca aat gat gat caa aca gct aaa aat gca gaa aat	6720
Ala Ile Asn Glu Ala Asn Asp Asp Gln Thr Ala Lys Asn Ala Glu Asn	
2225 2230 2235 2240	
aaa ggt att caa gat att ctt gat gtc aaa gtt cca agt cta gat gaa	6768
Lys Gly Ile Gln Asp Ile Leu Asp Val Lys Val Pro Ser Leu Asp Glu	
2245 2250 2255	
gtt aag aat aat gca aag caa gca att gct gat gcg tta gaa agt aag	6816
Val Lys Asn Asn Ala Lys Gln Ala Ile Ala Asp Ala Leu Glu Ser Lys	
2260 2265 2270	
cag aat gaa atc aat aag gca gtt aac ttg gat caa tct act aag caa	6864
Gln Asn Glu Ile Asn Lys Ala Val Asn Leu Asp Gln Ser Thr Lys Gln	
2275 2280 2285	
gac tta gtt aat caa gct aag act gct gca gaa aat gct aat aag aat	6912
Asp Leu Val Asn Gln Ala Lys Thr Ala Ala Glu Asn Ala Asn Lys Asn	
2290 2295 2300	
att gat tta gct aca act aat gac gaa gta ata gct gca agt aaa aag	6960

Ile Asp Leu Ala Thr Thr Asn Asp Glu Val Ile Ala Ala Ser Lys Lys 2305 2310 2315 2320	
ggt gta caa aat att gaa aat att att gtc cca gcc cca agt aca aat Gly Val Gln Asn Ile Glu Asn Ile Ile Val Pro Ala Pro Ser Thr Asn 2325 2330 2335	7008
tca gac act tca aat att agt act gat caa act gat tcc gat gct aat Ser Asp Thr Ser Asn Ile Ser Thr Asp Gln Thr Asp Ser Asp Ala Asn 2340 2345 2350	7056
aag agc caa gca caa gat agt aat aag act tct aat aat gat att aac Lys Ser Gln Ala Gln Asp Ser Asn Lys Thr Ser Asn Asn Asp Ile Asn 2355 2360 2365	7104
aag aat act gat aat cca aag cat agt aaa tct ggt aaa agt tcg gtg Lys Asn Thr Asp Asn Pro Lys His Ser Lys Ser Gly Lys Ser Ser Val 2370 2375 2380	7152
tct ctt gat gat aaa aag aat caa gca att aat gag ctt act aaa gta Ser Leu Asp Asp Lys Lys Asn Gln Ala Ile Asn Glu Leu Thr Lys Val 2385 2390 2395 2400	7200
gct gaa gct aag aaa gca gct att aat agt acc aat att tct gct gat Ala Glu Ala Lys Lys Ala Ala Ile Asn Ser Thr Asn Ile Ser Ala Asp 2405 2410 2415	7248
gct aaa gca aga ctt aac gct caa gta gat cgt gaa ttg gca cgt ggt Ala Lys Ala Arg Leu Asn Ala Gln Val Asp Arg Glu Leu Ala Arg Gly 2420 2425 2430	7296
aaa aat agt att agc caa gct aga aat tca gaa gaa tta aca agt agt Lys Asn Ser Ile Ser Gln Ala Arg Asn Ser Glu Glu Leu Thr Ser Ser 2435 2440 2445	7344
aag aat aca gca att gca acg att aat tca att agt gtt gct cca aag Lys Asn Thr Ala Ile Ala Thr Ile Asn Ser Ile Ser Val Ala Pro Lys 2450 2455 2460	7392
ggc acc caa ggg gta aat agt aga gaa aac tat ggc aat act gat tta Gly Thr Gln Gly Val Asn Ser Arg Glu Asn Tyr Gly Asn Thr Asp Leu 2465 2470 2475 2480	7440
aat aat aat agt att act gtt ggt gaa cgc cca att tct cac att cca Asn Asn Asn Ser Ile Thr Val Gly Glu Arg Pro Ile Ser His Ile Pro 2485 2490 2495	7488
act tct gat aaa caa gaa acc ttg cct caa act gga cat cat act aat Thr Ser Asp Lys Gln Glu Thr Leu Pro Gln Thr Gly His His Thr Asn 2500 2505 2510	7536
gaa ggc ttg aca att ctt ggt aca ttg gtt gcc ggt gta gca ggc tta Glu Gly Leu Thr Ile Leu Gly Thr Leu Val Ala Gly Val Ala Gly Leu 2515 2520 2525	7584
att aca ctt gca gga acc aag aag aga aaa gat Ile Thr Leu Ala Gly Thr Lys Lys Arg Lys Asp	7617

2530

2535

<210> 6

<211> 2539

<212> PRT

<213> Lactobacillus acidophilus

<400> 6

```

Met Thr Thr Ile Asn Asn Ala Lys Asp Ala Leu Asn Gly Asp Val Lys
 1           5           10           15
Lys Ala Ala Ser Lys Glu Ala Leu Gln Lys Ala Val Asp Glu Ala Pro
      20           25           30
Thr Val Lys Ser Asp Asp Ala Ala Tyr Tyr Asn Gly Ser Asp Glu Ala
      35           40           45
Lys Ala Ala Tyr Asp Lys Ala Ile Ser Ala Gly Gln Thr Val Leu Asn
      50           55           60
Asn Pro Asp Ala Thr Ala Thr Gln Ile Thr Asp Ala Leu Asn Ala Ile
      65           70           75
Asn Thr Ala Lys Gly Asp Phe Asp Gly Lys Thr Thr Asp Lys Ser Ala
      85           90           95
Leu Glu Thr Ala Ile Asn Asn Ser Lys Thr Val Lys Asp Ser Asn Asn
      100          105          110
Tyr Thr Asn Ala Asp Glu Thr Gln Lys Thr Ala Tyr Asp Ser Ala Val
      115          120          125
Thr Ser Ala Gln Ile Val Leu Asp Lys Thr Asn Ala Thr Gln Ala Glu
      130          135          140
Val Asn Gln Ala Leu Gln Asp Leu Glu Thr Ala Asn Asn Asn Leu Asn
      145          150          155          160
Gly Asp Ala Lys Thr Glu Ala Ala Asn Lys Ala Ala Leu Glu Ala Ala
      165          170          175
Val Lys Asp Ala Pro Asn Val Arg Asn Thr Pro Ala Tyr Tyr Asn Gly
      180          185          190
Thr Asn Glu Ala Gln Thr Thr Tyr Asn Asn Ala Ile Asn Ala Gly Gln
      195          200          205
Ala Val Leu Asp Gln Ala Asn Pro Ser Ala Asn Asp Val Lys Ser Ala
      210          215          220
Leu Asp Ala Ile Asn Ala Ala Lys Ala Asn Leu Lys Gly Glu Ala Thr
      225          230          235          240
Asn Thr Thr Ser Leu Glu Thr Ala Leu Thr Asn Ala Asn Asn Val Lys
      245          250          255
Asn Thr Gly Asn Tyr Thr Asn Ala Asp Gln Ala Lys Gln Glu Ala Leu
      260          265          270
Asn Asn Thr Ile Ile Ala Gly Gln Asp Leu Leu Lys Asn Thr Asn Ala
      275          280          285
Thr Gln Ala Glu Val Asp Asn Ala Ala Lys Ala Ile Thr Asn Ala Ile
      290          295          300
Asn Gly Leu Asn Gly Asp Thr Asn Leu Thr Asn Ala Lys Asn Ala Ala
      305          310          315          320
Thr Glu Asp Ile Gln Lys Ala Leu Asp Ser Lys Thr Thr Glu Ile Thr
      325          330          335
Asp Ala Thr Asn Ile Asp Gln Ala Thr Lys Asp Gln Leu Ile Ala Asp
      340          345          350
Ala Lys Lys Ala Ala Glu Asp Ala Asn Thr Ala Ile Asn Gln Ala Thr
      355          360          365
Asn Ala Asp Ala Val Asn Thr Ala Lys Thr Glu Gly Ile Ala Asn Ile
      370          375          380

```

Asn Lys Val Thr Val Pro Ser Leu Asp Asp Ala Lys Thr Lys Ala Ala
 385 390 395 400
 Lys Glu Ile Asp Gln Ala Leu Thr Asp Lys Thr Lys Glu Ile Thr Asp
 405 410 415
 Ala Glu Asn Ile Asp Gln Thr Thr Lys Asp Gln Leu Ile Lys Glu Ala
 420 425 430
 Thr Asp Ala Ala Asn Thr Ala Lys Asp Thr Ile Glu Lys Ser Thr Thr
 435 440 445
 Asn Asp Glu Ala Thr Lys Ala Gly Gln Asp Gly Val Asp Ala Val Asn
 450 455 460
 Asn Val Lys Val Pro Ser Val Thr Asp Ser Gln Asn Ala Ala Lys Asp
 465 470 475 480
 Ala Ile Asp Asp Ala Leu Asn Ala Lys Thr Lys Glu Ile Asn Asp Ala
 485 490 495
 Asn Asn Ile Asp Gln Thr Thr Lys Asp Gln Leu Ile Lys Glu Ala Thr
 500 505 510
 Asp Ala Ala Asn Asn Ala Lys Glu Ala Ile Asp Lys Ala Thr Thr Ala
 515 520 525
 Asp Ala Ile Lys Thr Ala Gln Asp Glu Gly Thr Thr Asn Ile Asn Asn
 530 535 540
 Val Thr Val Pro Ser Leu Glu Asp Ala Lys Lys Ala Ala Thr Lys Ala
 545 550 555 560
 Val Asp Asp Ala Leu Thr Ala Gln Thr Glu Val Ile Asn Lys Ala Asp
 565 570 575
 Asn Leu Ser Asp Ala Glu Lys Lys Asp Leu Ile Asp Gln Ala Thr Thr
 580 585 590
 Glu Ala Asn Lys Ala Lys Glu Ser Ile Glu Thr Ala Thr Thr Asn Asn
 595 600 605
 Glu Ala Ala Gln Ala Gly Lys Asp Gly Val Asp Ala Ile Asn Lys Ile
 610 615 620
 Val Pro Thr Ser Leu Asp Thr Val Lys Ser Asp Ala Asn Lys Ala Ile
 625 630 635 640
 Asp Asp Ala Leu Thr Lys Lys Leu Glu Glu Ile Asn Ser Ala Asn Ala
 645 650 655
 Leu Thr Thr Asp Glu Lys Thr Ala Leu Thr Gln Glu Ala Asn Thr Ala
 660 665 670
 Ala Ala Lys Ala Lys Glu Lys Ile Thr Asn Ala Thr Thr Asn Asp Ala
 675 680 685
 Val Ile Glu Ala Gln Asn Asn Gly Val Thr Ala Ile Asp Gly Ile Lys
 690 695 700
 Val Pro Thr Glu Ser Ala Val Lys Glu Ala Ala Lys Lys Ala Val Ala
 705 710 715 720
 Glu Ala Ala Thr Ala Lys Thr Asn Ala Ile Asp Ser Ser Asn Leu Thr
 725 730 735
 Ala Glu Glu Lys Ala Ala Leu Lys Gln Glu Val Thr Glu Ala Gln Thr
 740 745 750
 Ala Ala Asn Thr Ala Ile Asp Asn Ala Thr Thr Asn Ala Asp Val Thr
 755 760 765
 Glu Ala Lys Asp Lys Gly Ile Lys Ala Ile Asn Gly Ile Glu Val Pro
 770 775 780
 Asn Lys Ser Asp Thr Lys Gly Lys Ala Ile Thr Asp Leu Asn Asn Glu
 785 790 795 800
 Val Glu Asn Ala Lys Lys Ala Ile Asp Gln Asp Ser Asn Leu Thr Asp
 805 810 815
 Glu Glu Lys Gln Ala Ala Lys Asp Gln Ile Asp Ser Asp Ala Lys Thr
 820 825 830
 Ala Gln Asp Ala Ile Asn Asn Ala Lys Thr Asn Asp Asp Val Lys Asn

835	840	845
Ala Val Ala Ala Gly Thr Leu Ala Ile Asp Lys Asp Val Ala Asn Ala		
850	855	860
Ala Ile Asp Asn Ala Ala Ala Gly Lys Leu Lys Glu Ile Lys Asp Pro		
865	870	875
Leu Thr Ser Glu Glu Lys Gln Thr Tyr Thr Asp Leu Ile Asn Ser Glu		
885	890	895
Val Asn Asn Ala Lys Gln Asn Ile Ala Asn Ala Thr Thr Val Glu Glu		
900	905	910
Val Thr Thr Ala Gln Thr Asn Gly Val Asn Glu Ile Thr Asn Thr Lys		
915	920	925
Ile Pro Thr Thr Ser Ser Ala Lys Asp Lys Ala Ile Ala Ala Ile Asn		
930	935	940
Asp Ala Leu Gln Lys Lys Ser Asp Glu Ile Asn Asn Ala Ser Asn Ile		
945	950	955
Asn Thr Gln Glu Lys Thr Asp Leu Ile Lys Gln Ala Thr Glu Ala Ala		
965	970	975
Asn Thr Ala Lys Asp Asn Ile Asn Asn Ala Thr Thr Asn Ala Asp Val		
980	985	990
Lys Thr Ala Gln Thr Asn Gly Glu Lys Ala Ile Ala Asp Val Thr Val		
995	1000	1005
Pro Asn Leu Ser Asp Val Lys Lys Glu Asn Ile Asp Leu Ile Asn Lys		
1010	1015	1020
Ala Leu Asp Ala Lys Thr Asp Glu Ile Asn Asn Ala Ser Asn Leu Ser		
1025	1030	1035
Gln Asp Glu Lys Gln Ser Leu Ile Asn Asp Ala Thr Asn Ile Ala Thr		
1045	1050	1055
Glu Ala Ile Asn Asn Val Asn Gln Ser Gln Thr Asn Asp Asp Ala Lys		
1060	1065	1070
Ala Ala Ala Thr Ile Gly Val Gln Asn Ile Glu Asn Val Thr Ile Pro		
1075	1080	1085
Thr Leu Asp Asp Ala Lys Lys Asn Ala Asn Gln Ala Ile Asp Ala Ala		
1090	1095	1100
Leu Asn Ser Lys Val Asn Glu Ile Asn Asn Ala Ser Asn Leu Asn Asp		
1105	1110	1115
Thr Glu Lys Gln Lys Leu Val Asp Gln Ala Asn Asp Ala Ala Thr Thr		
1125	1130	1135
Ala Lys Asn Asn Val Glu Asn Ala Thr Thr Asn Asp Ala Ala Arg Asp		
1140	1145	1150
Ala Ala Asn Ala Gly Ile Asn Asn Ile Lys Gly Ile Thr Phe Thr Ser		
1155	1160	1165
Leu Glu Asp Ala Lys Asn Ala Ala Asn Thr Ala Ile Asp Asn Ala Phe		
1170	1175	1180
Gln Val Lys Thr Asp Glu Ile Asn Asn Ala Ser Asn Leu Ser Thr Glu		
1185	1190	1195
Glu Lys Gln Asp Leu Ile Asn Gln Ala Ser Glu Ala Ala Lys Asn Ala		
1205	1210	1215
Lys Asp Asn Ile Asn Asn Ala Thr Thr Asn Asp Ala Val Thr Asp Ala		
1220	1225	1230
Gln Asn Lys Gly Ile Ala Asp Ile Ala Asn Val Thr Val Pro Ser Leu		
1235	1240	1245
Asp Gln Val Lys Gln Asp Ala Ile Asn Ala Ile Lys Gln Val Gln Asp		
1250	1255	1260
Ala Lys Asn Lys Gln Ile Ser Asn Ala Ser Asn Leu Ser Ala Glu Glu		
1265	1270	1275
Gln Lys Glu Leu Thr Asp Gln Val Asp Lys Ile Ala Asn Asp Ala Ile		
1285	1290	1295

Ala Lys Ile Asn Asp Ala Ala Thr Thr Thr Asn Asp Ala Val Thr Ala
 1300 1305 1310
 Thr Cys Asp Glu Ala Ile Lys Gln Ile Thr Asp Leu Phe Ile Pro Thr
 1315 1320 1325
 Leu Asp Gly Ala Gln Thr Asp Ala Leu Asn Ala Ile Glu Ser Ala Lys
 1330 1335 1340
 Asn Ala Lys Leu Asn Asp Ile Asn Asn Ala Ala His Leu Thr Asp Gln
 1345 1350 1355 1360
 Glu Lys Gln Ala Leu Val Asp Gln Thr Asn Lys Ala Ala Asp Asp Ala
 1365 1370 1375
 Thr Lys Glu Ile Lys Gly Ala Gln Thr Asn Asp Ala Val Lys Ser Ala
 1380 1385 1390
 Glu Thr Ala Gly Leu Asp Asn Ile Asn Lys Val Thr Ile Pro Thr Leu
 1395 1400 1405
 Val Gln Lys Gln Gln Glu Ala Ile Gly Glu Leu Asn Val Ala Arg Asp
 1410 1415 1420
 Ala Lys Asn Arg Ala Ile Asp Asp Ala Thr Asp Leu Thr Thr Asp Glu
 1425 1430 1435 1440
 Lys Asn Ser Leu Lys Asp Lys Val Gln Ala Glu Tyr Ser Asn Ala Val
 1445 1450 1455
 Ser Asn Ile Thr Ser Ala Thr Thr Asp Glu Ala Val Thr Thr Ala Lys
 1460 1465 1470
 Glu Asn Gly Ile Asn Ala Ile Lys Asp Ile Glu Ile Pro Thr Lys Ser
 1475 1480 1485
 Ala Thr Lys Asp Gln Ala Thr Thr Asp Leu Lys Thr Ala Val Asp Glu
 1490 1495 1500
 Ala Lys Lys Ala Ile Asp Gln Asp Asn Asn Leu Asn Asn Glu Gln Lys
 1505 1510 1515 1520
 Gln Ala Ala Lys Asp Gln Ile Asp Ser Asp Ala Lys Lys Ala Gln Glu
 1525 1530 1535
 Ala Ile Asp Asn Ala Lys Thr Asp Glu Val Asn Ser Ala Val Asp
 1540 1545 1550
 Asn Gly Lys Leu Ala Ile Asp Lys Asp Ile Ala Asn Ala Ala Ile Asp
 1555 1560 1565
 Asn Ala Val Ala Gly Lys Lys Asp Glu Ile Ala Lys Ser Pro Leu Thr
 1570 1575 1580
 Asp Glu Glu Lys Thr Ala Leu Asn Asn Glu Val Asp Gln Lys Ala Gln
 1585 1590 1595 1600
 Asp Ala Lys Glu Ala Ile Asn Asn Ala Thr Thr Pro Glu Ala Val Thr
 1605 1610 1615
 Thr Ala Gln Asp Asn Gly Val Lys Asn Ile Asn Asp Thr Glu Val Pro
 1620 1625 1630
 Thr Glu Ser Thr Ala Lys Glu Ala Ala Lys Lys Ala Ile Ala Glu Ala
 1635 1640 1645
 Ala Glu Ala Lys Asn Asn Ala Ile Asp Ser Ser Asn Leu Thr Asp Glu
 1650 1655 1660
 Glu Lys Thr Ala Leu Lys Gln Glu Val Thr Asp Ala Gln Asn Ala Ala
 1665 1670 1675 1680
 Asn Thr Ala Ile Asp Asn Ala Thr Thr Asn Ala Ala Val Thr Glu Ala
 1685 1690 1695
 Glu Asp Asn Gly Ile Lys Ala Ile Asn Gly Ile Gly Ile Pro Thr Lys
 1700 1705 1710
 Ser Pro Ala Lys Asp Gln Ala Ile Thr Asp Leu Asn Asp Ala Val Asp
 1715 1720 1725
 Glu Ala Lys Lys Ala Ile Asp Gln Asp Asn Asn Leu Thr Asp Ala Glu
 1730 1735 1740
 Lys Gln Ala Ala Lys Asp Gln Ile Asp Ser Asp Ala Lys Lys Ala Gln

1745	1750	1755	1760
Glu Ala Ile Asp Asn Ala Lys Thr Asp Asp Glu Val Lys Thr Ala Val			
	1765	1770	1775
Asp Asn Gly Gln Leu Ala Ile Asp Lys Asp Val Ala Asn Ala Ala Ile			
	1780	1785	1790
Asp Asn Ala Val Ala Gly Lys Lys Ala Glu Ile Ala Lys Ala Pro Leu			
	1795	1800	1805
Thr Thr Asp Glu Ala Lys Asp Leu Asn Asp Leu Val Asp Gln Glu Ala			
	1810	1815	1820
Lys Ala Ala Lys Lys Ala Ile Asp Ser Ala Thr Thr Ile Pro Ala Val			
	1825	1830	1835
Asp Asp Ala Lys Asn Thr Gly Val Ala Ala Ile Asn Asn Ile Ala Val			
	1845	1850	1855
Pro Thr Thr Ser Ser Thr Lys Asp Gln Ala Asn Gln Thr Ile Asp Asp			
	1860	1865	1870
Ala Leu Ala Asn Lys Thr Lys Glu Ile Asn Asp Ala Thr Asn Leu Ser			
	1875	1880	1885
Asp Lys Gln Lys Gln Asp Leu Ile Asp Gln Ala Asn Glu Glu Ala Ala			
	1890	1895	1900
Lys Ala Lys Glu Asn Ile Lys Asn Ala Thr Ser Asn Glu Ala Val Asn			
	1905	1910	1915
Lys Ala Thr Thr Asp Gly Val Asp Ala Ile Ala Asn Val Thr Val Pro			
	1925	1930	1935
Ser Leu Asp Asp Ala Lys Lys Asp Ala Ser Gln Leu Ile Asp Asp Val			
	1940	1945	1950
Leu Lys Gln Lys Glu Asp Glu Ile Asn Asn Ala Ser His Leu Thr Asp			
	1955	1960	1965
Gln Glu Lys Gln Asp Leu Ile Asp Gln Ala Gln Asn Ala Ala Asp Glu			
	1970	1975	1980
Ala Lys Asp Lys Ile Asn Gln Ala Thr Thr Asn Asp Asp Val Ala Thr			
	1985	1990	1995
Glu Arg Asp Ala Gly Ala Glu Lys Ile Ala Asn Ile Val Val Pro Ser			
	2005	2010	2015
Leu Glu Asp Ala Lys Asp Lys Ala Thr Lys Ala Ile Asp Asn Ala Leu			
	2020	2025	2030
Ala Asp Lys Thr Lys Glu Ile Asn Asp Gln Thr Asn Leu Ser Asp Gln			
	2035	2040	2045
Glu Lys Asn Asp Leu Ile Asn Gln Ile Thr Asp Ile Ala Asp Lys Ala			
	2050	2055	2060
Lys Asp Lys Ile Asn Asn Ala Ala Thr Asp Ala Asp Ile Ala Lys Asn			
	2065	2070	2075
Glu Lys Asp Gly Ile Asp Ala Ile Val Asp Thr Lys Ile Pro Gly Leu			
	2085	2090	2095
Glu Asp His Lys Lys Asn Ala Ile Asn Ser Leu Asp Glu Ala Lys Ser			
	2100	2105	2110
Thr Lys Leu Ala Gln Ile Asp Gly Ala Thr His Leu Thr Ala Asn Glu			
	2115	2120	2125
Lys Thr Asp Leu Thr Gln Gln Val Asp Ala Glu Tyr Asn Lys Ala Leu			
	2130	2135	2140
Asp Glu Ile Asn Lys Ala Thr Thr Asn Asp Asp Ala Asp Lys Ala Ser			
	2145	2150	2155
Ala Asp Gly Val Glu Ala Ile Leu Asn Ile Lys Val Pro Ser Leu Asn			
	2165	2170	2175
Glu Lys Lys Gln Asp Ser Ile Asn Ala Leu Asn Glu Val Arg Asp Ala			
	2180	2185	2190
Lys Lys Asp Glu Ile Asn Lys Ala Thr Asn Leu Asn Gln Asn Glu Lys			
	2195	2200	2205

```

Asp Glu Leu Asn Lys Gln Val Asp Gln Ile Ala Asp Lys Ala Ile Asn
2210                2215                2220
Ala Ile Asn Glu Ala Asn Asp Asp Gln Thr Ala Lys Asn Ala Glu Asn
2225                2230                2235                2240
Lys Gly Ile Gln Asp Ile Leu Asp Val Lys Val Pro Ser Leu Asp Glu
2245                2250                2255
Val Lys Asn Asn Ala Lys Gln Ala Ile Ala Asp Ala Leu Glu Ser Lys
2260                2265                2270
Gln Asn Glu Ile Asn Lys Ala Val Asn Leu Asp Gln Ser Thr Lys Gln
2275                2280                2285
Asp Leu Val Asn Gln Ala Lys Thr Ala Ala Glu Asn Ala Asn Lys Asn
2290                2295                2300
Ile Asp Leu Ala Thr Thr Asn Asp Glu Val Ile Ala Ala Ser Lys Lys
2305                2310                2315                2320
Gly Val Gln Asn Ile Glu Asn Ile Ile Val Pro Ala Pro Ser Thr Asn
2325                2330                2335
Ser Asp Thr Ser Asn Ile Ser Thr Asp Gln Thr Asp Ser Asp Ala Asn
2340                2345                2350
Lys Ser Gln Ala Gln Asp Ser Asn Lys Thr Ser Asn Asn Asp Ile Asn
2355                2360                2365
Lys Asn Thr Asp Asn Pro Lys His Ser Lys Ser Gly Lys Ser Ser Val
2370                2375                2380
Ser Leu Asp Asp Lys Lys Asn Gln Ala Ile Asn Glu Leu Thr Lys Val
2385                2390                2395                2400
Ala Glu Ala Lys Lys Ala Ala Ile Asn Ser Thr Asn Ile Ser Ala Asp
2405                2410                2415
Ala Lys Ala Arg Leu Asn Ala Gln Val Asp Arg Glu Leu Ala Arg Gly
2420                2425                2430
Lys Asn Ser Ile Ser Gln Ala Arg Asn Ser Glu Glu Leu Thr Ser Ser
2435                2440                2445
Lys Asn Thr Ala Ile Ala Thr Ile Asn Ser Ile Ser Val Ala Pro Lys
2450                2455                2460
Gly Thr Gln Gly Val Asn Ser Arg Glu Asn Tyr Gly Asn Thr Asp Leu
2465                2470                2475                2480
Asn Asn Asn Ser Ile Thr Val Gly Glu Arg Pro Ile Ser His Ile Pro
2485                2490                2495
Thr Ser Asp Lys Gln Glu Thr Leu Pro Gln Thr Gly His His Thr Asn
2500                2505                2510
Glu Gly Leu Thr Ile Leu Gly Thr Leu Val Ala Gly Val Ala Gly Leu
2515                2520                2525
Ile Thr Leu Ala Gly Thr Lys Lys Arg Lys Asp
2530                2535

```

<210> 7

<211> 1773

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 649 - 67 kDa Myosin-crossreactive
streptococcal antigen

<220>

<221> CDS

<222> (1)...(1773)

<400> 7

```

atg tat tat tcc aat ggt aat tac gaa gca ttt gca gat cct aag aaa   48
Met Tyr Tyr Ser Asn Gly Asn Tyr Glu Ala Phe Ala Asp Pro Lys Lys
 1             5             10             15

cct gca ggc gtg gac aag aaa tct gct tat att att ggt agt ggt cta   96
Pro Ala Gly Val Asp Lys Lys Ser Ala Tyr Ile Ile Gly Ser Gly Leu
          20             25             30

gct ggt ctt tct aca gcc gta ttt tta gta cga gat gca caa atg aaa  144
Ala Gly Leu Ser Thr Ala Val Phe Leu Val Arg Asp Ala Gln Met Lys
      35             40             45

ggt gaa aat att cat att tta gaa gaa tta cca gtt gct ggt ggt tct  192
Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser
      50             55             60

ctt gat ggt gca gat cgt ccc aat gcg ggc ttt gtt gtt cgt ggt gga  240
Leu Asp Gly Ala Asp Arg Pro Asn Ala Gly Phe Val Val Arg Gly Gly
      65             70             75             80

cgc gaa atg gag aat cat ttt gaa tgt tta tgg gat atg tac cgc tca  288
Arg Glu Met Glu Asn His Phe Glu Cys Leu Trp Asp Met Tyr Arg Ser
          85             90             95

att cca agt ttg gaa gtt cca ggc gca tcg tat ctt gat gaa tat tat  336
Ile Pro Ser Leu Glu Val Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr
      100             105             110

tgg ctt gac aaa gaa gat ccc aat tca tca aat tgt cgt tta att tat  384
Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Ile Tyr
      115             120             125

aat cgt gga gat cgt ctt cca agt gat gga caa tat ggt tta ggc aaa  432
Asn Arg Gly Asp Arg Leu Pro Ser Asp Gly Gln Tyr Gly Leu Gly Lys
      130             135             140

tgt gct aat gaa att gtc aag ttg att atg acc cct gaa aag gaa att  480
Cys Ala Asn Glu Ile Val Lys Leu Ile Met Thr Pro Glu Lys Glu Ile
      145             150             155             160

gaa ggg caa act att gaa gaa ttt ttc agt gat gag ttc ttt aag act  528
Glu Gly Gln Thr Ile Glu Glu Phe Phe Ser Asp Glu Phe Phe Lys Thr
          165             170             175

aat ttc tgg aca tac tgg tca aca atg ttt gct ttt gaa aaa tgg cat  576
Asn Phe Trp Thr Tyr Trp Ser Thr Met Phe Ala Phe Glu Lys Trp His
          180             185             190

tca tta gcc gaa atg cgc cgt tat gca atg cgc ttt att cat cat att  624
Ser Leu Ala Glu Met Arg Arg Tyr Ala Met Arg Phe Ile His His Ile
      195             200             205

gat ggg ttg cct gat ttt act gcc tta aag ttt aat aag tat aat caa  672

```

Asp Gly Leu Pro Asp Phe Thr Ala Leu Lys Phe Asn Lys Tyr Asn Gln	
210 215 220	
tat gaa tca atg gtt aaa cca ctt ctt gca tat ctt aaa gat cat ggt	720
Tyr Glu Ser Met Val Lys Pro Leu Leu Ala Tyr Leu Lys Asp His Gly	
225 230 235 240	
gtg caa ttt gaa tat gac tgc cat gtt aag aat gtc gag gta gat cat	768
Val Gln Phe Glu Tyr Asp Cys His Val Lys Asn Val Glu Val Asp His	
245 250 255	
gaa ggc gac agt aaa att gcc aag aag att gtt atg acg cag aat ggc	816
Glu Gly Asp Ser Lys Ile Ala Lys Lys Ile Val Met Thr Gln Asn Gly	
260 265 270	
aaa gat aaa gaa att gat tta aca cat aat gac atc gtc ttt gta act	864
Lys Asp Lys Glu Ile Asp Leu Thr His Asn Asp Ile Val Phe Val Thr	
275 280 285	
aac ggt tca att act gaa agt tct act tat ggt gat cag aat act cca	912
Asn Gly Ser Ile Thr Glu Ser Ser Thr Tyr Gly Asp Gln Asn Thr Pro	
290 295 300	
gct cca att act aat gct aaa ggt gat tca tgg aag tta tgg gaa aat	960
Ala Pro Ile Thr Asn Ala Lys Gly Asp Ser Trp Lys Leu Trp Glu Asn	
305 310 315 320	
ttg gct aag caa gat cca gct ttc ggt cat cca gat gta ttc tgc gaa	1008
Leu Ala Lys Gln Asp Pro Ala Phe Gly His Pro Asp Val Phe Cys Glu	
325 330 335	
aac cta cca gaa cgt agt tgg ttt gtt tcc gca act gct aca ttg gag	1056
Asn Leu Pro Glu Arg Ser Trp Phe Val Ser Ala Thr Ala Thr Leu Glu	
340 345 350	
aat aag aag ctt gca cca tat ttt gag cgc tta acc aag cgc agt ttg	1104
Asn Lys Lys Leu Ala Pro Tyr Phe Glu Arg Leu Thr Lys Arg Ser Leu	
355 360 365	
tat gat ggt aag gtt aac aca ggt ggt att att act atc gtt gat tct	1152
Tyr Asp Gly Lys Val Asn Thr Gly Gly Ile Ile Thr Ile Val Asp Ser	
370 375 380	
aac tgg gaa ctt agt ttt act att cac cgt caa cca cat ttt aag agt	1200
Asn Trp Glu Leu Ser Phe Thr Ile His Arg Gln Pro His Phe Lys Ser	
385 390 395 400	
caa aac cca gac caa att gtt gtt tgg att tat gca ctt tat tca gat	1248
Gln Asn Pro Asp Gln Ile Val Val Trp Ile Tyr Ala Leu Tyr Ser Asp	
405 410 415	
act gaa ggt aac tat att aaa aag aga att gtt gat tgt act ggc aaa	1296
Thr Glu Gly Asn Tyr Ile Lys Lys Arg Ile Val Asp Cys Thr Gly Lys	
420 425 430	
gaa att gca gaa gag ttg ctt tac cac tta ggt gtt ccc gaa agc caa	1344
Glu Ile Ala Glu Glu Leu Leu Tyr His Leu Gly Val Pro Glu Ser Gln	

435	440	445	
att agt gaa ttg gcc agc gag gaa aat atg aat acc gta cca gtt tat			1392
Ile Ser Glu Leu Ala Ser Glu Glu Asn Met Asn Thr Val Pro Val Tyr			
450	455	460	
atg cca tat att act agt tac ttc atg cct cgt cgt gat ggt gat cgt			1440
Met Pro Tyr Ile Thr Ser Tyr Phe Met Pro Arg Arg Asp Gly Asp Arg			
465	470	475	480
cca gat gtt gtg cca gaa gga tca ata aac ctt gcc ttt att ggt aat			1488
Pro Asp Val Val Pro Glu Gly Ser Ile Asn Leu Ala Phe Ile Gly Asn			
	485	490	495
ttt gca gaa tct cca aca aga gat act gtg ttt act act gag tat tct			1536
Phe Ala Glu Ser Pro Thr Arg Asp Thr Val Phe Thr Thr Glu Tyr Ser			
	500	505	510
gtc aga aca gct atg gag gct gtt tat aca tta ctt aat gtt gat cgt			1584
Val Arg Thr Ala Met Glu Ala Val Tyr Thr Leu Leu Asn Val Asp Arg			
	515	520	525
ggc gta cca gaa gta ttt gac tca att tat gat att cgc cag ctt tta			1632
Gly Val Pro Glu Val Phe Asp Ser Ile Tyr Asp Ile Arg Gln Leu Leu			
	530	535	540
cgt gct atg tac tac atg tca gac aag aag aag cta gca gat caa gat			1680
Arg Ala Met Tyr Tyr Met Ser Asp Lys Lys Lys Leu Ala Asp Gln Asp			
	545	550	555
atg cct ctt cct gaa aag ctt gcc gta aag aca gga atg aga aag att			1728
Met Pro Leu Pro Glu Lys Leu Ala Val Lys Thr Gly Met Arg Lys Ile			
	565	570	575
aaa aag act tgg gta gaa gaa cta ctt aaa gaa gca aat tta gtc			1773
Lys Lys Thr Trp Val Glu Glu Leu Leu Lys Glu Ala Asn Leu Val			
	580	585	590

<210> 8

<211> 591

<212> PRT

<213> Lactobacillus acidophilus

<400> 8

Met Tyr Tyr Ser Asn Gly Asn Tyr Glu Ala Phe Ala Asp Pro Lys Lys	
1 5 10 15	
Pro Ala Gly Val Asp Lys Lys Ser Ala Tyr Ile Ile Gly Ser Gly Leu	
20 25 30	
Ala Gly Leu Ser Thr Ala Val Phe Leu Val Arg Asp Ala Gln Met Lys	
35 40 45	
Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser	
50 55 60	
Leu Asp Gly Ala Asp Arg Pro Asn Ala Gly Phe Val Val Arg Gly Gly	
65 70 75 80	
Arg Glu Met Glu Asn His Phe Glu Cys Leu Trp Asp Met Tyr Arg Ser	

- 26 -

Arg Ala Met Tyr Tyr Met Ser Asp Lys Lys Lys Leu Ala Asp Gln Asp
 545 550 555 560
 Met Pro Leu Pro Glu Lys Leu Ala Val Lys Thr Gly Met Arg Lys Ile
 565 570 575
 Lys Lys Thr Trp Val Glu Glu Leu Leu Lys Glu Ala Asn Leu Val
 580 585 590

<210> 9

<211> 1770

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 555 myosin-crossreactive antigen

<220>

<221> CDS

<222> (1)...(1770)

<400> 9

atg cat tat agt agt ggt aat tat gaa gct ttt gta aac gca agt aaa 48
 Met His Tyr Ser Ser Gly Asn Tyr Glu Ala Phe Val Asn Ala Ser Lys
 1 5 10 15

cct aag gat gtc gat cag aag tcc gca tat ctt gtt ggt tca ggt ttg 96
 Pro Lys Asp Val Asp Gln Lys Ser Ala Tyr Leu Val Gly Ser Gly Leu
 20 25 30

gca tcg ctt gct agt gct gta ttt tta att cgt gat ggt cac atg aag 144
 Ala Ser Leu Ala Ser Ala Val Phe Leu Ile Arg Asp Gly His Met Lys
 35 40 45

ggg gat aga att cat atc ctt gaa gaa ttg agc ctt cca ggt ggt tca 192
 Gly Asp Arg Ile His Ile Leu Glu Glu Leu Ser Leu Pro Gly Gly Ser
 50 55 60

atg gat ggg atc tat aat aag caa aaa gaa agc tac atc att cgt ggt 240
 Met Asp Gly Ile Tyr Asn Lys Gln Lys Glu Ser Tyr Ile Ile Arg Gly
 65 70 75 80

ggg cgt gaa atg gaa gcc cat ttt gaa tgc ttg tgg gac ttg ttt aga 288
 Gly Arg Glu Met Glu Ala His Phe Glu Cys Leu Trp Asp Leu Phe Arg
 85 90 95

tcg att cca tca gct gaa aat aaa gat gaa tcg gtc ctg gat gaa ttt 336
 Ser Ile Pro Ser Ala Glu Asn Lys Asp Glu Ser Val Leu Asp Glu Phe
 100 105 110

tac cgt tta aat aga aaa gat cca agt ttc gca aag act cgt gtc att 384
 Tyr Arg Leu Asn Arg Lys Asp Pro Ser Phe Ala Lys Thr Arg Val Ile
 115 120 125

gtt aac cgc gga cat gaa ctt cca act gac ggt caa tta ctt ctt act 432

Val	Asn	Arg	Gly	His	Glu	Leu	Pro	Thr	Asp	Gly	Gln	Leu	Leu	Leu	Thr		
130						135					140						
ccc	aag	gct	gtt	aaa	gaa	att	att	gat	ctt	tgc	tta	act	cct	gaa	aaa	480	
Pro	Lys	Ala	Val	Lys	Glu	Ile	Ile	Asp	Leu	Cys	Leu	Thr	Pro	Glu	Lys		
145					150					155					160		
gat	tta	caa	aat	aaa	aaa	att	aat	gaa	gtc	ttt	agt	aaa	gaa	ttt	ttt	528	
Asp	Leu	Gln	Asn	Lys	Lys	Ile	Asn	Glu	Val	Phe	Ser	Lys	Glu	Phe	Phe		
				165					170						175		
gaa	tca	aac	ttc	tgg	ctt	tac	tgg	tca	acg	atg	ttt	gcc	ttt	gag	cca	576	
Glu	Ser	Asn	Phe	Trp	Leu	Tyr	Trp	Ser	Thr	Met	Phe	Ala	Phe	Glu	Pro		
			180					185					190				
tgg	gca	agt	gcg	atg	gaa	atg	cgt	cgt	tac	tta	atg	cgt	ttt	gtt	caa	624	
Trp	Ala	Ser	Ala	Met	Glu	Met	Arg	Arg	Tyr	Leu	Met	Arg	Phe	Val	Gln		
	195						200					205					
cac	gtt	tct	aca	ctt	aag	aat	tta	tca	tca	cta	cgc	ttt	act	aag	tat	672	
His	Val	Ser	Thr	Leu	Lys	Asn	Leu	Ser	Ser	Leu	Arg	Phe	Thr	Lys	Tyr		
	210					215					220						
aac	caa	tat	gaa	tca	tta	att	tta	cca	atg	gtt	aaa	tac	ttg	aaa	gat	720	
Asn	Gln	Tyr	Glu	Ser	Leu	Ile	Leu	Pro	Met	Val	Lys	Tyr	Leu	Lys	Asp		
225					230					235					240		
cgc	ggc	gtg	caa	ttc	cat	tac	aac	acc	gtt	gtt	gat	aat	atc	ttt	gtt	768	
Arg	Gly	Val	Gln	Phe	His	Tyr	Asn	Thr	Val	Val	Asp	Asn	Ile	Phe	Val		
				245				250						255			
aac	cgt	tca	aat	ggc	gaa	aag	att	gct	aag	caa	att	ctt	tta	act	gaa	816	
Asn	Arg	Ser	Asn	Gly	Glu	Lys	Ile	Ala	Lys	Gln	Ile	Leu	Leu	Thr	Glu		
			260					265					270				
aac	ggc	gaa	aaa	aag	agc	atc	gat	tta	aca	gaa	aat	gac	ctc	gtc	ttc	864	
Asn	Gly	Glu	Lys	Lys	Ser	Ile	Asp	Leu	Thr	Glu	Asn	Asp	Leu	Val	Phe		
		275					280					285					
gtt	act	aac	ggc	tca	att	act	gaa	agt	aca	act	tat	ggc	gat	aac	ttg	912	
Val	Thr	Asn	Gly	Ser	Ile	Thr	Glu	Ser	Thr	Thr	Tyr	Gly	Asp	Asn	Leu		
	290					295					300						
cac	cca	gct	tct	gag	gaa	cat	aaa	tta	ggc	gct	act	tgg	aaa	tta	tgg	960	
His	Pro	Ala	Ser	Glu	Glu	His	Lys	Leu	Gly	Ala	Thr	Trp	Lys	Leu	Trp		
305					310					315					320		
caa	aac	ttg	gca	gcg	caa	gat	gat	gac	ttc	ggc	cac	cca	gat	gtc	ttc	1008	
Gln	Asn	Leu	Ala	Ala	Gln	Asp	Asp	Asp	Phe	Gly	His	Pro	Asp	Val	Phe		
				325					330					335			
tgc	aag	gat	att	cca	aag	gct	aac	tgg	gta	atg	tct	gct	aca	att	act	1056	
Cys	Lys	Asp	Ile	Pro	Lys	Ala	Asn	Trp	Val	Met	Ser	Ala	Thr	Ile	Thr		
			340					345					350				
ttt	aag	aat	aat	gat	att	gtg	cca	ttc	att	gaa	gca	gtt	aat	aag	aag	1104	
Phe	Lys	Asn	Asn	Asp	Ile	Val	Pro	Phe	Ile	Glu	Ala	Val	Asn	Lys	Lys		

355	360	365	
gat cca cac agc ggc tca att gta act agt ggg cct act acg att aag Asp Pro His Ser Gly Ser Ile Val Thr Ser Gly Pro Thr Thr Ile Lys 370 375 380			1152
gat tct aac tgg cta ctt ggt tat tca atc agt cgt cag cct cac ttt Asp Ser Asn Trp Leu Leu Gly Tyr Ser Ile Ser Arg Gln Pro His Phe 385 390 395 400			1200
gaa gca caa aag cct aac gaa ttg att gta tgg ctt tat ggt ttg ttc Glu Ala Gln Lys Pro Asn Glu Leu Ile Val Trp Leu Tyr Gly Leu Phe 405 410 415			1248
tca gac acc aaa ggt aac tat gtt gaa aag act atg cct gac tgt aac Ser Asp Thr Lys Gly Asn Tyr Val Glu Lys Thr Met Pro Asp Cys Asn 420 425 430			1296
ggg att gaa tta tgt gaa gaa tgg ctt tac cac atg ggt gtt cct gaa Gly Ile Glu Leu Cys Glu Glu Trp Leu Tyr His Met Gly Val Pro Glu 435 440 445			1344
gaa aga atc cca gaa atg gct tca gct gct acg act att cca gca cac Glu Arg Ile Pro Glu Met Ala Ser Ala Ala Thr Thr Ile Pro Ala His 450 455 460			1392
atg cca tat att act tca tac ttc atg cca aga gca tta ggc gac aga Met Pro Tyr Ile Thr Ser Tyr Phe Met Pro Arg Ala Leu Gly Asp Arg 465 470 475 480			1440
ccc aag gtt gtg cca gac cac tca aag aac ttg gcc ttc att ggt aac Pro Lys Val Val Pro Asp His Ser Lys Asn Leu Ala Phe Ile Gly Asn 485 490 495			1488
ttt gct gaa acg cca aga gac act gtc ttt acc act gaa tac tct gtc Phe Ala Glu Thr Pro Arg Asp Thr Val Phe Thr Thr Glu Tyr Ser Val 500 505 510			1536
aga act gcg atg gaa gct gta tac acc ttg ctt aac att gat cgt ggt Arg Thr Ala Met Glu Ala Val Tyr Thr Leu Leu Asn Ile Asp Arg Gly 515 520 525			1584
gtg cca gaa gta ttt gca tct gcc ttc gat gtc aga atg ctc atg aac Val Pro Glu Val Phe Ala Ser Ala Phe Asp Val Arg Met Leu Met Asn 530 535 540			1632
gca atg tac tac ttg aat gat caa aag aag ctt gaa gat ctt gat ttg Ala Met Tyr Tyr Leu Asn Asp Gln Lys Lys Leu Glu Asp Leu Asp Leu 545 550 555 560			1680
cct att gct gaa aag ttg gca att aag ggg atg ctc aag aaa gtt aag Pro Ile Ala Glu Lys Leu Ala Ile Lys Gly Met Leu Lys Lys Val Lys 565 570 575			1728
ggc act tat ata gag gaa ttg ctt aag aag tat aag ttg gtt Gly Thr Tyr Ile Glu Glu Leu Leu Lys Lys Tyr Lys Leu Val 580 585 590			1770

<210> 10
 <211> 590
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 10
 Met His Tyr Ser Ser Gly Asn Tyr Glu Ala Phe Val Asn Ala Ser Lys
 1 5 10 15
 Pro Lys Asp Val Asp Gln Lys Ser Ala Tyr Leu Val Gly Ser Gly Leu
 20 25 30
 Ala Ser Leu Ala Ser Ala Val Phe Leu Ile Arg Asp Gly His Met Lys
 35 40 45
 Gly Asp Arg Ile His Ile Leu Glu Glu Leu Ser Leu Pro Gly Gly Ser
 50 55 60
 Met Asp Gly Ile Tyr Asn Lys Gln Lys Glu Ser Tyr Ile Ile Arg Gly
 65 70 75 80
 Gly Arg Glu Met Glu Ala His Phe Glu Cys Leu Trp Asp Leu Phe Arg
 85 90 95
 Ser Ile Pro Ser Ala Glu Asn Lys Asp Glu Ser Val Leu Asp Glu Phe
 100 105 110
 Tyr Arg Leu Asn Arg Lys Asp Pro Ser Phe Ala Lys Thr Arg Val Ile
 115 120 125
 Val Asn Arg Gly His Glu Leu Pro Thr Asp Gly Gln Leu Leu Leu Thr
 130 135 140
 Pro Lys Ala Val Lys Glu Ile Ile Asp Leu Cys Leu Thr Pro Glu Lys
 145 150 155 160
 Asp Leu Gln Asn Lys Lys Ile Asn Glu Val Phe Ser Lys Glu Phe Phe
 165 170 175
 Glu Ser Asn Phe Trp Leu Tyr Trp Ser Thr Met Phe Ala Phe Glu Pro
 180 185 190
 Trp Ala Ser Ala Met Glu Met Arg Arg Tyr Leu Met Arg Phe Val Gln
 195 200 205
 His Val Ser Thr Leu Lys Asn Leu Ser Ser Leu Arg Phe Thr Lys Tyr
 210 215 220
 Asn Gln Tyr Glu Ser Leu Ile Leu Pro Met Val Lys Tyr Leu Lys Asp
 225 230 235 240
 Arg Gly Val Gln Phe His Tyr Asn Thr Val Val Asp Asn Ile Phe Val
 245 250 255
 Asn Arg Ser Asn Gly Glu Lys Ile Ala Lys Gln Ile Leu Leu Thr Glu
 260 265 270
 Asn Gly Glu Lys Lys Ser Ile Asp Leu Thr Glu Asn Asp Leu Val Phe
 275 280 285
 Val Thr Asn Gly Ser Ile Thr Glu Ser Thr Thr Tyr Gly Asp Asn Leu
 290 295 300
 His Pro Ala Ser Glu Glu His Lys Leu Gly Ala Thr Trp Lys Leu Trp
 305 310 315 320
 Gln Asn Leu Ala Ala Gln Asp Asp Asp Phe Gly His Pro Asp Val Phe
 325 330 335
 Cys Lys Asp Ile Pro Lys Ala Asn Trp Val Met Ser Ala Thr Ile Thr
 340 345 350
 Phe Lys Asn Asn Asp Ile Val Pro Phe Ile Glu Ala Val Asn Lys Lys
 355 360 365
 Asp Pro His Ser Gly Ser Ile Val Thr Ser Gly Pro Thr Thr Ile Lys
 370 375 380

Asp Ser Asn Trp Leu Leu Gly Tyr Ser Ile Ser Arg Gln Pro His Phe
 385 390 395 400
 Glu Ala Gln Lys Pro Asn Glu Leu Ile Val Trp Leu Tyr Gly Leu Phe
 405 410 415
 Ser Asp Thr Lys Gly Asn Tyr Val Glu Lys Thr Met Pro Asp Cys Asn
 420 425 430
 Gly Ile Glu Leu Cys Glu Glu Trp Leu Tyr His Met Gly Val Pro Glu
 435 440 445
 Glu Arg Ile Pro Glu Met Ala Ser Ala Ala Thr Thr Ile Pro Ala His
 450 455 460
 Met Pro Tyr Ile Thr Ser Tyr Phe Met Pro Arg Ala Leu Gly Asp Arg
 465 470 475 480
 Pro Lys Val Val Pro Asp His Ser Lys Asn Leu Ala Phe Ile Gly Asn
 485 490 495
 Phe Ala Glu Thr Pro Arg Asp Thr Val Phe Thr Thr Glu Tyr Ser Val
 500 505 510
 Arg Thr Ala Met Glu Ala Val Tyr Thr Leu Leu Asn Ile Asp Arg Gly
 515 520 525
 Val Pro Glu Val Phe Ala Ser Ala Phe Asp Val Arg Met Leu Met Asn
 530 535 540
 Ala Met Tyr Tyr Leu Asn Asp Gln Lys Lys Leu Glu Asp Leu Asp Leu
 545 550 555 560
 Pro Ile Ala Glu Lys Leu Ala Ile Lys Gly Met Leu Lys Lys Val Lys
 565 570 575
 Gly Thr Tyr Ile Glu Glu Leu Leu Lys Lys Tyr Lys Leu Val
 580 585 590

<210> 11

<211> 687

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1244 - sortase SrtA

<220>

<221> CDS

<222> (1)...(687)

<400> 11

atg gca aag aat aaa caa aag agt agt gtt act acg att tta gtt aga 48
 Met Ala Lys Asn Lys Gln Lys Ser Ser Val Thr Thr Ile Leu Val Arg
 1 5 10 15

att gtt gcg gtt ctt ttg tta gtt ata ggt ttg gtc ctt ata ttt aat 96
 Ile Val Ala Val Leu Leu Leu Val Ile Gly Leu Val Leu Ile Phe Asn
 20 25 30

aaa caa att agt aat caa atg atc aag cat aat caa cag tca gct ttg 144
 Lys Gln Ile Ser Asn Gln Met Ile Lys His Asn Gln Gln Ser Ala Leu
 35 40 45

aca aca cta act aaa aaa caa gtt gaa gca aat caa aag aaa aaa ggt 192

```

Thr Thr Leu Thr Lys Lys Gln Val Glu Ala Asn Gln Lys Lys Lys Gly
  50                               55                               60

atg tat gac ttt agt aag gtg aag tcg atg aat atg ggg caa gct gca 240
Met Tyr Asp Phe Ser Lys Val Lys Ser Met Asn Met Gly Gln Ala Ala
  65                               70                               75                               80

cga tca cag gtt aag aaa act tct gga gca att ggt gca ctt gca gtg 288
Arg Ser Gln Val Lys Lys Thr Ser Gly Ala Ile Gly Ala Leu Ala Val
                               85                               90                               95

cct gat gta aat atg tat ttg cca atc atg ctt ggt tta tca gat gat 336
Pro Asp Val Asn Met Tyr Leu Pro Ile Met Leu Gly Leu Ser Asp Asp
                               100                              105                              110

gca atg tct acg ggc ggc gga acc atg cgg gca gat caa gta atg ggg 384
Ala Met Ser Thr Gly Gly Gly Thr Met Arg Ala Asp Gln Val Met Gly
                               115                              120                              125

aag ggg aat tat cca ctt gca ggc cat tat atg act gct aag ggt att 432
Lys Gly Asn Tyr Pro Leu Ala Gly His Tyr Met Thr Ala Lys Gly Ile
                               130                              135                              140

ctt ttt tca cca ctt gaa gat gta aaa aag gga caa aga atc tat tta 480
Leu Phe Ser Pro Leu Glu Asp Val Lys Lys Gly Gln Arg Ile Tyr Leu
145                               150                               155                               160

act aat tta aag aaa atc tat att tat cgt att tac atg aaa aag att 528
Thr Asn Leu Lys Lys Ile Tyr Ile Tyr Arg Ile Tyr Met Lys Lys Ile
                               165                              170                              175

gta gat cca tct gca gtt tgg tta gtt aat aat act aag aaa aat att 576
Val Asp Pro Ser Ala Val Trp Leu Val Asn Asn Thr Lys Lys Asn Ile
                               180                              185                              190

gta act tta att act tgt gcg gac ggt ggt act aat cgc tgg gct att 624
Val Thr Leu Ile Thr Cys Ala Asp Gly Gly Thr Asn Arg Trp Ala Ile
                               195                              200                              205

cgg ggt aat ttg att aaa act gaa aaa gca aca gat gaa aat ttg aag 672
Arg Gly Asn Leu Ile Lys Thr Glu Lys Ala Thr Asp Glu Asn Leu Lys
210                               215                               220

gtt ttc aaa tta aag
Val Phe Lys Leu Lys
225

```

<210> 12

<211> 229

<212> PRT

<213> Lactobacillus acidophilus

<400> 12

```

Met Ala Lys Asn Lys Gln Lys Ser Ser Val Thr Thr Ile Leu Val Arg
  1           5           10           15
Ile Val Ala Val Leu Leu Leu Val Ile Gly Leu Val Leu Ile Phe Asn

```

		20						25					30				
Lys	Gln	Ile	Ser	Asn	Gln	Met	Ile	Lys	His	Asn	Gln	Gln	Ser	Ala	Leu		
		35					40					45					
Thr	Thr	Leu	Thr	Lys	Lys	Gln	Val	Glu	Ala	Asn	Gln	Lys	Lys	Lys	Gly		
		50				55					60						
Met	Tyr	Asp	Phe	Ser	Lys	Val	Lys	Ser	Met	Asn	Met	Gly	Gln	Ala	Ala		
65					70					75				80			
Arg	Ser	Gln	Val	Lys	Lys	Thr	Ser	Gly	Ala	Ile	Gly	Ala	Leu	Ala	Val		
			85						90					95			
Pro	Asp	Val	Asn	Met	Tyr	Leu	Pro	Ile	Met	Leu	Gly	Leu	Ser	Asp	Asp		
		100						105					110				
Ala	Met	Ser	Thr	Gly	Gly	Gly	Thr	Met	Arg	Ala	Asp	Gln	Val	Met	Gly		
		115					120					125					
Lys	Gly	Asn	Tyr	Pro	Leu	Ala	Gly	His	Tyr	Met	Thr	Ala	Lys	Gly	Ile		
130					135						140						
Leu	Phe	Ser	Pro	Leu	Glu	Asp	Val	Lys	Lys	Gly	Gln	Arg	Ile	Tyr	Leu		
145					150					155					160		
Thr	Asn	Leu	Lys	Lys	Ile	Tyr	Ile	Tyr	Arg	Ile	Tyr	Met	Lys	Lys	Ile		
			165					170						175			
Val	Asp	Pro	Ser	Ala	Val	Trp	Leu	Val	Asn	Asn	Thr	Lys	Lys	Asn	Ile		
		180					185						190				
Val	Thr	Leu	Ile	Thr	Cys	Ala	Asp	Gly	Gly	Thr	Asn	Arg	Trp	Ala	Ile		
	195						200					205					
Arg	Gly	Asn	Leu	Ile	Lys	Thr	Glu	Lys	Ala	Thr	Asp	Glu	Asn	Leu	Lys		
210						215					220						
Val	Phe	Lys	Leu	Lys													
225																	

<210> 13

<211> 1929

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1609 - mucus binding protein precursor

<220>

<221> CDS

<222> (1)...(1929)

<400> 13

atg	tct	cta	ttt	ggt	aaa	aag	aaa	aaa	gct	atc	gtt	aat	tat	ata	gat	48
Met	Ser	Leu	Phe	Gly	Lys	Lys	Lys	Lys	Ala	Ile	Val	Asn	Tyr	Ile	Asp	
1				5					10					15		

ttg	gac	aat	gat	aaa	aat	aat	atc	gct	aca	tca	ggt	gaa	ttg	tta	ggt	96
Leu	Asp	Asn	Asp	Lys	Asn	Asn	Ile	Ala	Thr	Ser	Gly	Glu	Leu	Leu	Gly	
			20					25					30			

aat	gtt	ggt	gaa	gag	att	ggt	tac	agt	agt	tca	gat	cag	att	gat	gct	144
Asn	Val	Gly	Glu	Glu	Ile	Gly	Tyr	Ser	Ser	Ser	Asp	Gln	Ile	Asp	Ala	
		35					40					45				

tta aaa aag caa ggt tat gtt ctt gta aat aat agt ttt gat ccg agt	192
Leu Lys Lys Gln Gly Tyr Val Leu Val Asn Asn Ser Phe Asp Pro Ser	
50 55 60	
gat aaa cca act ttt tca aat gaa gat gtt caa act tat act att tca	240
Asp Lys Pro Thr Phe Ser Asn Glu Asp Val Gln Thr Tyr Thr Ile Ser	
65 70 75 80	
ttt aaa cat gat gta gaa gca gtt gat aaa cct aat tct gat ttt gga	288
Phe Lys His Asp Val Glu Ala Val Asp Lys Pro Asn Ser Asp Phe Gly	
85 90 95	
att agt gaa agt gat tta caa aaa gtg ggt acg caa act gtc cat tat	336
Ile Ser Glu Ser Asp Leu Gln Lys Val Gly Thr Gln Thr Val His Tyr	
100 105 110	
gaa ggt gct gct act aga aca cca aaa gat aat gtg agt cag gtt gtt	384
Glu Gly Ala Ala Thr Arg Thr Pro Lys Asp Asn Val Ser Gln Val Val	
115 120 125	
ttt aaa cgt agt gta gtc tat gat aaa ata cta aaa aaa atc att agt	432
Phe Lys Arg Ser Val Val Tyr Asp Lys Ile Leu Lys Lys Ile Ile Ser	
130 135 140	
act tca aca tgg atg cct gaa aag caa agc ttt tta ttg atc gct aca	480
Thr Ser Thr Trp Met Pro Glu Lys Gln Ser Phe Leu Leu Ile Ala Thr	
145 150 155 160	
cct gaa gtt tcg gga tat act act gtt caa act act gtg ggt ggt gaa	528
Pro Glu Val Ser Gly Tyr Thr Thr Val Gln Thr Thr Val Gly Gly Glu	
165 170 175	
acg gta act cct gaa gat tgt gat cgt aat tat gtt gtt gaa tat gat	576
Thr Val Thr Pro Glu Asp Cys Asp Arg Asn Tyr Val Val Glu Tyr Asp	
180 185 190	
att aat cat caa cca tct gtc gct gat caa aaa gta gct gtt aaa tat	624
Ile Asn His Gln Pro Ser Val Ala Asp Gln Lys Val Ala Val Lys Tyr	
195 200 205	
gtc gat caa gat cta gaa aat aaa gaa att act gaa gat ata tta act	672
Val Asp Gln Asp Leu Glu Asn Lys Glu Ile Thr Glu Asp Ile Leu Thr	
210 215 220	
ggg atg cca aat tcc ttg gta gat tat gat cct aaa gct act att gaa	720
Gly Met Pro Asn Ser Leu Val Asp Tyr Asp Pro Lys Ala Thr Ile Glu	
225 230 235 240	
aga ctc gaa agt gac gaa gga tac gct tta gta aat aat ggt tat aat	768
Arg Leu Glu Ser Asp Glu Gly Tyr Ala Leu Val Asn Asn Gly Tyr Asn	
245 250 255	
cct gcg ggt gaa gta caa ttt tat agc aac aat gac gat tat gtg cct	816
Pro Ala Gly Glu Val Gln Phe Tyr Ser Asn Asn Asp Asp Tyr Val Pro	
260 265 270	
gtc ttt gtt atg aca atg aag cac act atc ggt caa gta gat agt gaa	864

Val Phe Val Met Thr Met Lys His Thr Ile Gly Gln Val Asp Ser Glu	
275 280 285	
cat cct gat agt aaa gta aat aag aac gaa tat gat aaa gat gtc gca	912
His Pro Asp Ser Lys Val Asn Lys Asn Glu Tyr Asp Lys Asp Val Ala	
290 295 300	
ttt act att aat tat gaa gga gca gat gct gct act cct gtt aac aat	960
Phe Thr Ile Asn Tyr Glu Gly Ala Asp Ala Ala Thr Pro Val Asn Asn	
305 310 315 320	
gtt caa aga tca cac tgg agt cgt agt tta acc gtt gat cgt gtt act	1008
Val Gln Arg Ser His Trp Ser Arg Ser Leu Thr Val Asp Arg Val Thr	
325 330 335	
ggt gaa att tta cct gga ggt aaa tat aca act gat tgg aaa gtg gat	1056
Gly Glu Ile Leu Pro Gly Gly Lys Tyr Thr Thr Asp Trp Lys Val Asp	
340 345 350	
cgt gaa aag tat gat gat gtt gat gtt cca gta gtt gat gga tat cac	1104
Arg Glu Lys Tyr Asp Asp Val Asp Val Pro Val Val Asp Gly Tyr His	
355 360 365	
acc gat gtt aaa atg atc aaa ggt gcc gag gtt aca cga gaa aat att	1152
Thr Asp Val Lys Met Ile Lys Gly Ala Glu Val Thr Arg Glu Asn Ile	
370 375 380	
att aga aca gta aat tat gtt gct aat ggc cat att att cca gtg gat	1200
Ile Arg Thr Val Asn Tyr Val Ala Asn Gly His Ile Ile Pro Val Asp	
385 390 395 400	
tct gat ggt aaa gaa att gtt ggt gca cca cat cca gtc ttt caa act	1248
Ser Asp Gly Lys Glu Ile Val Gly Ala Pro His Pro Val Phe Gln Thr	
405 410 415	
gat cca aat gat cca act caa gtg att act gat gaa cca gtg cca aag	1296
Asp Pro Asn Asp Pro Thr Gln Val Ile Thr Asp Glu Pro Val Pro Lys	
420 425 430	
att gat gga tac aag tgt aat ttg gca act att aca ccg tat aat cca	1344
Ile Asp Gly Tyr Lys Cys Asn Leu Ala Thr Ile Thr Pro Tyr Asn Pro	
435 440 445	
gca aaa gat atg gaa gtt aag tat aag gca gaa gat tct gat gtt tta	1392
Ala Lys Asp Met Glu Val Lys Tyr Lys Ala Glu Asp Ser Asp Val Leu	
450 455 460	
gta att tct gtt ggt gat aag aaa ccc aag tca gaa act aaa gca gtt	1440
Val Ile Ser Val Gly Asp Lys Lys Pro Lys Ser Glu Thr Lys Ala Val	
465 470 475 480	
tca gtg gaa aag ccg gtt gtt aaa cct gac cct aaa ccg gaa aat act	1488
Ser Val Glu Lys Pro Val Val Lys Pro Asp Pro Lys Pro Glu Asn Thr	
485 490 495	
aat tca gta act caa cct gct gtt act caa gat caa aat cat gat cat	1536
Asn Ser Val Thr Gln Pro Ala Val Thr Gln Asp Gln Asn His Asp His	

500	505	510	
gat caa gtt gct ata att aac ttt	ata gat ctt gac cat	gat ggt aaa	1584
Asp Gln Val Ala Ile Ile Asn Phe	Ile Asp Leu Asp His	Asp Gly Lys	
515	520	525	
caa ctg acc tca tct ggt cca cta act ggt aag	cca ggt gaa agc att		1632
Gln Leu Thr Ser Ser Gly Pro Leu Thr Gly Lys	Pro Gly Glu Ser Ile		
530	535	540	
aac gat ttg tat agt aca gaa tta cca tta aag gcg atc gag cgt gca			1680
Asn Asp Leu Tyr Ser Thr Glu Leu Pro Leu Lys Ala Ile Glu Arg Ala			
545	550	555	560
ggg tat cat gtt gtc ttt aat ggc ttt gat gat aat ggt aca att caa			1728
Gly Tyr His Val Val Phe Asn Gly Phe Asp Asp Asn Gly Thr Ile Gln			
565	570	575	
aga ttt gac aat aat gat tta atg aca caa gtg ttt aca att ggt ttg			1776
Arg Phe Asp Asn Asn Asp Leu Met Thr Gln Val Phe Thr Ile Gly Leu			
580	585	590	
cgt aaa ata agt gat gaa cag caa act tca att gga ctt gat gca tta			1824
Arg Lys Ile Ser Asp Glu Gln Gln Thr Ser Ile Gly Leu Asp Ala Leu			
595	600	605	
aag aaa ctt gat ctt cat aat aat gag gat gtt gct gca att gcc ttt			1872
Lys Lys Leu Asp Leu His Asn Asn Glu Asp Val Ala Ala Ile Ala Phe			
610	615	620	
gga gtt gct tca act atc att agt tta att gga tta atc ggt aat aaa			1920
Gly Val Ala Ser Thr Ile Ile Ser Leu Ile Gly Leu Ile Gly Asn Lys			
625	630	635	640
aac gat aag			1929
Asn Asp Lys			

<210> 14

<211> 643

<212> PRT

<213> Lactobacillus acidophilus

<400> 14

Met Ser Leu Phe Gly Lys Lys Lys Lys Ala Ile Val Asn Tyr Ile Asp	
1 5 10 15	
Leu Asp Asn Asp Lys Asn Asn Ile Ala Thr Ser Gly Glu Leu Leu Gly	
20 25 30	
Asn Val Gly Glu Glu Ile Gly Tyr Ser Ser Ser Asp Gln Ile Asp Ala	
35 40 45	
Leu Lys Lys Gln Gly Tyr Val Leu Val Asn Asn Ser Phe Asp Pro Ser	
50 55 60	
Asp Lys Pro Thr Phe Ser Asn Glu Asp Val Gln Thr Tyr Thr Ile Ser	
65 70 75 80	
Phe Lys His Asp Val Glu Ala Val Asp Lys Pro Asn Ser Asp Phe Gly	
85 90 95	

```

Ile Ser Glu Ser Asp Leu Gln Lys Val Gly Thr Gln Thr Val His Tyr
      100      105      110
Glu Gly Ala Ala Thr Arg Thr Pro Lys Asp Asn Val Ser Gln Val Val
      115      120      125
Phe Lys Arg Ser Val Val Tyr Asp Lys Ile Leu Lys Lys Ile Ile Ser
      130      135      140
Thr Ser Thr Trp Met Pro Glu Lys Gln Ser Phe Leu Leu Ile Ala Thr
      145      150      155      160
Pro Glu Val Ser Gly Tyr Thr Thr Val Gln Thr Thr Val Gly Gly Glu
      165      170      175
Thr Val Thr Pro Glu Asp Cys Asp Arg Asn Tyr Val Val Glu Tyr Asp
      180      185      190
Ile Asn His Gln Pro Ser Val Ala Asp Gln Lys Val Ala Val Lys Tyr
      195      200      205
Val Asp Gln Asp Leu Glu Asn Lys Glu Ile Thr Glu Asp Ile Leu Thr
      210      215      220
Gly Met Pro Asn Ser Leu Val Asp Tyr Asp Pro Lys Ala Thr Ile Glu
      225      230      235      240
Arg Leu Glu Ser Asp Glu Gly Tyr Ala Leu Val Asn Asn Gly Tyr Asn
      245      250      255
Pro Ala Gly Glu Val Gln Phe Tyr Ser Asn Asn Asp Asp Tyr Val Pro
      260      265      270
Val Phe Val Met Thr Met Lys His Thr Ile Gly Gln Val Asp Ser Glu
      275      280      285
His Pro Asp Ser Lys Val Asn Lys Asn Glu Tyr Asp Lys Asp Val Ala
      290      295      300
Phe Thr Ile Asn Tyr Glu Gly Ala Asp Ala Ala Thr Pro Val Asn Asn
      305      310      315      320
Val Gln Arg Ser His Trp Ser Arg Ser Leu Thr Val Asp Arg Val Thr
      325      330      335
Gly Glu Ile Leu Pro Gly Gly Lys Tyr Thr Thr Asp Trp Lys Val Asp
      340      345      350
Arg Glu Lys Tyr Asp Asp Val Asp Val Pro Val Val Asp Gly Tyr His
      355      360      365
Thr Asp Val Lys Met Ile Lys Gly Ala Glu Val Thr Arg Glu Asn Ile
      370      375      380
Ile Arg Thr Val Asn Tyr Val Ala Asn Gly His Ile Ile Pro Val Asp
      385      390      395      400
Ser Asp Gly Lys Glu Ile Val Gly Ala Pro His Pro Val Phe Gln Thr
      405      410      415
Asp Pro Asn Asp Pro Thr Gln Val Ile Thr Asp Glu Pro Val Pro Lys
      420      425      430
Ile Asp Gly Tyr Lys Cys Asn Leu Ala Thr Ile Thr Pro Tyr Asn Pro
      435      440      445
Ala Lys Asp Met Glu Val Lys Tyr Lys Ala Glu Asp Ser Asp Val Leu
      450      455      460
Val Ile Ser Val Gly Asp Lys Lys Pro Lys Ser Glu Thr Lys Ala Val
      465      470      475      480
Ser Val Glu Lys Pro Val Val Lys Pro Asp Pro Lys Pro Glu Asn Thr
      485      490      495
Asn Ser Val Thr Gln Pro Ala Val Thr Gln Asp Gln Asn His Asp His
      500      505      510
Asp Gln Val Ala Ile Ile Asn Phe Ile Asp Leu Asp His Asp Gly Lys
      515      520      525
Gln Leu Thr Ser Ser Gly Pro Leu Thr Gly Lys Pro Gly Glu Ser Ile
      530      535      540
Asn Asp Leu Tyr Ser Thr Glu Leu Pro Leu Lys Ala Ile Glu Arg Ala

```

```

545          550          555          560
Gly Tyr His Val Val Phe Asn Gly Phe Asp Asp Asn Gly Thr Ile Gln
          565          570          575
Arg Phe Asp Asn Asn Asp Leu Met Thr Gln Val Phe Thr Ile Gly Leu
          580          585          590
Arg Lys Ile Ser Asp Glu Gln Gln Thr Ser Ile Gly Leu Asp Ala Leu
          595          600          605
Lys Lys Leu Asp Leu His Asn Asn Glu Asp Val Ala Ala Ile Ala Phe
          610          615          620
Gly Val Ala Ser Thr Ile Ile Ser Leu Ile Gly Leu Ile Gly Asn Lys
625          630          635          640
Asn Asp Lys

```

<210> 15

<211> 3051

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1377 - mucus binding protein precursor

<220>

<221> CDS

<222> (1)...(3051)

<400> 15

```

atg aaa tta gcc tat gac gat tgg cgt aaa aat aaa gaa aag aat tat 48
Met Lys Leu Ala Tyr Asp Asp Trp Arg Lys Asn Lys Glu Lys Asn Tyr
  1          5          10          15

cct ttt gcg ggt tac act gta gag att gat tca tta tcg aat gct cca 96
Pro Phe Ala Gly Tyr Thr Val Glu Ile Asp Ser Leu Ser Asn Ala Pro
          20          25          30

tta aca aat gga ggt acc tac act atc aat ttg gga acc gaa act cgc 144
Leu Thr Asn Gly Gly Thr Tyr Thr Ile Asn Leu Gly Thr Glu Thr Arg
          35          40          45

ctt tat aat gaa cca tat tgg gta ata act tca cgc act att cat tat 192
Leu Tyr Asn Glu Pro Tyr Trp Val Ile Thr Ser Arg Thr Ile His Tyr
          50          55          60

gta aaa tat ggt cta acc ggt tct gat agt gtt gct tct cca gat gtg 240
Val Lys Tyr Gly Leu Thr Gly Ser Asp Ser Val Ala Ser Pro Asp Val
          65          70          75          80

atc cag gaa ggt cat tca aat gta acc agt tct aaa aat aat cca gtg 288
Ile Gln Glu Gly His Ser Asn Val Thr Ser Ser Lys Asn Asn Pro Val
          85          90          95

gta aat aac ttt aat tta gaa aaa gat ggt cat cac tat gtg agt tat 336
Val Asn Asn Phe Asn Leu Glu Lys Asp Gly His His Tyr Val Ser Tyr

```

100										105					110					
gaa	acg	gtt	caa	aga	tcg	tat	aat	gta	gct	tct	ggt	att	cct	gat	ggg	384				
Glu	Thr	Val	Gln	Arg	Ser	Tyr	Asn	Val	Ala	Ser	Gly	Ile	Pro	Asp	Gly					
115					120					125										
atg	aca	gat	aat	aaa	ggt	aat	atg	aat	tct	att	att	atc	ttt	gat	gga	432				
Met	Thr	Asp	Asn	Lys	Gly	Asn	Met	Asn	Ser	Ile	Ile	Ile	Phe	Asp	Gly					
130					135					140										
cag	ata	aac	cca	act	att	act	gat	tgg	gtt	act	cca	gat	cct	gat	gta	480				
Gln	Ile	Asn	Pro	Thr	Ile	Thr	Asp	Trp	Val	Thr	Pro	Asp	Pro	Asp	Val					
145					150					155					160					
act	caa	acc	aaa	tca	ccg	ggc	aag	aat	ctt	tct	aat	aaa	att	cca	aca	528				
Thr	Gln	Thr	Lys	Ser	Pro	Gly	Lys	Asn	Leu	Ser	Asn	Lys	Ile	Pro	Thr					
165					170					175										
aat	ggt	gaa	tct	tac	aat	tac	ctc	tat	aga	aag	ttc	tat	cat	cat	aac	576				
Asn	Gly	Glu	Ser	Tyr	Asn	Tyr	Leu	Tyr	Arg	Lys	Phe	Tyr	His	His	Asn					
180					185					190										
tat	tat	gat	aaa	gat	ggt	aac	ttc	cat	cag	aag	aca	tat	ctt	cct	aat	624				
Tyr	Tyr	Asp	Lys	Asp	Gly	Asn	Phe	His	Gln	Lys	Thr	Tyr	Leu	Pro	Asn					
195					200					205										
aat	gaa	gga	gag	cca	att	act	att	act	tac	tac	cac	aac	caa	cct	gta	672				
Asn	Glu	Gly	Glu	Pro	Ile	Thr	Ile	Thr	Tyr	Tyr	His	Asn	Gln	Pro	Val					
210					215					220										
gat	ctt	tca	ttt	gaa	gat	att	tca	aag	att	gat	cct	caa	gat	tta	agt	720				
Asp	Leu	Ser	Phe	Glu	Asp	Ile	Ser	Lys	Ile	Asp	Pro	Gln	Asp	Leu	Ser					
225					230					235					240					
ggg	agc	aac	tat	tct	gct	act	aac	gaa	tta	acg	aca	aag	aac	gat	gat	768				
Gly	Ser	Asn	Tyr	Ser	Ala	Thr	Asn	Glu	Leu	Thr	Thr	Lys	Asn	Asp	Asp					
245					250					255										
agt	aat	caa	tac	aat	gtt	tac	gat	gca	tca	aat	ggt	act	aaa	agt	tta	816				
Ser	Asn	Gln	Tyr	Asn	Val	Tyr	Asp	Ala	Ser	Asn	Gly	Thr	Lys	Ser	Leu					
260					265					270										
agt	caa	gta	att	agt	gat	att	gaa	gcg	aaa	ggt	tac	aag	ctt	gtt	tca	864				
Ser	Gln	Val	Ile	Ser	Asp	Ile	Glu	Ala	Lys	Gly	Tyr	Lys	Leu	Val	Ser					
275					280					285										
att	act	aac	gat	gac	gat	gat	tct	caa	acc	gac	ttg	aag	ggc	aac	agt	912				
Ile	Thr	Asn	Asp	Asp	Asp	Asp	Ser	Gln	Thr	Asp	Leu	Lys	Gly	Asn	Ser					
290					295					300										
tca	att	gat	tta	atc	tat	aac	aaa	gat	ggt	gtt	tgg	aag	agt	gca	act	960				
Ser	Ile	Asp	Leu	Ile	Tyr	Asn	Lys	Asp	Gly	Val	Trp	Lys	Ser	Ala	Thr					
305					310					315					320					
ggt	ggg	gat	aat	gct	gat	aac	ttg	att	cat	aag	cgc	tac	act	atc	aag	1008				
Gly	Gly	Asp	Asn	Ala	Asp	Asn	Leu	Ile	His	Lys	Arg	Tyr	Thr	Ile	Lys					
325					330					335										

ttt gtt cat gac gta aaa cct aca act aaa aat act tct gta agc cgt	1056
Phe Val His Asp Val Lys Pro Thr Thr Lys Asn Thr Ser Val Ser Arg	
340 345 350	
aac att cac tat gtg gct gac gaa ggc aat agc aag tat gaa gta ttg	1104
Asn Ile His Tyr Val Ala Asp Glu Gly Asn Ser Lys Tyr Glu Val Leu	
355 360 365	
aag aat cct gat act caa act gtt aac ttt gaa cgt act gct tat att	1152
Lys Asn Pro Asp Thr Gln Thr Val Asn Phe Glu Arg Thr Ala Tyr Ile	
370 375 380	
gat caa gtt act aag caa gaa gtt att aag aat gca gat ggt act tac	1200
Asp Gln Val Thr Lys Gln Glu Val Ile Lys Asn Ala Asp Gly Thr Tyr	
385 390 395 400	
agt gaa tta cca gct gac ttc aag cca act tgg aaa gct gtt gga act	1248
Ser Glu Leu Pro Ala Asp Phe Lys Pro Thr Trp Lys Ala Val Gly Thr	
405 410 415	
gat aac ttt gat aaa atc caa aag gat aga ttt aac aag gat gaa ggt	1296
Asp Asn Phe Asp Lys Ile Gln Lys Asp Arg Phe Asn Lys Asp Glu Gly	
420 425 430	
aag gtt cct ggc gtt tgg gaa att gaa cgt gct aac tat gat gat cca	1344
Lys Val Pro Gly Val Trp Glu Ile Glu Arg Ala Asn Tyr Asp Asp Pro	
435 440 445	
gag gga act caa tta acg gat aac ttt gct cct aaa gtt gca aat gtt	1392
Glu Gly Thr Gln Leu Thr Asp Asn Phe Ala Pro Lys Val Ala Asn Val	
450 455 460	
gat gct gct aag act tat aat gat att tat ctt gtt tac aaa caa aaa	1440
Asp Ala Ala Lys Thr Tyr Asn Asp Ile Tyr Leu Val Tyr Lys Gln Lys	
465 470 475 480	
gct caa tat aat att cac tac att gat gtt aat ggt gta gaa gat aaa	1488
Ala Gln Tyr Asn Ile His Tyr Ile Asp Val Asn Gly Val Glu Asp Lys	
485 490 495	
aac act tat act cca act gac ggt tat gaa ctt acc gat cat tta gtt	1536
Asn Thr Tyr Thr Pro Thr Asp Gly Tyr Glu Leu Thr Asp His Leu Val	
500 505 510	
cct aac gtt ggt gaa ggt aaa ggt atc ttt att ggc gac act cca gat	1584
Pro Asn Val Gly Glu Gly Lys Gly Ile Phe Ile Gly Asp Thr Pro Asp	
515 520 525	
gct acg cag aag tta tgg agc cca gca gac tac gaa aag gct gga tat	1632
Ala Thr Gln Lys Leu Trp Ser Pro Ala Asp Tyr Glu Lys Ala Gly Tyr	
530 535 540	
gtt tta gtt ggt tta tct gat aat gcc aaa ggc gat tta ctc ggt aag	1680
Val Leu Val Gly Leu Ser Asp Asn Ala Lys Gly Asp Leu Leu Gly Lys	
545 550 555 560	

caa acc tta act aag gac gtt caa gat caa tac gtt tac ttg aag cat	1728
Gln Thr Leu Thr Lys Asp Val Gln Asp Gln Tyr Val Tyr Leu Lys His	
565 570 575	
gca atc acc cct tca act gat aag aca cct aaa gaa gac gtg aag gcc	1776
Ala Ile Thr Pro Ser Thr Asp Lys Thr Pro Lys Glu Asp Val Lys Ala	
580 585 590	
gaa act gtc agt caa gta cgt act att tca tat cgg gat gct gaa act	1824
Glu Thr Val Ser Gln Val Arg Thr Ile Ser Tyr Arg Asp Ala Glu Thr	
595 600 605	
ggg gaa aag att aca gat gaa tta aag aag tac ggt att act gct aat	1872
Gly Glu Lys Ile Thr Asp Glu Leu Lys Lys Tyr Gly Ile Thr Ala Asn	
610 615 620	
gtt cct gac att acg caa act atc gat tat gtt cgt gtg cct ctt tat	1920
Val Pro Asp Ile Thr Gln Thr Ile Asp Tyr Val Arg Val Pro Leu Tyr	
625 630 635 640	
gat gca ttt aag ggt atg ttt tta ggc ttt gca gca att caa act gat	1968
Asp Ala Phe Lys Gly Met Phe Leu Gly Phe Ala Ala Ile Gln Thr Asp	
645 650 655	
gca aaa ggt ttt gct aag ctt gat agt aac ggt aaa cca gag atc aag	2016
Ala Lys Gly Phe Ala Lys Leu Asp Ser Asn Gly Lys Pro Glu Ile Lys	
660 665 670	
aaa gat act aat ggc caa cca att att gct act cga gat gat aag gca	2064
Lys Asp Thr Asn Gly Gln Pro Ile Ile Ala Thr Arg Asp Asp Lys Ala	
675 680 685	
tca tgg gtt cca act ggt gaa cat act gac tat cca gaa caa ggc tca	2112
Ser Trp Val Pro Thr Gly Glu His Thr Asp Tyr Pro Glu Gln Gly Ser	
690 695 700	
cct gat tta act aag tat ggg tat gta aag gaa agc tca tta gaa caa	2160
Pro Asp Leu Thr Lys Tyr Gly Tyr Val Lys Glu Ser Ser Leu Glu Gln	
705 710 715 720	
aag act aat aac aag gat ggc gca cag gta gat gct aaa gac ggt gac	2208
Lys Thr Asn Asn Lys Asp Gly Ala Gln Val Asp Ala Lys Asp Gly Asp	
725 730 735	
cca act caa tcc ggt ggc cac gtg gat gtt tac tac ttc cac gaa caa	2256
Pro Thr Gln Ser Gly Gly His Val Asp Val Tyr Tyr Phe His Glu Gln	
740 745 750	
gaa gat atc act tat gtg aat ccg aag ttt aat att gac caa aag gat	2304
Glu Asp Ile Thr Tyr Val Asn Pro Lys Phe Asn Ile Asp Gln Lys Asp	
755 760 765	
ctt gaa aag acc ttt aaa aga acg att atc tac cgt ggt acc aaa gac	2352
Leu Glu Lys Thr Phe Lys Arg Thr Ile Ile Tyr Arg Gly Thr Lys Asp	
770 775 780	
ggg cat act tat gaa gat gta aat ggt tca cca gat ggc act cat aag	2400

Gly His Thr Tyr Glu Asp Val Asn Gly Ser Pro Asp Gly Thr His Lys 785 790 795 800	
tat gtt cag act acc acc ttt act cgt aag gcg att gta gat gca gta Tyr Val Gln Thr Thr Thr Phe Thr Arg Lys Ala Ile Val Asp Ala Val 805 810 815	2448
acg aaa aaa gtg att aaa tat act cct tgg aca tca act aaa aca act Thr Lys Lys Val Ile Lys Tyr Thr Pro Trp Thr Ser Thr Lys Thr Thr 820 825 830	2496
tta gta gaa gtt att tct aag aca cct act gaa gtg ggt tat gac aat Leu Val Glu Val Ile Ser Lys Thr Pro Thr Glu Val Gly Tyr Asp Asn 835 840 845	2544
gtt gat att aaa tca gtt tct gca cgt act gtt gat cca gat aag gat Val Asp Ile Lys Ser Val Ser Ala Arg Thr Val Asp Pro Asp Lys Asp 850 855 860	2592
cca gaa gat tta ggt aca aca gtt gta act tat act gtc aac cca act Pro Glu Asp Leu Gly Thr Thr Val Val Thr Tyr Thr Val Asn Pro Thr 865 870 875 880	2640
cca aca cct gaa cca aat cca ggt aat ggc ggt aac acc agc gat ggt Pro Thr Pro Glu Pro Asn Pro Gly Asn Gly Asn Thr Ser Asp Gly 885 890 895	2688
gga aat act cct gat gga ggc tca gaa caa cca aat aat cct ggt aac Gly Asn Thr Pro Asp Gly Gly Ser Glu Gln Pro Asn Asn Pro Gly Asn 900 905 910	2736
aac aat gaa gtt cca ggt aac ccg ggc ggt gac aat gaa aca cct aag Asn Asn Glu Val Pro Gly Asn Pro Gly Gly Asp Asn Glu Thr Pro Lys 915 920 925	2784
gaa act cca act cct aag gat gat aag act aca cca gaa aaa cca gat Glu Thr Pro Thr Pro Lys Asp Asp Lys Thr Thr Pro Glu Lys Pro Asp 930 935 940	2832
gaa cat gac gat ttg aaa ttg aag tca cct gac gaa cat aac cat act Glu His Asp Asp Leu Lys Leu Lys Ser Pro Asp Glu His Asn His Thr 945 950 955 960	2880
cca aag aag gaa gtt aac aag act tca aat aat act cca cgt agc gaa Pro Lys Lys Glu Val Asn Lys Thr Ser Asn Asn Thr Pro Arg Ser Glu 965 970 975	2928
cgc tgg aac tca aac aaa tct cct aaa tca gaa aac gta aat aat gta Arg Trp Asn Ser Asn Lys Ser Pro Lys Ser Glu Asn Val Asn Asn Val 980 985 990	2976
aca ggt tct aat tcc gca gtt aaa tct acc aat agt cct gaa aca gta Thr Gly Ser Asn Ser Ala Val Lys Ser Thr Asn Ser Pro Glu Thr Val 995 1000 1005	3024
aag gaa aat act tta ccg cag act ggt Lys Glu Asn Thr Leu Pro Gln Thr Gly	3051

1010

1015

<210> 16

<211> 1017

<212> PRT

<213> Lactobacillus acidophilus

<400> 16

```

Met Lys Leu Ala Tyr Asp Asp Trp Arg Lys Asn Lys Glu Lys Asn Tyr
 1          5          10          15
Pro Phe Ala Gly Tyr Thr Val Glu Ile Asp Ser Leu Ser Asn Ala Pro
          20          25          30
Leu Thr Asn Gly Gly Thr Tyr Thr Ile Asn Leu Gly Thr Glu Thr Arg
          35          40          45
Leu Tyr Asn Glu Pro Tyr Trp Val Ile Thr Ser Arg Thr Ile His Tyr
          50          55          60
Val Lys Tyr Gly Leu Thr Gly Ser Asp Ser Val Ala Ser Pro Asp Val
          65          70          75          80
Ile Gln Glu Gly His Ser Asn Val Thr Ser Ser Lys Asn Asn Pro Val
          85          90          95
Val Asn Asn Phe Asn Leu Glu Lys Asp Gly His His Tyr Val Ser Tyr
          100          105          110
Glu Thr Val Gln Arg Ser Tyr Asn Val Ala Ser Gly Ile Pro Asp Gly
          115          120          125
Met Thr Asp Asn Lys Gly Asn Met Asn Ser Ile Ile Ile Phe Asp Gly
          130          135          140
Gln Ile Asn Pro Thr Ile Thr Asp Trp Val Thr Pro Asp Pro Asp Val
          145          150          155          160
Thr Gln Thr Lys Ser Pro Gly Lys Asn Leu Ser Asn Lys Ile Pro Thr
          165          170          175
Asn Gly Glu Ser Tyr Asn Tyr Leu Tyr Arg Lys Phe Tyr His His Asn
          180          185          190
Tyr Tyr Asp Lys Asp Gly Asn Phe His Gln Lys Thr Tyr Leu Pro Asn
          195          200          205
Asn Glu Gly Glu Pro Ile Thr Ile Thr Tyr Tyr His Asn Gln Pro Val
          210          215          220
Asp Leu Ser Phe Glu Asp Ile Ser Lys Ile Asp Pro Gln Asp Leu Ser
          225          230          235          240
Gly Ser Asn Tyr Ser Ala Thr Asn Glu Leu Thr Thr Lys Asn Asp Asp
          245          250          255
Ser Asn Gln Tyr Asn Val Tyr Asp Ala Ser Asn Gly Thr Lys Ser Leu
          260          265          270
Ser Gln Val Ile Ser Asp Ile Glu Ala Lys Gly Tyr Lys Leu Val Ser
          275          280          285
Ile Thr Asn Asp Asp Asp Asp Ser Gln Thr Asp Leu Lys Gly Asn Ser
          290          295          300
Ser Ile Asp Leu Ile Tyr Asn Lys Asp Gly Val Trp Lys Ser Ala Thr
          305          310          315          320
Gly Gly Asp Asn Ala Asp Asn Leu Ile His Lys Arg Tyr Thr Ile Lys
          325          330          335
Phe Val His Asp Val Lys Pro Thr Thr Lys Asn Thr Ser Val Ser Arg
          340          345          350
Asn Ile His Tyr Val Ala Asp Glu Gly Asn Ser Lys Tyr Glu Val Leu
          355          360          365
Lys Asn Pro Asp Thr Gln Thr Val Asn Phe Glu Arg Thr Ala Tyr Ile
          370          375          380

```

Asp Gln Val Thr Lys Gln Glu Val Ile Lys Asn Ala Asp Gly Thr Tyr
 385 390 395
 Ser Glu Leu Pro Ala Asp Phe Lys Pro Thr Trp Lys Ala Val Gly Thr
 405 410 415
 Asp Asn Phe Asp Lys Ile Gln Lys Asp Arg Phe Asn Lys Asp Glu Gly
 420 425 430
 Lys Val Pro Gly Val Trp Glu Ile Glu Arg Ala Asn Tyr Asp Asp Pro
 435 440 445
 Glu Gly Thr Gln Leu Thr Asp Asn Phe Ala Pro Lys Val Ala Asn Val
 450 455 460
 Asp Ala Ala Lys Thr Tyr Asn Asp Ile Tyr Leu Val Tyr Lys Gln Lys
 465 470 475 480
 Ala Gln Tyr Asn Ile His Tyr Ile Asp Val Asn Gly Val Glu Asp Lys
 485 490 495
 Asn Thr Tyr Thr Pro Thr Asp Gly Tyr Glu Leu Thr Asp His Leu Val
 500 505 510
 Pro Asn Val Gly Glu Gly Lys Gly Ile Phe Ile Gly Asp Thr Pro Asp
 515 520 525
 Ala Thr Gln Lys Leu Trp Ser Pro Ala Asp Tyr Glu Lys Ala Gly Tyr
 530 535 540
 Val Leu Val Gly Leu Ser Asp Asn Ala Lys Gly Asp Leu Leu Gly Lys
 545 550 555 560
 Gln Thr Leu Thr Lys Asp Val Gln Asp Gln Tyr Val Tyr Leu Lys His
 565 570 575
 Ala Ile Thr Pro Ser Thr Asp Lys Thr Pro Lys Glu Asp Val Lys Ala
 580 585 590
 Glu Thr Val Ser Gln Val Arg Thr Ile Ser Tyr Arg Asp Ala Glu Thr
 595 600 605
 Gly Glu Lys Ile Thr Asp Glu Leu Lys Lys Tyr Gly Ile Thr Ala Asn
 610 615 620
 Val Pro Asp Ile Thr Gln Thr Ile Asp Tyr Val Arg Val Pro Leu Tyr
 625 630 635 640
 Asp Ala Phe Lys Gly Met Phe Leu Gly Phe Ala Ala Ile Gln Thr Asp
 645 650 655
 Ala Lys Gly Phe Ala Lys Leu Asp Ser Asn Gly Lys Pro Glu Ile Lys
 660 665 670
 Lys Asp Thr Asn Gly Gln Pro Ile Ala Thr Arg Asp Asp Lys Ala
 675 680 685
 Ser Trp Val Pro Thr Gly Glu His Thr Asp Tyr Pro Glu Gln Gly Ser
 690 695 700
 Pro Asp Leu Thr Lys Tyr Gly Tyr Val Lys Glu Ser Ser Leu Glu Gln
 705 710 715 720
 Lys Thr Asn Asn Lys Asp Gly Ala Gln Val Asp Ala Lys Asp Gly Asp
 725 730 735
 Pro Thr Gln Ser Gly Gly His Val Asp Val Tyr Tyr Phe His Glu Gln
 740 745 750
 Glu Asp Ile Thr Tyr Val Asn Pro Lys Phe Asn Ile Asp Gln Lys Asp
 755 760 765
 Leu Glu Lys Thr Phe Lys Arg Thr Ile Ile Tyr Arg Gly Thr Lys Asp
 770 775 780
 Gly His Thr Tyr Glu Asp Val Asn Gly Ser Pro Asp Gly Thr His Lys
 785 790 795 800
 Tyr Val Gln Thr Thr Phe Thr Arg Lys Ala Ile Val Asp Ala Val
 805 810 815
 Thr Lys Lys Val Ile Lys Tyr Thr Pro Trp Thr Ser Thr Lys Thr Thr
 820 825 830
 Leu Val Glu Val Ile Ser Lys Thr Pro Thr Glu Val Gly Tyr Asp Asn

835	840	845
Val Asp Ile Lys Ser Val Ser Ala Arg Thr Val Asp Pro Asp Lys Asp		
850	855	860
Pro Glu Asp Leu Gly Thr Thr Val Val Thr Tyr Thr Val Asn Pro Thr		
865	870	875
Pro Thr Pro Glu Pro Asn Pro Gly Asn Gly Gly Asn Thr Ser Asp Gly		
885	890	895
Gly Asn Thr Pro Asp Gly Gly Ser Glu Gln Pro Asn Asn Pro Gly Asn		
900	905	910
Asn Asn Glu Val Pro Gly Asn Pro Gly Gly Asp Asn Glu Thr Pro Lys		
915	920	925
Glu Thr Pro Thr Pro Lys Asp Asp Lys Thr Thr Pro Glu Lys Pro Asp		
930	935	940
Glu His Asp Asp Leu Lys Leu Lys Ser Pro Asp Glu His Asn His Thr		
945	950	955
Pro Lys Lys Glu Val Asn Lys Thr Ser Asn Asn Thr Pro Arg Ser Glu		
965	970	975
Arg Trp Asn Ser Asn Lys Ser Pro Lys Ser Glu Asn Val Asn Asn Val		
980	985	990
Thr Gly Ser Asn Ser Ala Val Lys Ser Thr Asn Ser Pro Glu Thr Val		
995	1000	1005
Lys Glu Asn Thr Leu Pro Gln Thr Gly		
1010	1015	

<210> 17

<211> 12978

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1392 - mucus binding protein precursor Mub

<220>

<221> CDS

<222> (1)...(12978)

<400> 17

atg gtt tca aaa aat aat cgt gca aag caa atg gaa aat gtt gca gag	48
Met Val Ser Lys Asn Asn Arg Ala Lys Gln Met Glu Asn Val Ala Glu	
1 5 10 15	

cgc caa cca cat ttt agt att cgt aaa tta acg att ggt gct gct tct	96
Arg Gln Pro His Phe Ser Ile Arg Lys Leu Thr Ile Gly Ala Ala Ser	
20 25 30	

gtt ctt ttg agt aca aca ctt tgg atg agt gta aat aca agt agt gtg	144
Val Leu Leu Ser Thr Thr Leu Trp Met Ser Val Asn Thr Ser Ser Val	
35 40 45	

cat gct gag aat att gat aac agt gac aat gat gca cat gaa gct aca	192
His Ala Glu Asn Ile Asp Asn Ser Asp Asn Asp Ala His Glu Ala Thr	
50 55 60	

gag agc aat act gaa acg ccg agc att aat gat gat aca aaa gta gtt	240
Glu Ser Asn Thr Glu Thr Pro Ser Ile Asn Asp Asp Thr Lys Val Val	
65 70 75 80	
ggt gaa tca aac agc aat ata act tct tct aac gat gta aat gct ggt	288
Val Glu Ser Asn Ser Asn Ile Thr Ser Ser Asn Asp Val Asn Ala Gly	
85 90 95	
aat aat gga gca gaa act aat gat act aat aat gaa gta act gct tca	336
Asn Asn Gly Ala Glu Thr Asn Asp Thr Asn Asn Glu Val Thr Ala Ser	
100 105 110	
gaa gat act agc aag gga tta act gtt gat aat aaa gat gca tct gtt	384
Glu Asp Thr Ser Lys Gly Leu Thr Val Asp Asn Lys Asp Ala Ser Val	
115 120 125	
caa tct act gtt aag tca tca gat gaa gta aaa aag agt gaa tca act	432
Gln Ser Thr Val Lys Ser Ser Asp Glu Val Lys Lys Ser Glu Ser Thr	
130 135 140	
gag caa aaa tca gct aaa aca gct caa aat tct act tta aat aac aat	480
Glu Gln Lys Ser Ala Lys Thr Ala Gln Asn Ser Thr Leu Asn Asn Asn	
145 150 155 160	
aca gta aat aca gaa aaa gca gaa tca aat gta gct gct aaa agt aat	528
Thr Val Asn Thr Glu Lys Ala Glu Ser Asn Val Ala Ala Lys Ser Asn	
165 170 175	
gca gat aca gca aag tct act caa cag agc agt gca gct tct tct gct	576
Ala Asp Thr Ala Lys Ser Thr Gln Gln Ser Ser Ala Ala Ser Ser Ala	
180 185 190	
aat caa gtt agt tcc aat gct gat tta aca caa aat cag gca att aac	624
Asn Gln Val Ser Ser Asn Ala Asp Leu Thr Gln Asn Gln Ala Ile Asn	
195 200 205	
tct act act caa gtt gaa gct aat aat tca act aat gat aaa aag gct	672
Ser Thr Thr Gln Val Glu Ala Asn Asn Ser Thr Asn Asp Lys Lys Ala	
210 215 220	
aat aac gat act gct gat ttg agt aat att ggc tta aag gga att gaa	720
Asn Asn Asp Thr Ala Asp Leu Ser Asn Ile Gly Leu Lys Gly Ile Glu	
225 230 235 240	
act aat aag att ccg gaa act act gat ttg cct gta agt gag ttg att	768
Thr Asn Lys Ile Pro Glu Thr Thr Asp Leu Pro Val Ser Glu Leu Ile	
245 250 255	
aaa tct tat aat aac aac tct aac agt aat gaa gtt aat gtt aac caa	816
Lys Ser Tyr Asn Asn Asn Ser Asn Ser Asn Glu Val Asn Val Asn Gln	
260 265 270	
ggt agt ggc tta cgt gct gct caa tta ttt gct gct tca ttt att gca	864
Val Ser Gly Leu Arg Ala Ala Gln Leu Phe Ala Ala Ser Phe Ile Ala	
275 280 285	
aca caa aac act gga aca ggt aat aac ggt gca gta aat att gat aca	912

Thr	Gln	Asn	Thr	Gly	Thr	Gly	Asn	Asn	Gly	Ala	Val	Asn	Ile	Asp	Thr		
290						295					300						
tat	aag	cct	gac	ttt	aat	ctc	acc	gaa	aat	cca	gcc	tat	cag	caa	tat	960	
Tyr	Lys	Pro	Asp	Phe	Asn	Leu	Thr	Glu	Asn	Pro	Ala	Tyr	Gln	Gln	Tyr		
305				310					315						320		
ttt	gca	gca	att	ccg	gct	gat	caa	tat	gca	ttt	caa	tct	tat	gaa	gta	1008	
Phe	Ala	Ala	Ile	Pro	Ala	Asp	Gln	Tyr	Ala	Phe	Gln	Ser	Tyr	Glu	Val		
				325					330					335			
gta	agt	act	ggg	caa	aag	att	gta	gtt	aca	aca	gat	cgt	aat	aat	att	1056	
Val	Ser	Thr	Gly	Gln	Lys	Ile	Val	Val	Thr	Thr	Asp	Arg	Asn	Asn	Ile		
			340					345					350				
ggg	aac	aat	att	aga	ttc	tac	aat	gtt	aga	aat	ggg	agt	gct	caa	ctt	1104	
Gly	Asn	Asn	Ile	Arg	Phe	Tyr	Asn	Val	Arg	Asn	Gly	Ser	Ala	Gln	Leu		
		355					360					365					
gtt	tac	caa	atg	acc	aga	gat	acc	cag	acc	aat	gca	agt	ggg	agt	gta	1152	
Val	Tyr	Gln	Met	Thr	Arg	Asp	Thr	Gln	Thr	Asn	Ala	Ser	Gly	Ser	Val		
	370					375					380						
gta	aaa	aat	aga	cca	agt	tta	caa	ggg	act	ttt	acc	act	gct	ggg	gtt	1200	
Val	Lys	Asn	Arg	Pro	Ser	Leu	Gln	Gly	Thr	Phe	Thr	Thr	Ala	Gly	Val		
385					390				395						400		
gca	agt	aat	tca	aca	tat	aag	ggc	ggg	acc	tat	aac	tgg	tct	ctt	aac	1248	
Ala	Ser	Asn	Ser	Thr	Tyr	Lys	Gly	Gly	Thr	Tyr	Asn	Trp	Ser	Leu	Asn		
				405				410						415			
caa	aca	gac	act	gta	aac	ttt	cct	gga	att	ggg	aat	ttg	aag	att	ggg	1296	
Gln	Thr	Asp	Thr	Val	Asn	Phe	Pro	Gly	Ile	Gly	Asn	Leu	Lys	Ile	Gly		
			420					425					430				
cgt	att	gac	att	act	gct	ggg	agt	agt	aat	tct	cca	gta	gac	aat	ggg	1344	
Arg	Ile	Asp	Ile	Thr	Ala	Gly	Ser	Ser	Asn	Ser	Pro	Val	Asp	Asn	Gly		
		435					440					445					
aca	ggg	gct	ttt	gta	acc	gat	aat	tct	cat	cga	att	aca	cct	act	tgg	1392	
Thr	Gly	Ala	Phe	Val	Thr	Asp	Asn	Ser	His	Arg	Ile	Thr	Pro	Thr	Trp		
	450					455					460						
gat	caa	ggg	ctt	cca	ata	gaa	ggg	att	gtt	tca	gga	aag	act	tgg	aat	1440	
Asp	Gln	Gly	Leu	Pro	Ile	Glu	Gly	Ile	Val	Ser	Gly	Lys	Thr	Trp	Asn		
465					470					475					480		
agt	gca	ggg	tcc	aac	atc	cca	gat	aaa	gtt	act	caa	aat	att	tgg	tat	1488	
Ser	Ala	Gly	Ser	Asn	Ile	Pro	Asp	Lys	Val	Thr	Gln	Asn	Ile	Trp	Tyr		
				485					490					495			
gtt	gat	gct	gaa	aca	ggg	aaa	gtt	ctt	agt	cat	aag	act	agt	gac	gaa	1536	
Val	Asp	Ala	Glu	Thr	Gly	Lys	Val	Leu	Ser	His	Lys	Thr	Ser	Asp	Glu		
			500					505					510				
gct	ttc	aat	ggc	tct	agt	tat	gat	tca	act	gat	aat	ggc	gtg	aaa	aca	1584	
Ala	Phe	Asn	Gly	Ser	Ser	Tyr	Asp	Ser	Thr	Asp	Asn	Gly	Val	Lys	Thr		

515	520	525	
att agt aaa gac ggt aaa gct tat cag tta att gat aga ggc tct gat Ile Ser Lys Asp Gly Lys Ala Tyr Gln Leu Ile Asp Arg Gly Ser Asp 530 535 540			1632
ggg ctt tat gat cca agt gac ttt agt gat att tta aat aag caa tta Gly Leu Tyr Asp Pro Ser Asp Phe Ser Asp Ile Leu Asn Lys Gln Leu 545 550 555 560			1680
gct act aat aat ggt tta cca att act att ggt gat gtt cta tct act Ala Thr Asn Asn Gly Leu Pro Ile Thr Ile Gly Asp Val Leu Ser Thr 565 570 575			1728
cct ctt aaa gga act tta cgt gat ggt cga att ggt aat att aaa ggt Pro Leu Lys Gly Thr Leu Arg Asp Gly Arg Ile Gly Asn Ile Lys Gly 580 585 590			1776
tct att act aat ttt caa gga acg cgc gca tat atg cgt ctc caa aca Ser Ile Thr Asn Phe Gln Gly Thr Arg Ala Tyr Met Arg Leu Gln Thr 595 600 605			1824
aag act gac gga act att gat tta aac act tat act ttt gat cca ggt Lys Thr Asp Gly Thr Ile Asp Leu Asn Thr Tyr Thr Phe Asp Pro Gly 610 615 620			1872
tct act aga ggt aac ttg aat act gga tta agt caa gct gat gtt gct Ser Thr Arg Gly Asn Leu Asn Thr Gly Leu Ser Gln Ala Asp Val Ala 625 630 635 640			1920
cca ggc caa aca gtt atg ggt gct ggt gac act agt ggt tca ggg gcc Pro Gly Gln Thr Val Met Gly Ala Gly Asp Thr Ser Gly Ser Gly Ala 645 650 655			1968
ttc tac aat ggt act cgc cca ggc aat cgt gat att atc ttt cta tat Phe Tyr Asn Gly Thr Arg Pro Gly Asn Arg Asp Ile Ile Phe Leu Tyr 660 665 670			2016
aat gct gaa gca aac aag caa aat gct aac att act ttc gtt aac gat Asn Ala Glu Ala Asn Lys Gln Asn Ala Asn Ile Thr Phe Val Asn Asp 675 680 685			2064
gat act ggt gca agt tta agt cca caa caa aat tct agt ggg gat gca Asp Thr Gly Ala Ser Leu Ser Pro Gln Gln Asn Ser Ser Gly Asp Ala 690 695 700			2112
ggg agt caa atc acc ttt gac aat gca ggt act act gtt act aac ttg Gly Ser Gln Ile Thr Phe Asp Asn Ala Gly Thr Thr Val Thr Asn Leu 705 710 715 720			2160
att agc caa ggt tac gtt tac aac ggt aca act ggt aat ggc gta act Ile Ser Gln Gly Tyr Val Tyr Asn Gly Thr Thr Gly Asn Gly Val Thr 725 730 735			2208
aat gga tca gct ggt ggt agc ttt act agt gtt ggt ttt cca gct tac Asn Gly Ser Ala Gly Gly Ser Phe Thr Ser Val Gly Phe Pro Ala Tyr 740 745 750			2256

gat aac gat gac aac acc aac caa gca ttt gtt gtt cac ttt aag aac	2304
Asp Asn Asp Asp Asn Thr Asn Gln Ala Phe Val Val His Phe Lys Asn	
755 760 765	
cca gta caa act act act tac cgc caa ggt act gag gaa tct aag acc	2352
Pro Val Gln Thr Thr Thr Tyr Arg Gln Gly Thr Glu Ser Lys Thr	
770 775 780	
atc aat cgt aca att aac tac tat gat aag gta act ggt gaa aag att	2400
Ile Asn Arg Thr Ile Asn Tyr Tyr Asp Lys Val Thr Gly Glu Lys Ile	
785 790 795 800	
cca tct aac tta att tca caa aac cca gtt act gat tca gta act ttc	2448
Pro Ser Asn Leu Ile Ser Gln Asn Pro Val Thr Asp Ser Val Thr Phe	
805 810 815	
act cgt act caa gtt ttg gat caa gat ggt aag gtt gta ggt tac ggt	2496
Thr Arg Thr Gln Val Leu Asp Gln Asp Gly Lys Val Val Gly Tyr Gly	
820 825 830	
act att tca act gat ggt aaa tca ttt aga aat caa gat tgg cat act	2544
Thr Ile Ser Thr Asp Gly Lys Ser Phe Arg Asn Gln Asp Trp His Thr	
835 840 845	
gct gct ggt gaa agt agt act caa ttt gat gct aag cgt tca agt gat	2592
Ala Ala Gly Glu Ser Ser Thr Gln Phe Asp Ala Lys Arg Ser Ser Asp	
850 855 860	
ctt agt gca tat aac tac act gct cct gaa ttc caa gat gga act aat	2640
Leu Ser Ala Tyr Asn Tyr Thr Ala Pro Glu Phe Gln Asp Gly Thr Asn	
865 870 875 880	
gca agc att gta gca gct cat gaa gtg act cca act act caa gat ctc	2688
Ala Ser Ile Val Ala Ala His Glu Val Thr Pro Thr Thr Gln Asp Leu	
885 890 895	
gtt tac aat gtt tac tac ggt cac caa act caa caa gta act act aat	2736
Val Tyr Asn Val Tyr Tyr Gly His Gln Thr Gln Gln Val Thr Thr Asn	
900 905 910	
gaa gat gta acg cgt cgt ttc cac tac atc ttt act gat ggc act acg	2784
Glu Asp Val Thr Arg Arg Phe His Tyr Ile Phe Thr Asp Gly Thr Thr	
915 920 925	
cca gaa agc cat tta act cct caa gca gat caa aaa gta acc ttt act	2832
Pro Glu Ser His Leu Thr Pro Gln Ala Asp Gln Lys Val Thr Phe Thr	
930 935 940	
gga act gct act aag gac tta gta act ggc aag acc ggt gat act gtt	2880
Gly Thr Ala Thr Lys Asp Leu Val Thr Gly Lys Thr Gly Asp Thr Val	
945 950 955 960	
tgg act cca tcg act ggt aca tta gct caa gtt gct ggt caa act gtt	2928
Trp Thr Pro Ser Thr Gly Thr Leu Ala Gln Val Ala Gly Gln Thr Val	
965 970 975	

gcc ggc tac cac att act ggt aac gta aat gct aac gct gat ggt agt 2976
 Ala Gly Tyr His Ile Thr Gly Asn Val Asn Ala Asn Ala Asp Gly Ser
 980 985 990

gcg aat gcc gtt acg gta aac cca gat tct ggc gat att gat gta act 3024
 Ala Asn Ala Val Thr Val Asn Pro Asp Ser Gly Asp Ile Asp Val Thr
 995 1000 1005

gtt gtt tac act cca gat gct aag act cca gat act cca caa aaa gct 3072
 Val Val Tyr Thr Pro Asp Ala Lys Thr Pro Asp Thr Pro Gln Lys Ala
 1010 1015 1020

aag gtt act att tac gat aag act gaa aat aat aag caa tta tct aat 3120
 Lys Val Thr Ile Tyr Asp Lys Thr Glu Asn Asn Lys Gln Leu Ser Asn
 1025 1030 1035 1040

ttt gaa aat aac aat ggt aca aag ggt agt gca atc agc ttt gac ggt 3168
 Phe Glu Asn Asn Asn Gly Thr Lys Gly Ser Ala Ile Ser Phe Asp Gly
 1045 1050 1055

gaa cca caa acc ctt caa gct tac tta aat tca ggc tac gta ttt gat 3216
 Glu Pro Gln Thr Leu Gln Ala Tyr Leu Asn Ser Gly Tyr Val Phe Asp
 1060 1065 1070

agt gca act gat gcc aat ggt aat tca att ggt act gcc tca aac att 3264
 Ser Ala Thr Asp Ala Asn Gly Asn Ser Ile Gly Thr Ala Ser Asn Ile
 1075 1080 1085

acc ttt gga aac ttt gat agt gtt gat ggc aat gtt caa agc ttt aac 3312
 Thr Phe Gly Asn Phe Asp Ser Val Asp Gly Asn Val Gln Ser Phe Asn
 1090 1095 1100

att tat ttg gtt cac gga act gat act aag act gaa aag gca acg act 3360
 Ile Tyr Leu Val His Gly Thr Asp Thr Lys Thr Glu Lys Ala Thr Thr
 1105 1110 1115 1120

aat gct cat gtt cac tat gtt gta gca ggc aac gaa gct aat aag cca 3408
 Asn Ala His Val His Tyr Val Val Ala Gly Asn Glu Ala Asn Lys Pro
 1125 1130 1135

gct gct ccg gca gat agt cca act caa aca atc aac tgg acc aga act 3456
 Ala Ala Pro Ala Asp Ser Pro Thr Gln Thr Ile Asn Trp Thr Arg Thr
 1140 1145 1150

aac act act gac aag gtt act ggt gca act act gaa gga act tgg act 3504
 Asn Thr Thr Asp Lys Val Thr Gly Ala Thr Thr Glu Gly Thr Trp Thr
 1155 1160 1165

cca gac aag aac ggt ttt act agt gta act tca cct gat ctt act aat 3552
 Pro Asp Lys Asn Gly Phe Thr Ser Val Thr Ser Pro Asp Leu Thr Asn
 1170 1175 1180

tac act cca gat caa gct gtt gct aac ttt act aca cca cag cct aac 3600
 Tyr Thr Pro Asp Gln Ala Val Ala Asn Phe Thr Thr Pro Gln Pro Asn
 1185 1190 1195 1200

cgt gat caa gta gta act gtt gta tat aat cca aat cca gaa gtt gct 3648

Arg Asp Gln Val Val Thr Val Val Tyr Asn Pro Asn Pro Glu Val Ala	
1205 1210 1215	
caa aaa gct gac cta gtt gtt tat gac aag act gat aat aat aag gaa	3696
Gln Lys Ala Asp Leu Val Val Tyr Asp Lys Thr Asp Asn Asn Lys Glu	
1220 1225 1230	
ctt aac aac ttc gat aat agt ggt aaa act ggt act caa att tca ttt	3744
Leu Asn Asn Phe Asp Asn Ser Gly Lys Thr Gly Thr Gln Ile Ser Phe	
1235 1240 1245	
agt ggt tct gca aat tac gtt gct gac tta att gct aaa ggt tac aag	3792
Ser Gly Ser Ala Asn Tyr Val Ala Asp Leu Ile Ala Lys Gly Tyr Lys	
1250 1255 1260	
att gat agt ttt gta aat gat caa aac caa act tct aac cca act tca	3840
Ile Asp Ser Phe Val Asn Asp Gln Asn Gln Thr Ser Asn Pro Thr Ser	
1265 1270 1275 1280	
tat gat caa atc agt ttc agt aac ttc gat aat aat agt gct agt gac	3888
Tyr Asp Gln Ile Ser Phe Ser Asn Phe Asp Asn Asn Ser Ala Ser Asp	
1285 1290 1295	
caa cac ttt aag ttg tac tta gtt cac gat act gaa aac gta aca gat	3936
Gln His Phe Lys Leu Tyr Leu Val His Asp Thr Glu Asn Val Thr Asp	
1300 1305 1310	
aag aag act act act tca act gtt cac tac gtt gtt tca gat ggt aag	3984
Lys Lys Thr Thr Thr Ser Thr Val His Tyr Val Val Ser Asp Gly Lys	
1315 1320 1325	
act aac cca cca tct gat aat act caa acg att act tgg act cgt cca	4032
Thr Asn Pro Pro Ser Asp Asn Thr Gln Thr Ile Thr Trp Thr Arg Pro	
1330 1335 1340	
gga act aag gat aag gtc aca ggt gta aca act cca act gga aac tgg	4080
Gly Thr Lys Asp Lys Val Thr Gly Val Thr Thr Pro Thr Gly Asn Trp	
1345 1350 1355 1360	
act act ccg gac aac tat acg gat gta cca acg cca aat ctt gat gga	4128
Thr Thr Pro Asp Asn Tyr Thr Asp Val Pro Thr Pro Asn Leu Asp Gly	
1365 1370 1375	
tac act cca gat aag act aat gtt cca gca cca act cca gat cca aat	4176
Tyr Thr Pro Asp Lys Thr Asn Val Pro Ala Pro Thr Pro Asp Pro Asn	
1380 1385 1390	
caa aac cca aca act gtt gtt act tac aat cct aag act cca gaa gca	4224
Gln Asn Pro Thr Thr Val Val Thr Tyr Asn Pro Lys Thr Pro Glu Ala	
1395 1400 1405	
cca act tac acg ggt act acc gag aat aag act gta act cgt aca atc	4272
Pro Thr Tyr Thr Gly Thr Thr Glu Asn Lys Thr Val Thr Arg Thr Ile	
1410 1415 1420	
aac tac tat gac aag gta act ggt gaa aag att cca gct aac tta att	4320
Asn Tyr Tyr Asp Lys Val Thr Gly Glu Lys Ile Pro Ala Asn Leu Ile	

1425	1430	1435	1440	
agt gat aat cca	aca act caa aac gta	act tta tca cgt act cat gtt	4368	
Ser Asp Asn Pro Thr	Thr Gln Asn Val Thr	Leu Ser Arg Thr His Val		
	1445	1450	1455	
gtt tca tca act ggt	caa gac atg ggc tat ggg	act gtt agt gct gat	4416	
Val Ser Ser Thr	Gly Gln Asp Met Gly	Tyr Gly Thr Val Ser Ala Asp		
	1460	1465	1470	
ggg aag aca ttt act	aaa gcg aca act gtt	gat ggt tgg aac act ggt	4464	
Gly Lys Thr Phe Thr	Lys Ala Thr Thr Val	Asp Gly Trp Asn Thr Gly		
	1475	1480	1485	
gac tgg gct caa gta	act tca cca gat ctt	tca aac gca ggg tac act	4512	
Asp Trp Ala Gln Val	Thr Ser Pro Asp Leu	Ser Asn Ala Gly Tyr Thr		
	1490	1495	1500	
gct cca gat tta gct	caa gct gat caa gta	act gtt gat gca aac act	4560	
Ala Pro Asp Leu Ala	Gln Ala Asp Gln Val	Thr Val Asp Ala Asn Thr		
	1505	1510	1515	1520
aag gat gct gtg gtt	aat gtt tac tac ggt	cac caa act gaa gta att	4608	
Lys Asp Ala Val Val	Asn Val Tyr Tyr Gly	His Gln Thr Glu Val Ile		
	1525	1530	1535	
aca cca aag act cca	cat aat cct ggt gga	agt att aac cct aat gat	4656	
Thr Pro Lys Thr Pro	His Asn Pro Gly Gly	Ser Ile Asn Pro Asn Asp		
	1540	1545	1550	
cca cgt aat aag cca	tca gtt tac cca gat	ggg tta act aag gaa gct	4704	
Pro Arg Asn Lys Pro	Ser Val Tyr Pro Asp	Gly Leu Thr Lys Glu Ala		
	1555	1560	1565	
tta act act gaa gta	act cgt cac att aac	tat gtt ggt gtg aat gaa	4752	
Leu Thr Thr Glu Val	Thr Arg His Ile Asn	Tyr Val Gly Val Asn Glu		
	1570	1575	1580	
gac gga act act act	cca gta aat ggc tca	cca gat ggt aag aat act	4800	
Asp Gly Thr Thr Thr	Pro Val Asn Gly Ser	Pro Asp Gly Lys Asn Thr		
	1585	1590	1595	1600
tat act caa acc gtt	tcc ttt gaa cgt aat	gcc gtg atc gat aag gta	4848	
Tyr Thr Gln Thr Val	Ser Phe Glu Arg Asn	Ala Val Ile Asp Lys Val		
	1605	1610	1615	
act ggt caa att ttg	ggc tac agt act gat	ggc act act aat gta act	4896	
Thr Gly Gln Ile Leu	Gly Tyr Ser Thr Asp	Gly Thr Thr Asn Val Thr		
	1620	1625	1630	
ata act gat aag gac	cgt gct tgg acg cca	aca acc caa aac atg gat	4944	
Ile Thr Asp Lys Asp	Arg Ala Trp Thr Pro	Thr Thr Gln Asn Met Asp		
	1635	1640	1645	
tct gta gct tct aag	act cct agt gaa gta	ggc tat gac aag gtt gac	4992	
Ser Val Ala Ser Lys	Thr Pro Ser Glu Val	Gly Tyr Asp Lys Val Asp		
	1650	1655	1660	

att tca act gtt ggg ggc gta act gtt tac cca ggt caa aaa gtt aac	5040
Ile Ser Thr Val Gly Gly Val Thr Val Tyr Pro Gly Gln Lys Val Asn	
1665 1670 1675 1680	
gat gta act gtc act tac act aag aac aag tca cct gaa gtt act caa	5088
Asp Val Thr Val Thr Tyr Thr Lys Asn Lys Ser Pro Glu Val Thr Gln	
1685 1690 1695	
aag gcc act ctt gaa att atc gat aac aac gat act aac gca cct aag	5136
Lys Ala Thr Leu Glu Ile Ile Asp Asn Asn Asp Thr Asn Ala Pro Lys	
1700 1705 1710	
caa tta gct tca ttc agt aat gaa ggt aag agt gaa gat caa att aac	5184
Gln Leu Ala Ser Phe Ser Asn Glu Gly Lys Ser Glu Asp Gln Ile Asn	
1715 1720 1725	
ttc gct aac tca aat gaa atc ctt caa agt tac tta agc caa ggc tac	5232
Phe Ala Asn Ser Asn Glu Ile Leu Gln Ser Tyr Leu Ser Gln Gly Tyr	
1730 1735 1740	
aag gtt caa aag act gct ggt aac ctt agt gga gat gct caa agt ggc	5280
Lys Val Gln Lys Thr Ala Gly Asn Leu Ser Gly Asp Ala Gln Ser Gly	
1745 1750 1755 1760	
tac act tac cct act tac ggt aat act acg caa gac ttc aag att tac	5328
Tyr Thr Tyr Pro Thr Tyr Gly Asn Thr Thr Gln Asp Phe Lys Ile Tyr	
1765 1770 1775	
ttg att cac gat att gca gat aag act gaa act gct aca gca act gct	5376
Leu Ile His Asp Ile Ala Asp Lys Thr Glu Thr Ala Thr Ala Thr Ala	
1780 1785 1790	
caa gtt cac tat gtt gtt gct gat aat ggt gta caa gct cca gca gat	5424
Gln Val His Tyr Val Val Ala Asp Asn Gly Val Gln Ala Pro Ala Asp	
1795 1800 1805	
agt gat ctt caa act att act tac act aga act aat aga gtt gat aag	5472
Ser Asp Leu Gln Thr Ile Thr Tyr Thr Arg Thr Asn Arg Val Asp Lys	
1810 1815 1820	
gta act ggc gca act gta aat gaa ggt act tgg caa gct gat aag agt	5520
Val Thr Gly Ala Thr Val Asn Glu Gly Thr Trp Gln Ala Asp Lys Ser	
1825 1830 1835 1840	
gtc ttt act gat gta aaa tca cca gat ctt tct aaa gat ggt tac act	5568
Val Phe Thr Asp Val Lys Ser Pro Asp Leu Ser Lys Asp Gly Tyr Thr	
1845 1850 1855	
ccg agt ctt gaa aat gtt caa ttt aat gct cca gag cgt aat gta aac	5616
Pro Ser Leu Glu Asn Val Gln Phe Asn Ala Pro Glu Arg Asn Val Asn	
1860 1865 1870	
caa cgt gta act gtt gtt tac aac cgt tct gct caa gct gct gat tta	5664
Gln Arg Val Thr Val Val Tyr Asn Arg Ser Ala Gln Ala Ala Asp Leu	
1875 1880 1885	

caa atc att gac gac aat gat cca caa aac caa cgt gta ttg gca act	5712
Gln Ile Ile Asp Asp Asn Pro Gln Asn Gln Arg Val Leu Ala Thr	
1890 1895 1900	
tac tca gca ggt ggc gaa tca ggt aag caa att agc ttt gat ggt tca	5760
Tyr Ser Ala Gly Gly Glu Ser Gly Lys Gln Ile Ser Phe Asp Gly Ser	
1905 1910 1915 1920	
aac act caa ctt caa act tac ttg aac aat ggt tat aca ttt gaa aag	5808
Asn Thr Gln Leu Gln Thr Tyr Leu Asn Asn Gly Tyr Thr Phe Glu Lys	
1925 1930 1935	
tat gaa ggt caa ggt atg agt ggg gat gcc caa aat ggc ttc act tac	5856
Tyr Glu Gly Gln Gly Met Ser Gly Asp Ala Gln Asn Gly Phe Thr Tyr	
1940 1945 1950	
cca agc ttt gat aat gat tct caa tct aac caa agc ttc aag att tac	5904
Pro Ser Phe Asp Asn Asp Ser Gln Ser Asn Gln Ser Phe Lys Ile Tyr	
1955 1960 1965	
ttg aaa cac gca act gct aat aag act gca act gca act act act gct	5952
Leu Lys His Ala Thr Ala Asn Lys Thr Ala Thr Ala Thr Thr Thr Ala	
1970 1975 1980	
cat gtt cac tac atc atg gca gat ggt act aag gct cct gat gat agt	6000
His Val His Tyr Ile Met Ala Asp Gly Thr Lys Ala Pro Asp Asp Ser	
1985 1990 1995 2000	
gca att caa act att aac tgg acg cag act aac act gtt gac cga gta	6048
Ala Ile Gln Thr Ile Asn Trp Thr Gln Thr Asn Thr Val Asp Arg Val	
2005 2010 2015	
act ggt gca act ata aat gaa ggt act tgg tct tct gat aag aat gct	6096
Thr Gly Ala Thr Ile Asn Glu Gly Thr Trp Ser Ser Asp Lys Asn Ala	
2020 2025 2030	
ttt act gat gtt gat tca cca aca gta act ggg tac act cca ggt act	6144
Phe Thr Asp Val Asp Ser Pro Thr Val Thr Gly Tyr Thr Pro Gly Thr	
2035 2040 2045	
aag act gta aaa ttt gct act cca gaa cgt ggt gtt aac caa gtt gta	6192
Lys Thr Val Lys Phe Ala Thr Pro Glu Arg Gly Val Asn Gln Val Val	
2050 2055 2060	
aat gtt gtt tac act aag gat gct cca act cca gat cga caa aat gct	6240
Asn Val Val Tyr Thr Lys Asp Ala Pro Thr Pro Asp Arg Gln Asn Ala	
2065 2070 2075 2080	
ttg gtt gtt tac caa gac gta aat gat cca gct cat ccg gtt gat tta	6288
Leu Val Val Tyr Gln Asp Val Asn Asp Pro Ala His Pro Val Asp Leu	
2085 2090 2095	
ggg caa agt gat caa tta act ggt caa gca ggc tat agc att aac tac	6336
Gly Gln Ser Asp Gln Leu Thr Gly Gln Ala Gly Tyr Ser Ile Asn Tyr	
2100 2105 2110	
agc act gct aat aag att gat gaa tac gaa aaa caa ggt tac gta tta	6384

Ser Thr Ala Asn Lys Ile Asp Glu Tyr Glu Lys Gln Gly Tyr Val Leu	
2115 2120 2125	
gta tca aac ggc ttt gat gca aat ggt act aag cca agc ttt gac aat	6432
Val Ser Asn Gly Phe Asp Ala Asn Gly Thr Lys Pro Ser Phe Asp Asn	
2130 2135 2140	
ggt aac ggt aat act caa aca ttc tat gta acc ttt aag cat ggt att	6480
Val Asn Gly Asn Thr Gln Thr Phe Tyr Val Thr Phe Lys His Gly Ile	
2145 2150 2155 2160	
caa cct gtg acg cca aca act cca ggt act cca gat caa cca atc aat	6528
Gln Pro Val Thr Pro Thr Thr Pro Gly Thr Pro Asp Gln Pro Ile Asn	
2165 2170 2175	
cct gat aat cca gat ggt cct aaa tac cca tca ggc act gat caa act	6576
Pro Asp Asn Pro Asp Gly Pro Lys Tyr Pro Ser Gly Thr Asp Gln Thr	
2180 2185 2190	
agc tta act aaa gat gta act cgt act gtt act tac gaa ggt gct ggc	6624
Ser Leu Thr Lys Asp Val Thr Arg Thr Val Thr Tyr Glu Gly Ala Gly	
2195 2200 2205	
aac caa act cca agt cct gta act gat act ctt cac ttc caa ggt aca	6672
Asn Gln Thr Pro Ser Pro Val Thr Asp Thr Leu His Phe Gln Gly Thr	
2210 2215 2220	
ggg tac tta gac aag gta act ggt aag tgg act gat gca aat ggt aag	6720
Gly Tyr Leu Asp Lys Val Thr Gly Lys Trp Thr Asp Ala Asn Gly Lys	
2225 2230 2235 2240	
aaa tta agt gat caa act aag ggg att act tgg acg att acc gat ggt	6768
Lys Leu Ser Asp Gln Thr Lys Gly Ile Thr Trp Thr Ile Thr Asp Gly	
2245 2250 2255	
act aag gat gaa ggt agt ttt aac tta gtt cca act aag cat att gat	6816
Thr Lys Asp Glu Gly Ser Phe Asn Leu Val Pro Thr Lys His Ile Asp	
2260 2265 2270	
ggg tac act tcc aag gtt gtg act aac ggt gct gac gat ggt aac ggt	6864
Gly Tyr Thr Ser Lys Val Val Thr Asn Gly Ala Asp Asp Gly Asn Gly	
2275 2280 2285	
aat gtt aag agc tac act ggt att act cat aca agc gac aat att aac	6912
Asn Val Lys Ser Tyr Thr Gly Ile Thr His Thr Ser Asp Asn Ile Asn	
2290 2295 2300	
gtg gta gtt caa tac aac cca att gtt gct gaa caa ggt aac tta att	6960
Val Val Val Gln Tyr Asn Pro Ile Val Ala Glu Gln Gly Asn Leu Ile	
2305 2310 2315 2320	
ggt aag ttc cat gat gat act gat aac aag gat ttg aca ggt gta ggt	7008
Val Lys Phe His Asp Asp Thr Asp Asn Lys Asp Leu Thr Gly Val Gly	
2325 2330 2335	
act gat act ggt act caa gat gtt ggt act caa gtc act tac aat cca	7056
Thr Asp Thr Gly Thr Gln Asp Val Gly Thr Gln Val Thr Tyr Asn Pro	

2340	2345	2350	
agt act gat tta act aat ctt gaa aat aag ggt tat gtt tat gta tca Ser Thr Asp Leu Thr Asn Leu Glu Asn Lys Gly Tyr Val Tyr Val Ser 2355 2360 2365			7104
act gat ggt aat att cct tca tca att gtt aag ggg acc act act gta Thr Asp Gly Asn Ile Pro Ser Ser Ile Val Lys Gly Thr Thr Thr Val 2370 2375 2380			7152
act atc cac gta aaa cat ggt act gtt cca gta act cca gac aat cca Thr Ile His Val Lys His Gly Thr Val Pro Val Thr Pro Asp Asn Pro 2385 2390 2395 2400			7200
ggt act cca gat caa cca att aac cct aac gat cca gat cca aat ggt Gly Thr Pro Asp Gln Pro Ile Asn Pro Asn Asp Pro Asp Pro Asn Gly 2405 2410 2415			7248
cct aag tat cca aca gga act gat aag gct tct att gat aag act att Pro Lys Tyr Pro Thr Gly Thr Asp Lys Ala Ser Ile Asp Lys Thr Ile 2420 2425 2430			7296
act cgt att gtt cat tac gaa ggt gcc gat caa tat act cca aat gat Thr Arg Ile Val His Tyr Glu Gly Ala Asp Gln Tyr Thr Pro Asn Asp 2435 2440 2445			7344
gtt aag caa cca gta cac ttc act gct aag ggc gtg ctt gac aag gta Val Lys Gln Pro Val His Phe Thr Ala Lys Gly Val Leu Asp Lys Val 2450 2455 2460			7392
act ggt gaa tgg att act cca tta gct tgg tca gaa gat caa aca ttt Thr Gly Glu Trp Ile Thr Pro Leu Ala Trp Ser Glu Asp Gln Thr Phe 2465 2470 2475 2480			7440
aat ggt gta aat agt cca aaa att cca ggc tac cat gta gaa agt gtt Asn Gly Val Asn Ser Pro Lys Ile Pro Gly Tyr His Val Glu Ser Val 2485 2490 2495			7488
gat aag gat aca act gat aat caa aac gtt gat agt gct aag att agc Asp Lys Asp Thr Thr Asp Asn Gln Asn Val Asp Ser Ala Lys Ile Ser 2500 2505 2510			7536
cac aca ggg gct gat tac aca gta act gtt aag tat gca aaa gat gct His Thr Gly Ala Asp Tyr Thr Val Thr Val Lys Tyr Ala Lys Asp Ala 2515 2520 2525			7584
gct cca act cca gat gct aca act gga aaa gta gct tac atc gat gat Ala Pro Thr Pro Asp Ala Thr Thr Gly Lys Val Ala Tyr Ile Asp Asp 2530 2535 2540			7632
act act aag aat act tta agg act gat tcg ctt agt ggt aat gtt gat Thr Thr Lys Asn Thr Leu Arg Thr Asp Ser Leu Ser Gly Asn Val Asp 2545 2550 2555 2560			7680
gct aat att gat tac act act caa gat aag atc agt aat tac atc aac Ala Asn Ile Asp Tyr Thr Thr Gln Asp Lys Ile Ser Asn Tyr Ile Asn 2565 2570 2575			7728

atg ggg tac aag tta gta tct aac aac ttc act gat ggt aag gaa atc	7776
Met Gly Tyr Lys Leu Val Ser Asn Asn Phe Thr Asp Gly Lys Glu Ile	
2580 2585 2590	
ttt aat aag gat gct tct aag aac agc ttt gaa gtt cac ttg gta cat	7824
Phe Asn Lys Asp Ala Ser Lys Asn Ser Phe Glu Val His Leu Val His	
2595 2600 2605	
gac acc gtt cca gta acc cca gac aat cca ggt act cca gat aag cca	7872
Asp Thr Val Pro Val Thr Pro Asp Asn Pro Gly Thr Pro Asp Lys Pro	
2610 2615 2620	
atc aac cct aac gat cca cgt cca cga agt gaa caa cct aag tat cca	7920
Ile Asn Pro Asn Asp Pro Arg Pro Arg Ser Glu Gln Pro Lys Tyr Pro	
2625 2630 2635 2640	
act ggt act agt gaa act gac ctt act aag gac att act cgt act gtt	7968
Thr Gly Thr Ser Glu Thr Asp Leu Thr Lys Asp Ile Thr Arg Thr Val	
2645 2650 2655	
cat tat tca ggt gct gat gaa tac act cca aat gat gtt aag caa cca	8016
His Tyr Ser Gly Ala Asp Glu Tyr Thr Pro Asn Asp Val Lys Gln Pro	
2660 2665 2670	
gta cac ttc act gct aag ggc gta ctt gac aag gta act ggt gaa tgg	8064
Val His Phe Thr Ala Lys Gly Val Leu Asp Lys Val Thr Gly Glu Trp	
2675 2680 2685	
att act cca tta act tgg tca gaa gat caa aca ttt aat ggt gta aat	8112
Ile Thr Pro Leu Thr Trp Ser Glu Asp Gln Thr Phe Asn Gly Val Asn	
2690 2695 2700	
agt cca aag att cca ggc tat cat gta gta agt gtt gat aaa gat gct	8160
Ser Pro Lys Ile Pro Gly Tyr His Val Val Ser Val Asp Lys Asp Ala	
2705 2710 2715 2720	
gat ggt act aat gtt gct tca tct aat gtt agc cac act ggt tcc gat	8208
Asp Gly Thr Asn Val Ala Ser Ser Asn Val Ser His Thr Gly Ser Asp	
2725 2730 2735	
tac act gtc aat gtt gta tat gct aag gat gct gta aag caa gct gaa	8256
Tyr Thr Val Asn Val Val Tyr Ala Lys Asp Ala Val Lys Gln Ala Glu	
2740 2745 2750	
aat gct aac tta cat att att gac ctt agc gat aac aac aaa gaa att	8304
Asn Ala Asn Leu His Ile Ile Asp Leu Ser Asp Asn Asn Lys Glu Ile	
2755 2760 2765	
gct aac ttt aat gat tct ggt gat gat aat gct gca att aac ttc aat	8352
Ala Asn Phe Asn Asp Ser Gly Asp Asp Asn Ala Ala Ile Asn Phe Asn	
2770 2775 2780	
ggc gca caa act act gtc gat gcc ttg atc aag ggt ggt tat aaa gtt	8400
Gly Ala Gln Thr Thr Val Asp Ala Leu Ile Lys Gly Gly Tyr Lys Val	
2785 2790 2795 2800	

aac agc att gtt caa gca act agt gat cct aat aac cca act aaa tat	8448
Asn Ser Ile Val Gln Ala Thr Ser Asp Pro Asn Asn Pro Thr Lys Tyr	
2805 2810 2815	
ggc act gaa tat tca agt gct gct agt caa tgg atg ttt gac gat aaa	8496
Gly Thr Glu Tyr Ser Ser Ala Ala Ser Gln Trp Met Phe Asp Asp Lys	
2820 2825 2830	
cct ggt gta gat caa tca ttc tat gta tat gta gaa cac gat tac gct	8544
Pro Gly Val Asp Gln Ser Phe Tyr Val Tyr Val Glu His Asp Tyr Ala	
2835 2840 2845	
cca att aat cca gaa aat gcc tat ggt aga act gat tta act caa aca	8592
Pro Ile Asn Pro Glu Asn Ala Tyr Gly Arg Thr Asp Leu Thr Gln Thr	
2850 2855 2860	
gta act gaa act gtt cac tac att gat gaa gct act aat aag cct gtt	8640
Val Thr Glu Thr Val His Tyr Ile Asp Glu Ala Thr Asn Lys Pro Val	
2865 2870 2875 2880	
gca act gat tac acc aat act ctt aca ttt aag ggt caa ggt aga gtt	8688
Ala Thr Asp Tyr Thr Asn Thr Leu Thr Phe Lys Gly Gln Gly Arg Val	
2885 2890 2895	
gat aag gta act ggt aag atg ctt aag atc aag agc att gaa aat ggt	8736
Asp Lys Val Thr Gly Lys Met Leu Lys Ile Lys Ser Ile Glu Asn Gly	
2900 2905 2910	
caa att act tat gat tac aat gta gcc aat gaa att gat atc agt agt	8784
Gln Ile Thr Tyr Asp Tyr Asn Val Ala Asn Glu Ile Asp Ile Ser Ser	
2915 2920 2925	
gct aag tta agt gac ttt gct tgg tca act ccg act act ttg caa aaa	8832
Ala Lys Leu Ser Asp Phe Ala Trp Ser Thr Pro Thr Thr Leu Gln Lys	
2930 2935 2940	
gta act tca cca act att gct ggt tac aca att gat gct gct aag act	8880
Val Thr Ser Pro Thr Ile Ala Gly Tyr Thr Ile Asp Ala Ala Lys Thr	
2945 2950 2955 2960	
aca cca agt gaa tta gct gat ggt aat gac att aag gaa atc caa aat	8928
Thr Pro Ser Glu Leu Ala Asp Gly Asn Asp Ile Lys Glu Ile Gln Asn	
2965 2970 2975	
gtt gct tac gat cac ggt aac gta gaa gct act gtt tac tac aag gca	8976
Val Ala Tyr Asp His Gly Asn Val Glu Ala Thr Val Tyr Tyr Lys Ala	
2980 2985 2990	
aac cca gtt gaa act cac aag gct gga tta act att tat gca aat gga	9024
Asn Pro Val Glu Thr His Lys Ala Gly Leu Thr Ile Tyr Ala Asn Gly	
2995 3000 3005	
aat caa gta ggt act gcg agt gta act ggt gct aag gat act gct att	9072
Asn Gln Val Gly Thr Ala Ser Val Thr Gly Ala Lys Asp Thr Ala Ile	
3010 3015 3020	
aac ttc agt agt gct tct gat att gtt gcg gct tac att tct aat ggt	9120

Asn Phe Ser Ser Ala Ser Asp Ile Val Ala Ala Tyr Ile Ser Asn Gly 3025 3030 3035 3040	
tac aaa ttt gat cac gct caa gat gta acc aac aat aaa gaa atg act Tyr Lys Phe Asp His Ala Gln Asp Val Thr Asn Asn Lys Glu Met Thr 3045 3050 3055	9168
ggc aag tca tac aat gag tta aac ttt ggt aac ttt gca act aca aat Gly Lys Ser Tyr Asn Glu Leu Asn Phe Gly Asn Phe Ala Thr Thr Asn 3060 3065 3070	9216
aat agt gat caa caa ttt gct atc tac tta act aag gat gaa aca cca Asn Ser Asp Gln Gln Phe Ala Ile Tyr Leu Thr Lys Asp Glu Thr Pro 3075 3080 3085	9264
gct aag act caa caa aat gct caa ttg act gtt cga gat gta act cct Ala Lys Thr Gln Gln Asn Ala Gln Leu Thr Val Arg Asp Val Thr Pro 3090 3095 3100	9312
ggc caa gaa atg gat tta ggt aat tac act caa cct ggt ctt gaa ggc Gly Gln Glu Met Asp Leu Gly Asn Tyr Thr Gln Pro Gly Leu Glu Gly 3105 3110 3115 3120	9360
gat aca att agc ttt agt agt gct caa gaa ttt gtt caa aac tta ttg Asp Thr Ile Ser Phe Ser Ser Ala Gln Glu Phe Val Gln Asn Leu Leu 3125 3130 3135	9408
aac aaa ggt tac gtt tgg gat ggt gct tca tat aac ggt act aac tta Asn Lys Gly Tyr Val Trp Asp Gly Ala Ser Tyr Asn Gly Thr Asn Leu 3140 3145 3150	9456
gaa gct act aac tat gct ggt att aac ttt ggt aat tat gac aac act Glu Ala Thr Asn Tyr Ala Gly Ile Asn Phe Gly Asn Tyr Asp Asn Thr 3155 3160 3165	9504
gat gat aag aat ggc att agt caa aaa tgg gta att aac tta gtt cat Asp Asp Lys Asn Gly Ile Ser Gln Lys Trp Val Ile Asn Leu Val His 3170 3175 3180	9552
ggc gta act cca gta aat cct gat cat cca gat gat aaa gat ggt ttt Gly Val Thr Pro Val Asn Pro Asp His Pro Asp Asp Lys Asp Gly Phe 3185 3190 3195 3200	9600
act aag gat tac ctt gat cgt aca att act cgt gat gta act tat gtt Thr Lys Asp Tyr Leu Asp Arg Thr Ile Thr Arg Asp Val Thr Tyr Val 3205 3210 3215	9648
tac gaa gat ggt agc caa gct gct gct cca gta cat cag gaa gca cat Tyr Glu Asp Gly Ser Gln Ala Ala Pro Val His Gln Glu Ala His 3220 3225 3230	9696
tac caa ggt tca ggt tac tta gat aat gta aca ggc aag tgg gta act Tyr Gln Gly Ser Gly Tyr Leu Asp Asn Val Thr Gly Lys Trp Val Thr 3235 3240 3245	9744
ggt gaa aat ggt aag atc act ggc ttg gct caa ggc tta act tgg act Val Glu Asn Gly Lys Ile Thr Gly Leu Ala Gln Gly Leu Thr Trp Thr 3250 3255 3260	9792

3250	3255	3260	
cca gat caa gat tca aca ttt gac caa att ggt gca aag aat att gaa			9840
Pro Asp Gln Asp Ser Thr Phe Asp Gln Ile Gly Ala Lys Asn Ile Glu			
3265	3270	3275	3280
ggg tac cat gta tct tct gta agc ggc aat gga att tca ggc ttc aca			9888
Gly Tyr His Val Ser Ser Val Ser Gly Asn Gly Ile Ser Gly Phe Thr			
3285	3290	3295	
gtt ggt caa gat ggt aca gtt ggt caa caa aca gtt act aaa gat act			9936
Val Gly Gln Asp Gly Thr Val Gly Gln Gln Thr Val Thr Lys Asp Thr			
3300	3305	3310	
cca agt tca aca att aga gtt gtt tat gtt aag act cca gta act cca			9984
Pro Ser Ser Thr Ile Arg Val Val Tyr Val Lys Thr Pro Val Thr Pro			
3315	3320	3325	
gtt cca gca aat ggt tca att gtt tac att gat gac act act ggt aat			10032
Val Pro Ala Asn Gly Ser Ile Val Tyr Ile Asp Asp Thr Thr Gly Asn			
3330	3335	3340	
aac ctt gag aat gct act ttc ggt ggt act gtt ggt gct aag att gac			10080
Asn Leu Glu Asn Ala Thr Phe Gly Gly Thr Val Gly Ala Lys Ile Asp			
3345	3350	3355	3360
tac act act gca gat aga att agt tac tat caa ggt aaa ggc tac aag			10128
Tyr Thr Thr Ala Asp Arg Ile Ser Tyr Tyr Gln Gly Lys Gly Tyr Lys			
3365	3370	3375	
ctt gta tct aac aac ttc acc gat ggc agc caa aca ttc aaa caa ggt			10176
Leu Val Ser Asn Asn Phe Thr Asp Gly Ser Gln Thr Phe Lys Gln Gly			
3380	3385	3390	
gaa aat aag ttt gaa gtt cat tta act cat gtg act gaa act aag gat			10224
Glu Asn Lys Phe Glu Val His Leu Thr His Val Thr Glu Thr Lys Asp			
3395	3400	3405	
gca act aag act att act cgt gat gta act tat gtt tac gaa gat ggt			10272
Ala Thr Lys Thr Ile Thr Arg Asp Val Thr Tyr Val Tyr Glu Asp Gly			
3410	3415	3420	
agt cag gct gat act cca gta caa caa aca att aca ttt act ggt aaa			10320
Ser Gln Ala Asp Thr Pro Val Gln Gln Thr Ile Thr Phe Thr Gly Lys			
3425	3430	3435	3440
act act agt gat aaa gta act gga tct gaa aag act act tgg aat aat			10368
Thr Thr Ser Asp Lys Val Thr Gly Ser Glu Lys Thr Thr Trp Asn Asn			
3445	3450	3455	
gaa agt caa acc ttc ggt gca act aaa gca att gat aca act aag tat			10416
Glu Ser Gln Thr Phe Gly Ala Thr Lys Ala Ile Asp Thr Thr Lys Tyr			
3460	3465	3470	
caa att gta ggt att aac gaa cgt aat act act gcc aat gtt gac aga			10464
Gln Ile Val Gly Ile Asn Glu Arg Asn Thr Thr Ala Asn Val Asp Arg			
3475	3480	3485	

gat act ggt gta gta gct agt gaa aca att act cca aat agt caa aat	10512
Asp Thr Gly Val Val Ala Ser Glu Thr Ile Thr Pro Asn Ser Gln Asn	
3490 3495 3500	
agt gca gtt gtc atc act ttg gca aac aaa cca gaa act cca att cca	10560
Ser Ala Val Val Ile Thr Leu Ala Asn Lys Pro Glu Thr Pro Ile Pro	
3505 3510 3515 3520	
gca aat ggt tca att acg tat tat gat gat act act gga aca act ctt	10608
Ala Asn Gly Ser Ile Thr Tyr Tyr Asp Asp Thr Thr Gly Thr Thr Leu	
3525 3530 3535	
gaa agc gct ggt ttc agt ggt agt gtt gga caa aag atc aat tac act	10656
Glu Ser Ala Gly Phe Ser Gly Ser Val Gly Gln Lys Ile Asn Tyr Thr	
3540 3545 3550	
act gcg gat aga att att aat tac gta aac aag ggt tat gat gtt gta	10704
Thr Ala Asp Arg Ile Ile Asn Tyr Val Asn Lys Gly Tyr Asp Val Val	
3555 3560 3565	
tcc aac aac ttc act gat ggc aac gaa aca ttc aaa caa ggt gac aac	10752
Ser Asn Asn Phe Thr Asp Gly Asn Glu Thr Phe Lys Gln Gly Asp Asn	
3570 3575 3580	
aag ttt gaa gtt cat ttg gta cat gcg act aca cca att acc cct gaa	10800
Lys Phe Glu Val His Leu Val His Ala Thr Thr Pro Ile Thr Pro Glu	
3585 3590 3595 3600	
aat ccg ggt aag cca ggt caa gaa gtt cca aat cca aat gat cca gaa	10848
Asn Pro Gly Lys Pro Gly Gln Glu Val Pro Asn Pro Asn Asp Pro Glu	
3605 3610 3615	
cac cca cac act att cct gcc aac ttt gta cca caa act ttg act cat	10896
His Pro His Thr Ile Pro Ala Asn Phe Val Pro Gln Thr Leu Thr His	
3620 3625 3630	
act gta act cgt gat gta act tat gtt tat gca gat ggt agt caa gct	10944
Thr Val Thr Arg Asp Val Thr Tyr Val Tyr Ala Asp Gly Ser Gln Ala	
3635 3640 3645	
agt gct cca gta cat caa aca ttt acc ttt aac ggt aac ggt gta att	10992
Ser Ala Pro Val His Gln Thr Phe Thr Phe Asn Gly Asn Gly Val Ile	
3650 3655 3660	
gat ctt gtg aca ggt caa tta gta act gtt gaa aac ggc aag atc act	11040
Asp Leu Val Thr Gly Gln Leu Val Thr Val Glu Asn Gly Lys Ile Thr	
3665 3670 3675 3680	
ggt gca ggt aag att act tgg aat gca gac agt cat aac ttc gat gca	11088
Gly Ala Gly Lys Ile Thr Trp Asn Ala Asp Ser His Asn Phe Asp Ala	
3685 3690 3695	
atc gat gca att gat cac gat ggt tac tac att tca aat gtt agt gaa	11136
Ile Asp Ala Ile Asp His Asp Gly Tyr Tyr Ile Ser Asn Val Ser Glu	
3700 3705 3710	

aat aac act aca gct aat gta gat aca aat aca ggt gcg gta gct ggt Asn Asn Thr Thr Ala Asn Val Asp Thr Asn Thr Gly Ala Val Ala Gly 3715 3720 3725	11184
gaa aca att act cca aat agt caa aat agt aca att att att act ttg Glu Thr Ile Thr Pro Asn Ser Gln Asn Ser Thr Ile Ile Ile Thr Leu 3730 3735 3740	11232
act aag aaa cca gat gta cca act cca gtt cca gag caa ggt tca att Thr Lys Lys Pro Asp Val Pro Thr Pro Val Pro Glu Gln Gly Ser Ile 3745 3750 3755 3760	11280
aaa gta act gtt cat gat gta aag act aac caa gat gtt cca ggc tat Lys Val Thr Val His Asp Val Lys Thr Asn Gln Asp Val Pro Gly Tyr 3765 3770 3775	11328
gat aaa gat agt ggc aaa caa aat act ggt aca agc ttt act tat gat Asp Lys Asp Ser Gly Lys Gln Asn Thr Gly Thr Ser Phe Thr Tyr Asp 3780 3785 3790	11376
aaa acc act aca att act gat ctt gag aac aaa ggt tac aag gta att Lys Thr Thr Thr Ile Thr Asp Leu Glu Asn Lys Gly Tyr Lys Val Ile 3795 3800 3805	11424
aat cct aat gtt gat att cca act aag gta tct aat att gat caa cat Asn Pro Asn Val Asp Ile Pro Thr Lys Val Ser Asn Ile Asp Gln His 3810 3815 3820	11472
att gtt atc tat gta gat cat aat gtg att cca gta act cca gat aag Ile Val Ile Tyr Val Asp His Asn Val Ile Pro Val Thr Pro Asp Lys 3825 3830 3835 3840	11520
cca ggc aat gga tta agt gaa aac gat ctt aat aag acg gtt acc gaa Pro Gly Asn Gly Leu Ser Glu Asn Asp Leu Asn Lys Thr Val Thr Glu 3845 3850 3855	11568
act gtt cac tat gtt gta aac ggt ggt gct act gaa gct cca gca gat Thr Val His Tyr Val Val Asn Gly Gly Ala Thr Glu Ala Pro Ala Asp 3860 3865 3870	11616
aaa aca act agt ttg aaa ttt act ggt aca gct tat tat gat tca gta Lys Thr Thr Ser Leu Lys Phe Thr Gly Thr Ala Tyr Tyr Asp Ser Val 3875 3880 3885	11664
act aag aag tgg act gat gca aac ggt aat gaa tta tca gat caa tct Thr Lys Lys Trp Thr Asp Ala Asn Gly Asn Glu Leu Ser Asp Gln Ser 3890 3895 3900	11712
aag aat gtt act tgg act gct gaa aat ggt aat aag ttt gca gta gtg Lys Asn Val Thr Trp Thr Ala Glu Asn Gly Asn Lys Phe Ala Val Val 3905 3910 3915 3920	11760
gta act cca act ctt gaa ggt tat act cca agt gtt caa tct ggt tat Val Thr Pro Thr Leu Glu Gly Tyr Thr Pro Ser Val Gln Ser Gly Tyr 3925 3930 3935	11808
gat gat gga aat aag aat gtt aag gaa atc aat aac att act cca gat	11856

Asp Asp Gly Asn Lys Asn Val Lys Glu Ile Asn Asn Ile Thr Pro Asp	
3940 3945 3950	
tca ggt aat gta gaa gta act gta act tac aat aag aac aat gtt cca	11904
Ser Gly Asn Val Glu Val Thr Val Thr Tyr Asn Lys Asn Asn Val Pro	
3955 3960 3965	
act cct gta aag caa gga aca att gag att att tac cat gac act act	11952
Thr Pro Val Lys Gln Gly Thr Ile Glu Ile Ile Tyr His Asp Thr Thr	
3970 3975 3980	
gat aat gta gat att cca gga tat ggt cag agt cgg att aag gaa gat	12000
Asp Asn Val Asp Ile Pro Gly Tyr Gly Gln Ser Arg Ile Lys Glu Asp	
3985 3990 3995 4000	
gag ggt aca agc ttt agc tat aat cct aat gct aaa gat tta ccg gcc	12048
Glu Gly Thr Ser Phe Ser Tyr Asn Pro Asn Ala Lys Asp Leu Pro Ala	
4005 4010 4015	
ttg gaa agc aaa ggc tat gtt ctt gat ggt gaa tta cca aca att cca	12096
Leu Glu Ser Lys Gly Tyr Val Leu Asp Gly Glu Leu Pro Thr Ile Pro	
4020 4025 4030	
act aaa ttt aca gat ggt gat caa cgt gtg gta att aat gta aag cac	12144
Thr Lys Phe Thr Asp Gly Asp Gln Arg Val Val Ile Asn Val Lys His	
4035 4040 4045	
ggg aca act act gtt act cca gat aaa ccg ggc aaa cct ggt gat cca	12192
Gly Thr Thr Thr Val Thr Pro Asp Lys Pro Gly Lys Pro Gly Asp Pro	
4050 4055 4060	
att gat cct aat aat cca gat ggt cct aag tat cca gaa ggt acc ggt	12240
Ile Asp Pro Asn Asn Pro Asp Gly Pro Lys Tyr Pro Glu Gly Thr Gly	
4065 4070 4075 4080	
gaa aat aac tta aag gta act ggt aca caa act atc cat tac att ggt	12288
Glu Asn Asn Leu Lys Val Thr Gly Thr Gln Thr Ile His Tyr Ile Gly	
4085 4090 4095	
gca ggt gat aag act cca aag gat aat act caa agc ttc gaa ttt act	12336
Ala Gly Asp Lys Thr Pro Lys Asp Asn Thr Gln Ser Phe Glu Phe Thr	
4100 4105 4110	
aag caa att acc ttt gat aat gta act ggt aag att att aat gat tct	12384
Lys Gln Ile Thr Phe Asp Asn Val Thr Gly Lys Ile Ile Asn Asp Ser	
4115 4120 4125	
ggg tgg aat gta acc agt cat aca ttt ggc tct gaa gca act cct gta	12432
Gly Trp Asn Val Thr Ser His Thr Phe Gly Ser Glu Ala Thr Pro Val	
4130 4135 4140	
att gat ggc tac cat gct gat aag aca act gct gga ggc act act gta	12480
Ile Asp Gly Tyr His Ala Asp Lys Thr Thr Ala Gly Gly Thr Thr Val	
4145 4150 4155 4160	
act cct aat gac tta cat aag aca gta aca gta act tac aca cca aat	12528
Thr Pro Asn Asp Leu His Lys Thr Val Thr Val Thr Tyr Thr Pro Asn	

4165										4170					4175					
gtt ccg gct gta ccg aca cca act cca aca cct agt ccg gaa cca aag	12576																			
Val Pro Ala Val Pro Thr Pro Thr Pro Thr Pro Ser Pro Glu Pro Lys																				
4180 4185 4190																				
ccg gag aat act cca gtt gaa cca aat aca cca act cca act cca gat	12624																			
Pro Glu Asn Thr Pro Val Glu Pro Asn Thr Pro Thr Pro Thr Pro Asp																				
4195 4200 4205																				
att cca gat aat gta acc cca act cca gaa cca gaa aat aat aat gta	12672																			
Ile Pro Asp Asn Val Thr Pro Thr Pro Glu Pro Glu Asn Asn Asn Val																				
4210 4215 4220																				
aaa cct cat ggc gaa agc att gtt caa aag aat aat gac aat cca aag	12720																			
Lys Pro His Gly Glu Ser Ile Val Gln Lys Asn Asn Asp Asn Pro Lys																				
4225 4230 4235 4240																				
gtg gtt tca cat ggt caa tct ggt aat aat tgg aca gct cct cat ggt	12768																			
Val Val Ser His Gly Gln Ser Gly Asn Asn Trp Thr Ala Pro His Gly																				
4245 4250 4255																				
caa cat gtc gat caa agg ggt aac att gta act tct gat aat aga gtc	12816																			
Gln His Val Asp Gln Arg Gly Asn Ile Val Thr Ser Asp Asn Arg Val																				
4260 4265 4270																				
gtt ggt tat gtt gat caa aat ggt aaa gct cac tac act aaa ttg cca	12864																			
Val Gly Tyr Val Asp Gln Asn Gly Lys Ala His Tyr Thr Lys Leu Pro																				
4275 4280 4285																				
caa aca ggc gat gat caa act aat gat gtt gca gca gca ctt tta ggt	12912																			
Gln Thr Gly Asp Asp Gln Thr Asn Asp Val Ala Ala Ala Leu Leu Gly																				
4290 4295 4300																				
ggc gca gca gtc tca ctt ggt tta atc gga ctt gca ggt gtc aag aag	12960																			
Gly Ala Ala Val Ser Leu Gly Leu Ile Gly Leu Ala Gly Val Lys Lys																				
4305 4310 4315 4320																				
cgt aga aaa gaa gac aaa	12978																			
Arg Arg Lys Glu Asp Lys																				
4325																				

<210> 18

<211> 4326

<212> PRT

<213> Lactobacillus acidophilus

<400> 18

Met Val Ser Lys Asn Asn Arg Ala Lys Gln Met Glu Asn Val Ala Glu	
1 5 10 15	
Arg Gln Pro His Phe Ser Ile Arg Lys Leu Thr Ile Gly Ala Ala Ser	
20 25 30	
Val Leu Leu Ser Thr Thr Leu Trp Met Ser Val Asn Thr Ser Ser Val	
35 40 45	
His Ala Glu Asn Ile Asp Asn Ser Asp Asn Asp Ala His Glu Ala Thr	
50 55 60	

Glu	Ser	Asn	Thr	Glu	Thr	Pro	Ser	Ile	Asn	Asp	Asp	Thr	Lys	Val	Val
65					70					75					80
Val	Glu	Ser	Asn	Ser	Asn	Ile	Thr	Ser	Ser	Asn	Asp	Val	Asn	Ala	Gly
			85						90					95	
Asn	Asn	Gly	Ala	Glu	Thr	Asn	Asp	Thr	Asn	Asn	Glu	Val	Thr	Ala	Ser
			100					105					110		
Glu	Asp	Thr	Ser	Lys	Gly	Leu	Thr	Val	Asp	Asn	Lys	Asp	Ala	Ser	Val
		115						120				125			
Gln	Ser	Thr	Val	Lys	Ser	Ser	Asp	Glu	Val	Lys	Lys	Ser	Glu	Ser	Thr
		130					135					140			
Glu	Gln	Lys	Ser	Ala	Lys	Thr	Ala	Gln	Asn	Ser	Thr	Leu	Asn	Asn	Asn
145					150					155					160
Thr	Val	Asn	Thr	Glu	Lys	Ala	Glu	Ser	Asn	Val	Ala	Ala	Lys	Ser	Asn
			165						170					175	
Ala	Asp	Thr	Ala	Lys	Ser	Thr	Gln	Gln	Ser	Ser	Ala	Ala	Ser	Ser	Ala
			180						185					190	
Asn	Gln	Val	Ser	Ser	Asn	Ala	Asp	Leu	Thr	Gln	Asn	Gln	Ala	Ile	Asn
		195					200					205			
Ser	Thr	Thr	Gln	Val	Glu	Ala	Asn	Asn	Ser	Thr	Asn	Asp	Lys	Lys	Ala
		210				215						220			
Asn	Asn	Asp	Thr	Ala	Asp	Leu	Ser	Asn	Ile	Gly	Leu	Lys	Gly	Ile	Glu
225					230					235					240
Thr	Asn	Lys	Ile	Pro	Glu	Thr	Thr	Asp	Leu	Pro	Val	Ser	Glu	Leu	Ile
			245						250					255	
Lys	Ser	Tyr	Asn	Asn	Asn	Ser	Asn	Ser	Asn	Glu	Val	Asn	Val	Asn	Gln
			260					265					270		
Val	Ser	Gly	Leu	Arg	Ala	Ala	Gln	Leu	Phe	Ala	Ala	Ser	Phe	Ile	Ala
		275						280					285		
Thr	Gln	Asn	Thr	Gly	Thr	Gly	Asn	Asn	Gly	Ala	Val	Asn	Ile	Asp	Thr
		290				295						300			
Tyr	Lys	Pro	Asp	Phe	Asn	Leu	Thr	Glu	Asn	Pro	Ala	Tyr	Gln	Gln	Tyr
305					310					315					320
Phe	Ala	Ala	Ile	Pro	Ala	Asp	Gln	Tyr	Ala	Phe	Gln	Ser	Tyr	Glu	Val
			325						330					335	
Val	Ser	Thr	Gly	Gln	Lys	Ile	Val	Val	Thr	Thr	Asp	Arg	Asn	Asn	Ile
			340					345					350		
Gly	Asn	Asn	Ile	Arg	Phe	Tyr	Asn	Val	Arg	Asn	Gly	Ser	Ala	Gln	Leu
		355						360				365			
Val	Tyr	Gln	Met	Thr	Arg	Asp	Thr	Gln	Thr	Asn	Ala	Ser	Gly	Ser	Val
		370				375						380			
Val	Lys	Asn	Arg	Pro	Ser	Leu	Gln	Gly	Thr	Phe	Thr	Thr	Ala	Gly	Val
385					390					395					400
Ala	Ser	Asn	Ser	Thr	Tyr	Lys	Gly	Gly	Thr	Tyr	Asn	Trp	Ser	Leu	Asn
			405						410					415	
Gln	Thr	Asp	Thr	Val	Asn	Phe	Pro	Gly	Ile	Gly	Asn	Leu	Lys	Ile	Gly
			420					425					430		
Arg	Ile	Asp	Ile	Thr	Ala	Gly	Ser	Ser	Asn	Ser	Pro	Val	Asp	Asn	Gly
		435						440				445			
Thr	Gly	Ala	Phe	Val	Thr	Asp	Asn	Ser	His	Arg	Ile	Thr	Pro	Thr	Trp
		450				455						460			
Asp	Gln	Gly	Leu	Pro	Ile	Glu	Gly	Ile	Val	Ser	Gly	Lys	Thr	Trp	Asn
465					470					475					480
Ser	Ala	Gly	Ser	Asn	Ile	Pro	Asp	Lys	Val	Thr	Gln	Asn	Ile	Trp	Tyr
			485						490					495	
Val	Asp	Ala	Glu	Thr	Gly	Lys	Val	Leu	Ser	His	Lys	Thr	Ser	Asp	Glu
			500					505					510		
Ala	Phe	Asn	Gly	Ser	Ser	Tyr	Asp	Ser	Thr	Asp	Asn	Gly	Val	Lys	Thr

- 66 -

Ala Gly Tyr His Ile Thr Gly Asn Val Asn Ala Asn Ala Asp Gly Ser
 980 985 990
 Ala Asn Ala Val Thr Val Asn Pro Asp Ser Gly Asp Ile Asp Val Thr
 995 1000 1005
 Val Val Tyr Thr Pro Asp Ala Lys Thr Pro Asp Thr Pro Gln Lys Ala
 1010 1015 1020
 Lys Val Thr Ile Tyr Asp Lys Thr Glu Asn Asn Lys Gln Leu Ser Asn
 1025 1030 1035 1040
 Phe Glu Asn Asn Asn Gly Thr Lys Gly Ser Ala Ile Ser Phe Asp Gly
 1045 1050 1055
 Glu Pro Gln Thr Leu Gln Ala Tyr Leu Asn Ser Gly Tyr Val Phe Asp
 1060 1065 1070
 Ser Ala Thr Asp Ala Asn Gly Asn Ser Ile Gly Thr Ala Ser Asn Ile
 1075 1080 1085
 Thr Phe Gly Asn Phe Asp Ser Val Asp Gly Asn Val Gln Ser Phe Asn
 1090 1095 1100
 Ile Tyr Leu Val His Gly Thr Asp Thr Lys Thr Glu Lys Ala Thr Thr
 1105 1110 1115 1120
 Asn Ala His Val His Tyr Val Val Ala Gly Asn Glu Ala Asn Lys Pro
 1125 1130 1135
 Ala Ala Pro Ala Asp Ser Pro Thr Gln Thr Ile Asn Trp Thr Arg Thr
 1140 1145 1150
 Asn Thr Thr Asp Lys Val Thr Gly Ala Thr Thr Glu Gly Thr Trp Thr
 1155 1160 1165
 Pro Asp Lys Asn Gly Phe Thr Ser Val Thr Ser Pro Asp Leu Thr Asn
 1170 1175 1180
 Tyr Thr Pro Asp Gln Ala Val Ala Asn Phe Thr Thr Pro Gln Pro Asn
 1185 1190 1195 1200
 Arg Asp Gln Val Val Thr Val Val Tyr Asn Pro Asn Pro Glu Val Ala
 1205 1210 1215
 Gln Lys Ala Asp Leu Val Val Tyr Asp Lys Thr Asp Asn Asn Lys Glu
 1220 1225 1230
 Leu Asn Asn Phe Asp Asn Ser Gly Lys Thr Gly Thr Gln Ile Ser Phe
 1235 1240 1245
 Ser Gly Ser Ala Asn Tyr Val Ala Asp Leu Ile Ala Lys Gly Tyr Lys
 1250 1255 1260
 Ile Asp Ser Phe Val Asn Asp Gln Asn Gln Thr Ser Asn Pro Thr Ser
 1265 1270 1275 1280
 Tyr Asp Gln Ile Ser Phe Ser Asn Phe Asp Asn Asn Ser Ala Ser Asp
 1285 1290 1295
 Gln His Phe Lys Leu Tyr Leu Val His Asp Thr Glu Asn Val Thr Asp
 1300 1305 1310
 Lys Lys Thr Thr Thr Ser Thr Val His Tyr Val Val Ser Asp Gly Lys
 1315 1320 1325
 Thr Asn Pro Pro Ser Asp Asn Thr Gln Thr Ile Thr Trp Thr Arg Pro
 1330 1335 1340
 Gly Thr Lys Asp Lys Val Thr Gly Val Thr Thr Pro Thr Gly Asn Trp
 1345 1350 1355 1360
 Thr Thr Pro Asp Asn Tyr Thr Asp Val Pro Thr Pro Asn Leu Asp Gly
 1365 1370 1375
 Tyr Thr Pro Asp Lys Thr Asn Val Pro Ala Pro Thr Pro Asp Pro Asn
 1380 1385 1390
 Gln Asn Pro Thr Thr Val Val Thr Tyr Asn Pro Lys Thr Pro Glu Ala
 1395 1400 1405
 Pro Thr Tyr Thr Gly Thr Thr Glu Asn Lys Thr Val Thr Arg Thr Ile
 1410 1415 1420
 Asn Tyr Tyr Asp Lys Val Thr Gly Glu Lys Ile Pro Ala Asn Leu Ile

1425		1430		1435		1440
Ser Asp Asn Pro Thr Thr Gln Asn Val Thr Leu Ser Arg Thr His Val						
	1445		1450		1455	
Val Ser Ser Thr Gly Gln Asp Met Gly Tyr Gly Thr Val Ser Ala Asp						
	1460		1465		1470	
Gly Lys Thr Phe Thr Lys Ala Thr Thr Val Asp Gly Trp Asn Thr Gly						
	1475		1480		1485	
Asp Trp Ala Gln Val Thr Ser Pro Asp Leu Ser Asn Ala Gly Tyr Thr						
	1490		1495		1500	
Ala Pro Asp Leu Ala Gln Ala Asp Gln Val Thr Val Asp Ala Asn Thr						
1505		1510		1515		1520
Lys Asp Ala Val Val Asn Val Tyr Tyr Gly His Gln Thr Glu Val Ile						
	1525		1530		1535	
Thr Pro Lys Thr Pro His Asn Pro Gly Gly Ser Ile Asn Pro Asn Asp						
	1540		1545		1550	
Pro Arg Asn Lys Pro Ser Val Tyr Pro Asp Gly Leu Thr Lys Glu Ala						
	1555		1560		1565	
Leu Thr Thr Glu Val Thr Arg His Ile Asn Tyr Val Gly Val Asn Glu						
	1570		1575		1580	
Asp Gly Thr Thr Thr Pro Val Asn Gly Ser Pro Asp Gly Lys Asn Thr						
1585		1590		1595		1600
Tyr Thr Gln Thr Val Ser Phe Glu Arg Asn Ala Val Ile Asp Lys Val						
	1605		1610		1615	
Thr Gly Gln Ile Leu Gly Tyr Ser Thr Asp Gly Thr Thr Asn Val Thr						
	1620		1625		1630	
Ile Thr Asp Lys Asp Arg Ala Trp Thr Pro Thr Thr Gln Asn Met Asp						
	1635		1640		1645	
Ser Val Ala Ser Lys Thr Pro Ser Glu Val Gly Tyr Asp Lys Val Asp						
	1650		1655		1660	
Ile Ser Thr Val Gly Gly Val Thr Val Tyr Pro Gly Gln Lys Val Asn						
1665		1670		1675		1680
Asp Val Thr Val Thr Tyr Thr Lys Asn Lys Ser Pro Glu Val Thr Gln						
	1685		1690		1695	
Lys Ala Thr Leu Glu Ile Ile Asp Asn Asn Asp Thr Asn Ala Pro Lys						
	1700		1705		1710	
Gln Leu Ala Ser Phe Ser Asn Glu Gly Lys Ser Glu Asp Gln Ile Asn						
	1715		1720		1725	
Phe Ala Asn Ser Asn Glu Ile Leu Gln Ser Tyr Leu Ser Gln Gly Tyr						
	1730		1735		1740	
Lys Val Gln Lys Thr Ala Gly Asn Leu Ser Gly Asp Ala Gln Ser Gly						
1745		1750		1755		1760
Tyr Thr Tyr Pro Thr Tyr Gly Asn Thr Thr Gln Asp Phe Lys Ile Tyr						
	1765		1770		1775	
Leu Ile His Asp Ile Ala Asp Lys Thr Glu Thr Ala Thr Ala Thr Ala						
	1780		1785		1790	
Gln Val His Tyr Val Val Ala Asp Asn Gly Val Gln Ala Pro Ala Asp						
	1795		1800		1805	
Ser Asp Leu Gln Thr Ile Thr Tyr Thr Arg Thr Asn Arg Val Asp Lys						
	1810		1815		1820	
Val Thr Gly Ala Thr Val Asn Glu Gly Thr Trp Gln Ala Asp Lys Ser						
1825		1830		1835		1840
Val Phe Thr Asp Val Lys Ser Pro Asp Leu Ser Lys Asp Gly Tyr Thr						
	1845		1850		1855	
Pro Ser Leu Glu Asn Val Gln Phe Asn Ala Pro Glu Arg Asn Val Asn						
	1860		1865		1870	
Gln Arg Val Thr Val Val Tyr Asn Arg Ser Ala Gln Ala Ala Asp Leu						
	1875		1880		1885	

Gln Ile Ile Asp Asp Asn Asp Pro Gln Asn Gln Arg Val Leu Ala Thr
 1890 1895 1900
 Tyr Ser Ala Gly Gly Glu Ser Gly Lys Gln Ile Ser Phe Asp Gly Ser
 1905 1910 1915 1920
 Asn Thr Gln Leu Gln Thr Tyr Leu Asn Asn Gly Tyr Thr Phe Glu Lys
 1925 1930 1935
 Tyr Glu Gly Gln Gly Met Ser Gly Asp Ala Gln Asn Gly Phe Thr Tyr
 1940 1945 1950
 Pro Ser Phe Asp Asn Asp Ser Gln Ser Asn Gln Ser Phe Lys Ile Tyr
 1955 1960 1965
 Leu Lys His Ala Thr Ala Asn Lys Thr Ala Thr Ala Thr Thr Ala
 1970 1975 1980
 His Val His Tyr Ile Met Ala Asp Gly Thr Lys Ala Pro Asp Asp Ser
 1985 1990 1995 2000
 Ala Ile Gln Thr Ile Asn Trp Thr Gln Thr Asn Thr Val Asp Arg Val
 2005 2010 2015
 Thr Gly Ala Thr Ile Asn Glu Gly Thr Trp Ser Ser Asp Lys Asn Ala
 2020 2025 2030
 Phe Thr Asp Val Asp Ser Pro Thr Val Thr Gly Tyr Thr Pro Gly Thr
 2035 2040 2045
 Lys Thr Val Lys Phe Ala Thr Pro Glu Arg Gly Val Asn Gln Val Val
 2050 2055 2060
 Asn Val Val Tyr Thr Lys Asp Ala Pro Thr Pro Asp Arg Gln Asn Ala
 2065 2070 2075 2080
 Leu Val Val Tyr Gln Asp Val Asn Asp Pro Ala His Pro Val Asp Leu
 2085 2090 2095
 Gly Gln Ser Asp Gln Leu Thr Gly Gln Ala Gly Tyr Ser Ile Asn Tyr
 2100 2105 2110
 Ser Thr Ala Asn Lys Ile Asp Glu Tyr Glu Lys Gln Gly Tyr Val Leu
 2115 2120 2125
 Val Ser Asn Gly Phe Asp Ala Asn Gly Thr Lys Pro Ser Phe Asp Asn
 2130 2135 2140
 Val Asn Gly Asn Thr Gln Thr Phe Tyr Val Thr Phe Lys His Gly Ile
 2145 2150 2155 2160
 Gln Pro Val Thr Pro Thr Thr Pro Gly Thr Pro Asp Gln Pro Ile Asn
 2165 2170 2175
 Pro Asp Asn Pro Asp Gly Pro Lys Tyr Pro Ser Gly Thr Asp Gln Thr
 2180 2185 2190
 Ser Leu Thr Lys Asp Val Thr Arg Thr Val Thr Tyr Glu Gly Ala Gly
 2195 2200 2205
 Asn Gln Thr Pro Ser Pro Val Thr Asp Thr Leu His Phe Gln Gly Thr
 2210 2215 2220
 Gly Tyr Leu Asp Lys Val Thr Gly Lys Trp Thr Asp Ala Asn Gly Lys
 2225 2230 2235 2240
 Lys Leu Ser Asp Gln Thr Lys Gly Ile Thr Trp Thr Ile Thr Asp Gly
 2245 2250 2255
 Thr Lys Asp Glu Gly Ser Phe Asn Leu Val Pro Thr Lys His Ile Asp
 2260 2265 2270
 Gly Tyr Thr Ser Lys Val Val Thr Asn Gly Ala Asp Asp Gly Asn Gly
 2275 2280 2285
 Asn Val Lys Ser Tyr Thr Gly Ile Thr His Thr Ser Asp Asn Ile Asn
 2290 2295 2300
 Val Val Val Gln Tyr Asn Pro Ile Val Ala Glu Gln Gly Asn Leu Ile
 2305 2310 2315 2320
 Val Lys Phe His Asp Asp Thr Asp Asn Lys Asp Leu Thr Gly Val Gly
 2325 2330 2335
 Thr Asp Thr Gly Thr Gln Asp Val Gly Thr Gln Val Thr Tyr Asn Pro

- 70 -

Asn Ser Ile Val Gln Ala Thr Ser Asp Pro Asn Asn Pro Thr Lys Tyr
 2805 2810 2815
 Gly Thr Glu Tyr Ser Ser Ala Ala Ser Gln Trp Met Phe Asp Asp Lys
 2820 2825 2830
 Pro Gly Val Asp Gln Ser Phe Tyr Val Tyr Val Glu His Asp Tyr Ala
 2835 2840 2845
 Pro Ile Asn Pro Glu Asn Ala Tyr Gly Arg Thr Asp Leu Thr Gln Thr
 2850 2855 2860
 Val Thr Glu Thr Val His Tyr Ile Asp Glu Ala Thr Asn Lys Pro Val
 2865 2870 2875 2880
 Ala Thr Asp Tyr Thr Asn Thr Leu Thr Phe Lys Gly Gln Gly Arg Val
 2885 2890 2895
 Asp Lys Val Thr Gly Lys Met Leu Lys Ile Lys Ser Ile Glu Asn Gly
 2900 2905 2910
 Gln Ile Thr Tyr Asp Tyr Asn Val Ala Asn Glu Ile Asp Ile Ser Ser
 2915 2920 2925
 Ala Lys Leu Ser Asp Phe Ala Trp Ser Thr Pro Thr Thr Leu Gln Lys
 2930 2935 2940
 Val Thr Ser Pro Thr Ile Ala Gly Tyr Thr Ile Asp Ala Ala Lys Thr
 2945 2950 2955 2960
 Thr Pro Ser Glu Leu Ala Asp Gly Asn Asp Ile Lys Glu Ile Gln Asn
 2965 2970 2975
 Val Ala Tyr Asp His Gly Asn Val Glu Ala Thr Val Tyr Tyr Lys Ala
 2980 2985 2990
 Asn Pro Val Glu Thr His Lys Ala Gly Leu Thr Ile Tyr Ala Asn Gly
 2995 3000 3005
 Asn Gln Val Gly Thr Ala Ser Val Thr Gly Ala Lys Asp Thr Ala Ile
 3010 3015 3020
 Asn Phe Ser Ser Ala Ser Asp Ile Val Ala Ala Tyr Ile Ser Asn Gly
 3025 3030 3035 3040
 Tyr Lys Phe Asp His Ala Gln Asp Val Thr Asn Asn Lys Glu Met Thr
 3045 3050 3055
 Gly Lys Ser Tyr Asn Glu Leu Asn Phe Gly Asn Phe Ala Thr Thr Asn
 3060 3065 3070
 Asn Ser Asp Gln Gln Phe Ala Ile Tyr Leu Thr Lys Asp Glu Thr Pro
 3075 3080 3085
 Ala Lys Thr Gln Gln Asn Ala Gln Leu Thr Val Arg Asp Val Thr Pro
 3090 3095 3100
 Gly Gln Glu Met Asp Leu Gly Asn Tyr Thr Gln Pro Gly Leu Glu Gly
 3105 3110 3115 3120
 Asp Thr Ile Ser Phe Ser Ser Ala Gln Glu Phe Val Gln Asn Leu Leu
 3125 3130 3135
 Asn Lys Gly Tyr Val Trp Asp Gly Ala Ser Tyr Asn Gly Thr Asn Leu
 3140 3145 3150
 Glu Ala Thr Asn Tyr Ala Gly Ile Asn Phe Gly Asn Tyr Asp Asn Thr
 3155 3160 3165
 Asp Asp Lys Asn Gly Ile Ser Gln Lys Trp Val Ile Asn Leu Val His
 3170 3175 3180
 Gly Val Thr Pro Val Asn Pro Asp His Pro Asp Asp Lys Asp Gly Phe
 3185 3190 3195 3200
 Thr Lys Asp Tyr Leu Asp Arg Thr Ile Thr Arg Asp Val Thr Tyr Val
 3205 3210 3215
 Tyr Glu Asp Gly Ser Gln Ala Ala Ala Pro Val His Gln Glu Ala His
 3220 3225 3230
 Tyr Gln Gly Ser Gly Tyr Leu Asp Asn Val Thr Gly Lys Trp Val Thr
 3235 3240 3245
 Val Glu Asn Gly Lys Ile Thr Gly Leu Ala Gln Gly Leu Thr Trp Thr

3250	3255	3260
Pro Asp Gln Asp Ser Thr Phe Asp Gln Ile Gly Ala Lys Asn Ile Glu		
3265	3270	3275
Gly Tyr His Val Ser Ser Val Ser Gly Asn Gly Ile Ser Gly Phe Thr		3280
	3285	3290
Val Gly Gln Asp Gly Thr Val Gly Gln Gln Thr Val Thr Lys Asp Thr		3295
	3300	3305
Pro Ser Ser Thr Ile Arg Val Val Tyr Val Lys Thr Pro Val Thr Pro		3310
	3315	3320
Val Pro Ala Asn Gly Ser Ile Val Tyr Ile Asp Asp Thr Thr Gly Asn		3325
	3330	3335
Asn Leu Glu Asn Ala Thr Phe Gly Gly Thr Val Gly Ala Lys Ile Asp		3340
3345	3350	3355
Tyr Thr Thr Ala Asp Arg Ile Ser Tyr Tyr Gln Gly Lys Gly Tyr Lys		3360
	3365	3370
Leu Val Ser Asn Asn Phe Thr Asp Gly Ser Gln Thr Phe Lys Gln Gly		3375
	3380	3385
Glu Asn Lys Phe Glu Val His Leu Thr His Val Thr Glu Thr Lys Asp		3390
	3395	3400
Ala Thr Lys Thr Ile Thr Arg Asp Val Thr Tyr Val Tyr Glu Asp Gly		3405
	3410	3415
Ser Gln Ala Asp Thr Pro Val Gln Gln Thr Ile Thr Phe Thr Gly Lys		3420
3425	3430	3435
Thr Thr Ser Asp Lys Val Thr Gly Ser Glu Lys Thr Thr Trp Asn Asn		3440
	3445	3450
Glu Ser Gln Thr Phe Gly Ala Thr Lys Ala Ile Asp Thr Thr Lys Tyr		3455
	3460	3465
Gln Ile Val Gly Ile Asn Glu Arg Asn Thr Thr Ala Asn Val Asp Arg		3470
	3475	3480
Asp Thr Gly Val Val Ala Ser Glu Thr Ile Thr Pro Asn Ser Gln Asn		3485
	3490	3495
Ser Ala Val Val Ile Thr Leu Ala Asn Lys Pro Glu Thr Pro Ile Pro		3500
3505	3510	3515
Ala Asn Gly Ser Ile Thr Tyr Tyr Asp Asp Thr Thr Gly Thr Thr Leu		3520
	3525	3530
Glu Ser Ala Gly Phe Ser Gly Ser Val Gly Gln Lys Ile Asn Tyr Thr		3535
	3540	3545
Thr Ala Asp Arg Ile Ile Asn Tyr Val Asn Lys Gly Tyr Asp Val Val		3550
	3555	3560
Ser Asn Asn Phe Thr Asp Gly Asn Glu Thr Phe Lys Gln Gly Asp Asn		3565
	3570	3575
Lys Phe Glu Val His Leu Val His Ala Thr Thr Pro Ile Thr Pro Glu		3580
3585	3590	3595
Asn Pro Gly Lys Pro Gly Gln Glu Val Pro Asn Pro Asn Asp Pro Glu		3600
	3605	3610
His Pro His Thr Ile Pro Ala Asn Phe Val Pro Gln Thr Leu Thr His		3615
	3620	3625
Thr Val Thr Arg Asp Val Thr Tyr Val Tyr Ala Asp Gly Ser Gln Ala		3630
	3635	3640
Ser Ala Pro Val His Gln Thr Phe Thr Phe Asn Gly Asn Gly Val Ile		3645
	3650	3655
Asp Leu Val Thr Gly Gln Leu Val Thr Val Glu Asn Gly Lys Ile Thr		3660
3665	3670	3675
Gly Ala Gly Lys Ile Thr Trp Asn Ala Asp Ser His Asn Phe Asp Ala		3680
	3685	3690
Ile Asp Ala Ile Asp His Asp Gly Tyr Tyr Ile Ser Asn Val Ser Glu		3695
	3700	3705
		3710

Asn Asn Thr Thr Ala Asn Val Asp Thr Asn Thr Gly Ala Val Ala Gly
 3715 3720 3725
 Glu Thr Ile Thr Pro Asn Ser Gln Asn Ser Thr Ile Ile Ile Thr Leu
 3730 3735 3740
 Thr Lys Lys Pro Asp Val Pro Thr Pro Val Pro Glu Gln Gly Ser Ile
 3745 3750 3755 3760
 Lys Val Thr Val His Asp Val Lys Thr Asn Gln Asp Val Pro Gly Tyr
 3765 3770 3775
 Asp Lys Asp Ser Gly Lys Gln Asn Thr Gly Thr Ser Phe Thr Tyr Asp
 3780 3785 3790
 Lys Thr Thr Thr Ile Thr Asp Leu Glu Asn Lys Gly Tyr Lys Val Ile
 3795 3800 3805
 Asn Pro Asn Val Asp Ile Pro Thr Lys Val Ser Asn Ile Asp Gln His
 3810 3815 3820
 Ile Val Ile Tyr Val Asp His Asn Val Ile Pro Val Thr Pro Asp Lys
 3825 3830 3835 3840
 Pro Gly Asn Gly Leu Ser Glu Asn Asp Leu Asn Lys Thr Val Thr Glu
 3845 3850 3855
 Thr Val His Tyr Val Val Asn Gly Gly Ala Thr Glu Ala Pro Ala Asp
 3860 3865 3870
 Lys Thr Thr Ser Leu Lys Phe Thr Gly Thr Ala Tyr Tyr Asp Ser Val
 3875 3880 3885
 Thr Lys Lys Trp Thr Asp Ala Asn Gly Asn Glu Leu Ser Asp Gln Ser
 3890 3895 3900
 Lys Asn Val Thr Trp Thr Ala Glu Asn Gly Asn Lys Phe Ala Val Val
 3905 3910 3915 3920
 Val Thr Pro Thr Leu Glu Gly Tyr Thr Pro Ser Val Gln Ser Gly Tyr
 3925 3930 3935
 Asp Asp Gly Asn Lys Asn Val Lys Glu Ile Asn Asn Ile Thr Pro Asp
 3940 3945 3950
 Ser Gly Asn Val Glu Val Thr Val Thr Tyr Asn Lys Asn Asn Val Pro
 3955 3960 3965
 Thr Pro Val Lys Gln Gly Thr Ile Glu Ile Ile Tyr His Asp Thr Thr
 3970 3975 3980
 Asp Asn Val Asp Ile Pro Gly Tyr Gly Gln Ser Arg Ile Lys Glu Asp
 3985 3990 3995 4000
 Glu Gly Thr Ser Phe Ser Tyr Asn Pro Asn Ala Lys Asp Leu Pro Ala
 4005 4010 4015
 Leu Glu Ser Lys Gly Tyr Val Leu Asp Gly Glu Leu Pro Thr Ile Pro
 4020 4025 4030
 Thr Lys Phe Thr Asp Gly Asp Gln Arg Val Val Ile Asn Val Lys His
 4035 4040 4045
 Gly Thr Thr Thr Val Thr Pro Asp Lys Pro Gly Lys Pro Gly Asp Pro
 4050 4055 4060
 Ile Asp Pro Asn Asn Pro Asp Gly Pro Lys Tyr Pro Glu Gly Thr Gly
 4065 4070 4075 4080
 Glu Asn Asn Leu Lys Val Thr Gly Thr Gln Thr Ile His Tyr Ile Gly
 4085 4090 4095
 Ala Gly Asp Lys Thr Pro Lys Asp Asn Thr Gln Ser Phe Glu Phe Thr
 4100 4105 4110
 Lys Gln Ile Thr Phe Asp Asn Val Thr Gly Lys Ile Ile Asn Asp Ser
 4115 4120 4125
 Gly Trp Asn Val Thr Ser His Thr Phe Gly Ser Glu Ala Thr Pro Val
 4130 4135 4140
 Ile Asp Gly Tyr His Ala Asp Lys Thr Thr Ala Gly Gly Thr Thr Val
 4145 4150 4155 4160
 Thr Pro Asn Asp Leu His Lys Thr Val Thr Val Thr Tyr Thr Pro Asn

4165 4170 4175
 Val Pro Ala Val Pro Thr Pro Thr Pro Thr Pro Ser Pro Glu Pro Lys
 4180 4185 4190
 Pro Glu Asn Thr Pro Val Glu Pro Asn Thr Pro Thr Pro Thr Pro Asp
 4195 4200 4205
 Ile Pro Asp Asn Val Thr Pro Thr Pro Glu Pro Glu Asn Asn Val
 4210 4215 4220
 Lys Pro His Gly Glu Ser Ile Val Gln Lys Asn Asn Asp Asn Pro Lys
 4225 4230 4235 4240
 Val Val Ser His Gly Gln Ser Gly Asn Asn Trp Thr Ala Pro His Gly
 4245 4250 4255
 Gln His Val Asp Gln Arg Gly Asn Ile Val Thr Ser Asp Asn Arg Val
 4260 4265 4270
 Val Gly Tyr Val Asp Gln Asn Gly Lys Ala His Tyr Thr Lys Leu Pro
 4275 4280 4285
 Gln Thr Gly Asp Asp Gln Thr Asn Asp Val Ala Ala Ala Leu Leu Gly
 4290 4295 4300
 Gly Ala Ala Val Ser Leu Gly Leu Ile Gly Leu Ala Gly Val Lys Lys
 4305 4310 4315 4320
 Arg Arg Lys Glu Asp Lys
 4325

<210> 19

<211> 3624

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1709 - mucus binding protein precursor Mub

<220>

<221> CDS

<222> (1)...(3624)

<400> 19

atg gat aag aaa gaa gtg aaa aat agg ttt agt ttt agg aag tta tcc 48
 Met Asp Lys Lys Glu Val Lys Asn Arg Phe Ser Phe Arg Lys Leu Ser
 1 5 10 15

aca ggc tta gcg aca gta ttt tta gga tca att ttc ttt tgg aca aat 96
 Thr Gly Leu Ala Thr Val Phe Leu Gly Ser Ile Phe Phe Trp Thr Asn
 20 25 30

gga caa acg gtt caa gca gat agt gta gag cca gct agt gaa cag gct 144
 Gly Gln Thr Val Gln Ala Asp Ser Val Glu Pro Ala Ser Glu Gln Ala
 35 40 45

gta caa aat gtt gac tct caa gta cag gct gat aat act gtt tcg gaa 192
 Val Gln Asn Val Asp Ser Gln Val Gln Ala Asp Asn Thr Val Ser Glu
 50 55 60

aat acc gtt aat gaa gaa aat ggc tct act tcc gaa act act act gaa 240

Asn Thr Val Asn Glu Glu Asn Gly Ser Thr Ser Glu Thr Thr Thr Glu	
65 70 75 80	
ggt aag aca gaa atg ccg tct gtt gat aca aca tct caa gct aaa gat	288
Val Lys Thr Glu Met Pro Ser Val Asp Thr Thr Ser Gln Ala Lys Asp	
85 90 95	
gca gta gaa act tca gat aat aag aaa gtt gag ctc cct caa gga gaa	336
Ala Val Glu Thr Ser Asp Asn Lys Lys Val Glu Leu Pro Gln Gly Glu	
100 105 110	
gca gat aag cag gtt cca caa aag tta gag gtt aat aag agt aat caa	384
Ala Asp Lys Gln Val Pro Gln Lys Leu Glu Val Asn Lys Ser Asn Gln	
115 120 125	
gca gct gaa aca act gat aaa gat aca aag caa aat gct act tct gca	432
Ala Ala Glu Thr Thr Asp Lys Asp Thr Lys Gln Asn Ala Thr Ser Ala	
130 135 140	
aca cca gca caa ctt aat gaa aat aca gct cca gtt gtt gta aaa gct	480
Thr Pro Ala Gln Leu Asn Glu Asn Thr Ala Pro Val Val Val Lys Ala	
145 150 155 160	
aag tcg gaa gga aaa gaa gta gtt aag gct act gat ccg act gat tat	528
Lys Ser Glu Gly Lys Glu Val Val Lys Ala Thr Asp Pro Thr Asp Tyr	
165 170 175	
cca act gaa gtt ggt caa atc att gat caa gat aaa tat att tat caa	576
Pro Thr Glu Val Gly Gln Ile Ile Asp Gln Asp Lys Tyr Ile Tyr Gln	
180 185 190	
att ttg tcg ctt aat gat cgt agt ggc cga cct tct gat tcg aag ctg	624
Ile Leu Ser Leu Asn Asp Arg Ser Gly Arg Pro Ser Asp Ser Lys Leu	
195 200 205	
ggt ctt acc act aat aga aat gat cat aat gac aag aat atc tat gct	672
Val Leu Thr Thr Asn Arg Asn Asp His Asn Asp Lys Asn Ile Tyr Ala	
210 215 220	
tac gta gtt gat aga aat aat aga aga gta agt caa tca gtt aca gtt	720
Tyr Val Val Asp Arg Asn Asn Arg Arg Val Ser Gln Ser Val Thr Val	
225 230 235 240	
ggt gta gat caa cat act att att agt gtg aat ggt cgc gga tat caa	768
Gly Val Asp Gln His Thr Ile Ile Ser Val Asn Gly Arg Gly Tyr Gln	
245 250 255	
att tct aat acc ggc ggt agc aat gtc att gta gat ggc aaa gaa gtg	816
Ile Ser Asn Thr Gly Gly Ser Asn Val Ile Val Asp Gly Lys Glu Val	
260 265 270	
cca acg cag aat act tct act gtt act tcg ggt aat ggt act act agt	864
Pro Thr Gln Asn Thr Ser Thr Val Thr Ser Gly Asn Gly Thr Thr Ser	
275 280 285	
cca atc tat gga tta ggt aat act act cgt ggt gat tat tcc gca att	912
Pro Ile Tyr Gly Leu Gly Asn Thr Thr Arg Gly Asp Tyr Ser Ala Ile	

290	295	300	
ggt gaa atc cca cca gta tac act gaa aat tca gta atc aag tat tac			960
Gly Glu Ile Pro Pro Val Tyr Thr Glu Asn Ser Val Ile Lys Tyr Tyr			
305	310	315	320
tat cgt gat gaa aat ggt aat tta aaa gaa gct gaa agt tct gat cag			1008
Tyr Arg Asp Glu Asn Gly Asn Leu Lys Glu Ala Glu Ser Ser Asp Gln			
	325	330	335
tat cct aac gta aac gtt tcg ggt ctt act ggt caa gaa ttt gta att			1056
Tyr Pro Asn Val Asn Val Ser Gly Leu Thr Gly Gln Glu Phe Val Ile			
	340	345	350
cct aat gtg gat caa tat aag cgg gtt atc aag gga cgt tat tta aat			1104
Pro Asn Val Asp Gln Tyr Lys Arg Val Ile Lys Gly Arg Tyr Leu Asn			
	355	360	365
tca gat aat ttg cct aca ggt gat ttc acg gga acg att tct caa ttt			1152
Ser Asp Asn Leu Pro Thr Gly Asp Phe Thr Gly Thr Ile Ser Gln Phe			
	370	375	380
ggt gag ggg aaa tat tat aag aaa gtc tac tat gat tat ggt aca gat			1200
Gly Glu Gly Lys Tyr Tyr Lys Lys Val Tyr Tyr Asp Tyr Gly Thr Asp			
	385	390	400
gat gtg gat tat tac gta gta tat aac caa gtt tca cct gac ggc aca			1248
Asp Val Asp Tyr Tyr Val Val Tyr Asn Gln Val Ser Pro Asp Gly Thr			
	405	410	415
atg gat gtt agt ctc ttt aga ggt gac aat aat aca cct att gaa tca			1296
Met Asp Val Ser Leu Phe Arg Gly Asp Asn Asn Thr Pro Ile Glu Ser			
	420	425	430
aga agg gtg ggt cca ggt aga tct att cgt ttt acc agt cgt aac tat			1344
Arg Arg Val Gly Pro Gly Arg Ser Ile Arg Phe Thr Ser Arg Asn Tyr			
	435	440	445
act gct cgt aat cca tat gtg acc gaa aca cca cat gaa gta caa ttt			1392
Thr Ala Arg Asn Pro Tyr Val Thr Glu Thr Pro His Glu Val Gln Phe			
	450	455	460
att tac gat aaa tta ggt tcc att gtt cca gtc gat gaa gat ggt aac			1440
Ile Tyr Asp Lys Leu Gly Ser Ile Val Pro Val Asp Glu Asp Gly Asn			
	465	470	480
gta att ggc gac tta gtc caa ttc aat aat agt act gat cca act aag			1488
Val Ile Gly Asp Leu Val Gln Phe Asn Asn Ser Thr Asp Pro Thr Lys			
	485	490	495
gct gct gta acc gat tcg cca gtt att gct ggt tat aca att aag gat			1536
Ala Ala Val Thr Asp Ser Pro Val Ile Ala Gly Tyr Thr Ile Lys Asp			
	500	505	510
cct act caa aga gag att acc cca cat gat cct ggc aaa aat att aag			1584
Pro Thr Gln Arg Glu Ile Thr Pro His Asp Pro Gly Lys Asn Ile Lys			
	515	520	525

gta gtc tat gtt cgc aac cat gtg aca gca gct att aag tat atc gat	1632
Val Val Tyr Val Arg Asn His Val Thr Ala Ala Ile Lys Tyr Ile Asp	
530 535 540	
gat act gct ggc gat gac tta agt gcg tac aac aag tca att aca gct	1680
Asp Thr Ala Gly Asp Asp Leu Ser Ala Tyr Asn Lys Ser Ile Thr Ala	
545 550 555 560	
aag cca ggt gaa gca ctt aac tat act act aaa gat tca att aca gaa	1728
Lys Pro Gly Glu Ala Leu Asn Tyr Thr Thr Lys Asp Ser Ile Thr Glu	
565 570 575	
ctc cag aat aaa ggg tat gta tta gta agt gat aac ttc aat gta act	1776
Leu Gln Asn Lys Gly Tyr Val Leu Val Ser Asp Asn Phe Asn Val Thr	
580 585 590	
act atg cct gaa aat ggt ggt aat tac gaa gtt cac gta aag cat ggc	1824
Thr Met Pro Glu Asn Gly Gly Asn Tyr Glu Val His Val Lys His Gly	
595 600 605	
act aag aca atc gat cca gat aac cca act gat aag tac acc aag aag	1872
Thr Lys Thr Ile Asp Pro Asp Asn Pro Thr Asp Lys Tyr Thr Lys Lys	
610 615 620	
gat tta caa aaa aca gct act cgt acg att aat tat gtt gat gat caa	1920
Asp Leu Gln Lys Thr Ala Thr Arg Thr Ile Asn Tyr Val Asp Asp Gln	
625 630 635 640	
ggc aac aag att gca gaa tct gtg act tcc aca gtt gtt ttc aca ggg	1968
Gly Asn Lys Ile Ala Glu Ser Val Thr Ser Thr Val Val Phe Thr Gly	
645 650 655	
act ggt act gta gat gcc gta acc ggt aac tta gtg aac tta cat ccc	2016
Thr Gly Thr Val Asp Ala Val Thr Gly Asn Leu Val Asn Leu His Pro	
660 665 670	
gac ggt tcg att aaa gac caa aac ggt aag ctt act tgg act tac tca	2064
Asp Gly Ser Ile Lys Asp Gln Asn Gly Lys Leu Thr Trp Thr Tyr Ser	
675 680 685	
gtt gat ggc ggt gtt gta caa aaa agt gat act tac aca ttt agc gca	2112
Val Asp Gly Gly Val Val Gln Lys Ser Asp Thr Tyr Thr Phe Ser Ala	
690 695 700	
aca act gct cga cca act att gat cac aat aat tct act tac aac ttt	2160
Thr Thr Ala Arg Pro Thr Ile Asp His Asn Asn Ser Thr Tyr Asn Phe	
705 710 715 720	
act tct act act ccc gct gat tac aat gct ggc aat ggt gct gta tcg	2208
Thr Ser Thr Thr Pro Ala Asp Tyr Asn Ala Gly Asn Gly Ala Val Ser	
725 730 735	
agt tat cgt gtg aat agt act gat cca caa aac tta att gtt aat gtt	2256
Ser Tyr Arg Val Asn Ser Thr Asp Pro Gln Asn Leu Ile Val Asn Val	
740 745 750	

gtt tat acc aag caa gct atc tac cat gca ggt aag act gaa act aag Val Tyr Thr Lys Gln Ala Ile Tyr His Ala Gly Lys Thr Glu Thr Lys 755 760 765	2304
agt gta act cgc acc att aat tat tta gat ggt aag act ggc gaa aag Ser Val Thr Arg Thr Ile Asn Tyr Leu Asp Gly Lys Thr Gly Glu Lys 770 775 780	2352
ata cca act gat tta att gca act aac cca gtt gca caa aca gtt aat Ile Pro Thr Asp Leu Ile Ala Thr Asn Pro Val Ala Gln Thr Val Asn 785 790 795 800	2400
ttg cat cgt act gaa att att gat gac aac ggc aag gtg atc ggc tac Leu His Arg Thr Glu Ile Ile Asp Asp Asn Gly Lys Val Ile Gly Tyr 805 810 815	2448
ggg aca atc agt aaa gat ggt aaa tca tac act att aac aat gat tgg Gly Thr Ile Ser Lys Asp Gly Lys Ser Tyr Thr Ile Asn Asn Asp Trp 820 825 830	2496
gta gtc gac ggt aag tgg gca agt gta act tca cct gat tta tca gct Val Val Asp Gly Lys Trp Ala Ser Val Thr Ser Pro Asp Leu Ser Ala 835 840 845	2544
aag ggt tat aaa gct cca cgt ttt gaa aat ggt act tca gct gct aga Lys Gly Tyr Lys Ala Pro Arg Phe Glu Asn Gly Thr Ser Ala Ala Arg 850 855 860	2592
gtt gac gaa gta att gtt ggt agt ggt acc aaa gac gct act gtt aat Val Asp Glu Val Ile Val Gly Ser Gly Thr Lys Asp Ala Thr Val Asn 865 870 875 880	2640
gtt tat tac gat cat aat ttg atc cca att gga cca gat aat ttt gat Val Tyr Tyr Asp His Asn Leu Ile Pro Ile Gly Pro Asp Asn Phe Asp 885 890 895	2688
aag cat ggc gta gat cga agc cag att gag aag cag gtt aaa gaa aca Lys His Gly Val Asp Arg Ser Gln Ile Glu Lys Gln Val Lys Glu Thr 900 905 910	2736
gtt cat tat gta ggt gct ggc gat aag act cct gct gat cat gtg caa Val His Tyr Val Gly Ala Gly Asp Lys Thr Pro Ala Asp His Val Gln 915 920 925	2784
act tcg aag tgg acg cgc act att act att gat gcg gta act aaa gaa Thr Ser Lys Trp Thr Arg Thr Ile Thr Ile Asp Ala Val Thr Lys Glu 930 935 940	2832
gtt gta cct aat ggt caa tat aca act gat tgg aca att cca aag ggt Val Val Pro Asn Gly Gln Tyr Thr Thr Asp Trp Thr Ile Pro Lys Gly 945 950 955 960	2880
gag aag acc gag tat gct caa gta aat acg cca gta gtt aat ggc tac Glu Lys Thr Glu Tyr Ala Gln Val Asn Thr Pro Val Val Asn Gly Tyr 965 970 975	2928
tat gct gat caa gct aat gtt ccg gca acg act gta act caa aat gat	2976

Tyr Ala Asp Gln Ala Asn Val Pro Ala Thr Thr Val Thr Gln Asn Asp	
980 985 990	
att gaa aaa aca gta act tat aag caa att ggt agg att gtt cca gtt	3024
Ile Glu Lys Thr Val Thr Tyr Lys Gln Ile Gly Arg Ile Val Pro Val	
995 1000 1005	
gat cca aat ggt aag cca att cca gat gca cca act cca caa tat cct	3072
Asp Pro Asn Gly Lys Pro Ile Pro Asp Ala Pro Thr Pro Gln Tyr Pro	
1010 1015 1020	
aac gat cca acg gat ccg act aag gta ctt cct aat gta ccg gtg cca	3120
Asn Asp Pro Thr Asp Pro Thr Lys Val Leu Pro Asn Val Pro Val Pro	
1025 1030 1035 1040	
aat att cca ggc tac aag cca agt gtg cca aca gtt act cca act gac	3168
Asn Ile Pro Gly Tyr Lys Pro Ser Val Pro Thr Val Thr Pro Thr Asp	
1045 1050 1055	
cct ggc aag gat aca caa gtt cca tat aca ccg gta act cca act aat	3216
Pro Gly Lys Asp Thr Gln Val Pro Tyr Thr Pro Val Thr Pro Thr Asn	
1060 1065 1070	
cca gat aat cca gtc att cca acg cct caa ccg gaa cca aac cct gat	3264
Pro Asp Asn Pro Val Ile Pro Thr Pro Gln Pro Glu Pro Asn Pro Asp	
1075 1080 1085	
aat ggt aag gat aag ccg gtc gat cca tcc aag cca tca gat gat cca	3312
Asn Gly Lys Asp Lys Pro Val Asp Pro Ser Lys Pro Ser Asp Asp Pro	
1090 1095 1100	
gtt cat cct gaa tat cct ggt att aag agg gga cag gat aaa cct gat	3360
Val His Pro Glu Tyr Pro Gly Ile Lys Arg Gly Gln Asp Lys Pro Asp	
1105 1110 1115 1120	
aag gaa aag act gat aag aag aga aat ggc aag act aag ggt aaa gaa	3408
Lys Glu Lys Thr Asp Lys Lys Arg Asn Gly Lys Thr Lys Gly Lys Glu	
1125 1130 1135	
aat aca cct act gga aga gat gct gtt aag cga gct gga cga agc gat	3456
Asn Thr Pro Thr Gly Arg Asp Ala Val Lys Arg Ala Gly Arg Ser Asp	
1140 1145 1150	
gat gca ctt aaa tta gct agt gaa gct aaa aat cgc cgt atg act att	3504
Asp Ala Leu Lys Leu Ala Ser Glu Ala Lys Asn Arg Arg Met Thr Ile	
1155 1160 1165	
caa ggt aag aat gaa gaa tta cca caa gct ggt gaa gat cat aat gct	3552
Gln Gly Lys Asn Glu Glu Leu Pro Gln Ala Gly Glu Asp His Asn Ala	
1170 1175 1180	
atg gcg ttg att ggt ctt gca ttt gcc act ctt gct gga agt gta gtc	3600
Met Ala Leu Ile Gly Leu Ala Phe Ala Thr Leu Ala Gly Ser Val Val	
1185 1190 1195 1200	
ttt gct act gat agg aaa cgg aga	3624
Phe Ala Thr Asp Arg Lys Arg Arg	

1205

<210> 20
 <211> 1208
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 20

```

Met Asp Lys Lys Glu Val Lys Asn Arg Phe Ser Phe Arg Lys Leu Ser
 1          5          10          15
Thr Gly Leu Ala Thr Val Phe Leu Gly Ser Ile Phe Phe Trp Thr Asn
          20          25          30
Gly Gln Thr Val Gln Ala Asp Ser Val Glu Pro Ala Ser Glu Gln Ala
          35          40          45
Val Gln Asn Val Asp Ser Gln Val Gln Ala Asp Asn Thr Val Ser Glu
          50          55          60
Asn Thr Val Asn Glu Glu Asn Gly Ser Thr Ser Glu Thr Thr Thr Glu
          65          70          75          80
Val Lys Thr Glu Met Pro Ser Val Asp Thr Thr Ser Gln Ala Lys Asp
          85          90          95
Ala Val Glu Thr Ser Asp Asn Lys Lys Val Glu Leu Pro Gln Gly Glu
          100          105          110
Ala Asp Lys Gln Val Pro Gln Lys Leu Glu Val Asn Lys Ser Asn Gln
          115          120          125
Ala Ala Glu Thr Thr Asp Lys Asp Thr Lys Gln Asn Ala Thr Ser Ala
          130          135          140
Thr Pro Ala Gln Leu Asn Glu Asn Thr Ala Pro Val Val Val Lys Ala
          145          150          155          160
Lys Ser Glu Gly Lys Glu Val Val Lys Ala Thr Asp Pro Thr Asp Tyr
          165          170          175
Pro Thr Glu Val Gly Gln Ile Ile Asp Gln Asp Lys Tyr Ile Tyr Gln
          180          185          190
Ile Leu Ser Leu Asn Asp Arg Ser Gly Arg Pro Ser Asp Ser Lys Leu
          195          200          205
Val Leu Thr Thr Asn Arg Asn Asp His Asn Asp Lys Asn Ile Tyr Ala
          210          215          220
Tyr Val Val Asp Arg Asn Asn Arg Arg Val Ser Gln Ser Val Thr Val
          225          230          235          240
Gly Val Asp Gln His Thr Ile Ile Ser Val Asn Gly Arg Gly Tyr Gln
          245          250          255
Ile Ser Asn Thr Gly Gly Ser Asn Val Ile Val Asp Gly Lys Glu Val
          260          265          270
Pro Thr Gln Asn Thr Ser Thr Val Thr Ser Gly Asn Gly Thr Thr Ser
          275          280          285
Pro Ile Tyr Gly Leu Gly Asn Thr Thr Arg Gly Asp Tyr Ser Ala Ile
          290          295          300
Gly Glu Ile Pro Pro Val Tyr Thr Glu Asn Ser Val Ile Lys Tyr Tyr
          305          310          315          320
Tyr Arg Asp Glu Asn Gly Asn Leu Lys Glu Ala Glu Ser Ser Asp Gln
          325          330          335
Tyr Pro Asn Val Asn Val Ser Gly Leu Thr Gly Gln Glu Phe Val Ile
          340          345          350
Pro Asn Val Asp Gln Tyr Lys Arg Val Ile Lys Gly Arg Tyr Leu Asn
          355          360          365
Ser Asp Asn Leu Pro Thr Gly Asp Phe Thr Gly Thr Ile Ser Gln Phe
          370          375          380

```

Gly	Glu	Gly	Lys	Tyr	Tyr	Lys	Lys	Val	Tyr	Tyr	Asp	Tyr	Gly	Thr	Asp	385	390	395	400
Asp	Val	Asp	Tyr	Tyr	Val	Val	Tyr	Asn	Gln	Val	Ser	Pro	Asp	Gly	Thr	405	410	415	
Met	Asp	Val	Ser	Leu	Phe	Arg	Gly	Asp	Asn	Asn	Thr	Pro	Ile	Glu	Ser	420	425	430	
Arg	Arg	Val	Gly	Pro	Gly	Arg	Ser	Ile	Arg	Phe	Thr	Ser	Arg	Asn	Tyr	435	440	445	
Thr	Ala	Arg	Asn	Pro	Tyr	Val	Thr	Glu	Thr	Pro	His	Glu	Val	Gln	Phe	450	455	460	
Ile	Tyr	Asp	Lys	Leu	Gly	Ser	Ile	Val	Pro	Val	Asp	Glu	Asp	Gly	Asn	465	470	475	480
Val	Ile	Gly	Asp	Leu	Val	Gln	Phe	Asn	Asn	Ser	Thr	Asp	Pro	Thr	Lys	485	490	495	
Ala	Ala	Val	Thr	Asp	Ser	Pro	Val	Ile	Ala	Gly	Tyr	Thr	Ile	Lys	Asp	500	505	510	
Pro	Thr	Gln	Arg	Glu	Ile	Thr	Pro	His	Asp	Pro	Gly	Lys	Asn	Ile	Lys	515	520	525	
Val	Val	Tyr	Val	Arg	Asn	His	Val	Thr	Ala	Ala	Ile	Lys	Tyr	Ile	Asp	530	535	540	
Asp	Thr	Ala	Gly	Asp	Asp	Leu	Ser	Ala	Tyr	Asn	Lys	Ser	Ile	Thr	Ala	545	550	555	560
Lys	Pro	Gly	Glu	Ala	Leu	Asn	Tyr	Thr	Thr	Lys	Asp	Ser	Ile	Thr	Glu	565	570	575	
Leu	Gln	Asn	Lys	Gly	Tyr	Val	Leu	Val	Ser	Asp	Asn	Phe	Asn	Val	Thr	580	585	590	
Thr	Met	Pro	Glu	Asn	Gly	Gly	Asn	Tyr	Glu	Val	His	Val	Lys	His	Gly	595	600	605	
Thr	Lys	Thr	Ile	Asp	Pro	Asp	Asn	Pro	Thr	Asp	Lys	Tyr	Thr	Lys	Lys	610	615	620	
Asp	Leu	Gln	Lys	Thr	Ala	Thr	Arg	Thr	Ile	Asn	Tyr	Val	Asp	Asp	Gln	625	630	635	640
Gly	Asn	Lys	Ile	Ala	Glu	Ser	Val	Thr	Ser	Thr	Val	Val	Phe	Thr	Gly	645	650	655	
Thr	Gly	Thr	Val	Asp	Ala	Val	Thr	Gly	Asn	Leu	Val	Asn	Leu	His	Pro	660	665	670	
Asp	Gly	Ser	Ile	Lys	Asp	Gln	Asn	Gly	Lys	Leu	Thr	Trp	Thr	Tyr	Ser	675	680	685	
Val	Asp	Gly	Gly	Val	Val	Gln	Lys	Ser	Asp	Thr	Tyr	Thr	Phe	Ser	Ala	690	695	700	
Thr	Thr	Ala	Arg	Pro	Thr	Ile	Asp	His	Asn	Asn	Ser	Thr	Tyr	Asn	Phe	705	710	715	720
Thr	Ser	Thr	Thr	Pro	Ala	Asp	Tyr	Asn	Ala	Gly	Asn	Gly	Ala	Val	Ser	725	730	735	
Ser	Tyr	Arg	Val	Asn	Ser	Thr	Asp	Pro	Gln	Asn	Leu	Ile	Val	Asn	Val	740	745	750	
Val	Tyr	Thr	Lys	Gln	Ala	Ile	Tyr	His	Ala	Gly	Lys	Thr	Glu	Thr	Lys	755	760	765	
Ser	Val	Thr	Arg	Thr	Ile	Asn	Tyr	Leu	Asp	Gly	Lys	Thr	Gly	Glu	Lys	770	775	780	
Ile	Pro	Thr	Asp	Leu	Ile	Ala	Thr	Asn	Pro	Val	Ala	Gln	Thr	Val	Asn	785	790	795	800
Leu	His	Arg	Thr	Glu	Ile	Ile	Asp	Asp	Asn	Gly	Lys	Val	Ile	Gly	Tyr	805	810	815	
Gly	Thr	Ile	Ser	Lys	Asp	Gly	Lys	Ser	Tyr	Thr	Ile	Asn	Asn	Asp	Trp	820	825	830	
Val	Val	Asp	Gly	Lys	Trp	Ala	Ser	Val	Thr	Ser	Pro	Asp	Leu	Ser	Ala				

```
<210> 21
<211> 3522
<212> DNA
<213> Lactobacillus acidophilus

<220>
<221> misc_feature
<222> (0)...(0)
```

<223> ORF 1652 - mucus binding protein precursor; Mub

<220>

<221> CDS

<222> (1)...(3522)

<400> 21

atg gta cat gaa aaa aag aag atg aga aaa aat cat aag aag ata acc	48
Met Val His Glu Lys Lys Lys Met Arg Lys Asn His Lys Lys Ile Thr	
1 5 10 15	
cac aag ggt aaa aag ata acc acg ggg gcc gct tcc gta tta ctt gga	96
His Lys Gly Lys Lys Ile Thr Thr Gly Ala Ala Ser Val Leu Leu Gly	
20 25 30	
gct gga att gtg gta gga gca aat gct cgt cct gtc aaa gct aca agc	144
Ala Gly Ile Val Val Gly Ala Asn Ala Arg Pro Val Lys Ala Thr Ser	
35 40 45	
tca cgc gaa gat gaa att act gag gta gat act att aat gtg att agt	192
Ser Arg Glu Asp Glu Ile Thr Glu Val Asp Thr Ile Asn Val Ile Ser	
50 55 60	
agt gaa act gaa aaa gca gat gta gag caa aga aca gat act act gaa	240
Ser Glu Thr Glu Lys Ala Asp Val Glu Gln Arg Thr Asp Thr Thr Glu	
65 70 75 80	
act gta gaa aca gaa ggt aat gtg gat aat aca aat acg gaa gtt tct	288
Thr Val Glu Thr Glu Gly Asn Val Asp Asn Thr Asn Thr Glu Val Ser	
85 90 95	
gta cct ata gat gaa aca att aat act gaa gct caa gct gca aac aat	336
Val Pro Ile Asp Glu Thr Ile Asn Thr Glu Ala Gln Ala Ala Asn Asn	
100 105 110	
aca aca cag gtt gaa tca act gta gaa gat aca aca caa gaa gag act	384
Thr Thr Gln Val Glu Ser Thr Val Glu Asp Thr Thr Gln Glu Glu Thr	
115 120 125	
aca gaa acg caa caa aat cct tca gtg gat aat caa gag ccg gtt tta	432
Thr Glu Thr Gln Gln Asn Pro Ser Val Asp Asn Gln Glu Pro Val Leu	
130 135 140	
agt gat cct cct agt gtg gaa tca cca gaa gat tca gct aca gaa gtt	480
Ser Asp Pro Pro Ser Val Glu Ser Pro Glu Asp Ser Ala Thr Glu Val	
145 150 155 160	
aca act act aag aca act gat gaa gta aaa aat gca gct gat gaa gcc	528
Thr Thr Thr Lys Thr Thr Asp Glu Val Lys Asn Ala Ala Asp Glu Ala	
165 170 175	
aat aaa gaa aac aaa gat aag tta gat gcg gaa ata aat aag gct gag	576
Asn Lys Glu Asn Lys Asp Lys Leu Asp Ala Glu Ile Asn Lys Ala Glu	
180 185 190	
gat aat ggt cat aca gta act caa gat ggt gac aaa gta tat aag gct	624

Asp	Asn	Gly	His	Thr	Val	Thr	Gln	Asp	Gly	Asp	Lys	Val	Tyr	Lys	Ala		
	195						200					205					
gat	gca	act	aat	atc	gat	aag	ata	att	gaa	gat	ctt	aat	caa	ttt	act	672	
Asp	Ala	Thr	Asn	Ile	Asp	Lys	Ile	Ile	Glu	Asp	Leu	Asn	Gln	Phe	Thr		
	210					215					220						
gct	gat	caa	att	act	gat	att	gaa	act	aaa	tta	gct	aaa	tat	aaa	gaa	720	
Ala	Asp	Gln	Ile	Thr	Asp	Ile	Glu	Thr	Lys	Leu	Ala	Lys	Tyr	Lys	Glu		
	225				230					235					240		
gaa	cta	gaa	gcg	tac	aag	gct	gat	caa	gta	aga	tac	gaa	gct	gaa	ttg	768	
Glu	Leu	Glu	Ala	Tyr	Lys	Ala	Asp	Gln	Val	Arg	Tyr	Glu	Ala	Glu	Leu		
			245					250						255			
aag	aat	tat	caa	aca	gct	aag	gat	gct	tat	gtt	aaa	aaa	tta	gaa	gaa	816	
Lys	Asn	Tyr	Gln	Thr	Ala	Lys	Asp	Ala	Tyr	Val	Lys	Lys	Leu	Glu	Glu		
		260					265						270				
tgg	ggt	ctt	tat	aag	cca	ggc	gat	att	gat	cca	agt	gat	att	tca	cag	864	
Trp	Gly	Leu	Tyr	Lys	Pro	Gly	Asp	Ile	Asp	Pro	Ser	Asp	Ile	Ser	Gln		
	275					280						285					
agt	tta	att	tta	gga	gaa	gag	aaa	aac	tct	aaa	gtt	gaa	gtt	cta	aat	912	
Ser	Leu	Ile	Leu	Gly	Glu	Glu	Lys	Asn	Ser	Lys	Val	Glu	Val	Leu	Asn		
	290					295					300						
aag	gga	agt	gtc	gta	gat	gaa	gga	acc	ggc	agt	atc	tta	aat	ggc	tta	960	
Lys	Gly	Ser	Val	Val	Asp	Glu	Gly	Thr	Gly	Ser	Ile	Leu	Asn	Gly	Leu		
	305				310					315					320		
ttg	aat	cat	ttc	tac	acc	att	gat	gaa	aaa	ttc	gac	ggc	gag	ttc	ttg	1008	
Leu	Asn	His	Phe	Tyr	Thr	Ile	Asp	Glu	Lys	Phe	Asp	Gly	Glu	Phe	Leu		
			325					330						335			
aag	ctg	caa	tat	act	aac	tta	gag	aac	ata	act	tat	atg	ggt	aag	aat	1056	
Lys	Leu	Gln	Tyr	Thr	Asn	Leu	Glu	Asn	Ile	Thr	Tyr	Met	Gly	Lys	Asn		
		340						345					350				
atc	gat	agt	att	cag	att	atc	ttt	agt	ggt	tgg	aat	cct	aac	tat	aag	1104	
Ile	Asp	Ser	Ile	Gln	Ile	Ile	Phe	Ser	Gly	Trp	Asn	Pro	Asn	Tyr	Lys		
		355				360						365					
ggg	aaa	aat	gct	gat	aag	aga	act	tca	ggt	att	tat	ttc	agt	gac	aaa	1152	
Gly	Lys	Asn	Ala	Asp	Lys	Arg	Thr	Ser	Gly	Ile	Tyr	Phe	Ser	Asp	Lys		
	370					375					380						
tta	act	gac	ggt	ttt	ttc	tac	gta	aac	agc	gat	ggc	gta	acc	atg	gaa	1200	
Leu	Thr	Asp	Gly	Phe	Phe	Tyr	Val	Asn	Ser	Asp	Gly	Val	Thr	Met	Glu		
	385				390					395					400		
atg	att	ttg	ttt	gaa	aat	ggt	aaa	acc	att	aac	cta	gat	aaa	aat	tcc	1248	
Met	Ile	Leu	Phe	Glu	Asn	Gly	Lys	Thr	Ile	Asn	Leu	Asp	Lys	Asn	Ser		
			405					410						415			
gca	tat	att	act	gct	ggt	tcc	ttg	aac	agt	cag	ggt	aca	ggt	aat	gac	1296	
Ala	Tyr	Ile	Thr	Ala	Gly	Ser	Leu	Asn	Ser	Gln	Gly	Thr	Gly	Asn	Asp		

420	425	430	
tat att gaa aaa gct gaa ata ttt aac aat agt agc gaa tat ggc ggt Tyr Ile Glu Lys Ala Glu Ile Phe Asn Asn Ser Ser Glu Tyr Gly Gly 435 440 445			1344
agt gct gtt aca ttc cag gat tca ttc ata aga cgt cat gat ggt act Ser Ala Val Thr Phe Gln Asp Ser Phe Ile Arg Arg His Asp Gly Thr 450 455 460			1392
tat ggt ggg gat gtt cta tat gcg gac caa aat atc gaa gtt tta gcc Tyr Gly Gly Asp Val Leu Tyr Ala Asp Gln Asn Ile Glu Val Leu Ala 465 470 475 480			1440
gta tat cca ggt aaa gat caa act tta gaa gat gca att gaa gag cag Val Tyr Pro Gly Lys Asp Gln Thr Leu Glu Asp Ala Ile Glu Glu Gln 485 490 495			1488
aag aaa tta gct ctt gag gct gga tgg aag caa gaa att atc gat aag Lys Lys Leu Ala Leu Glu Ala Gly Trp Lys Gln Glu Ile Ile Asp Lys 500 505 510			1536
ttc att aac tgg gat agc tct acc gat cgc tca aag gca atc ttt ggc Phe Ile Asn Trp Asp Ser Ser Thr Asp Arg Ser Lys Ala Ile Phe Gly 515 520 525			1584
gca ggt gca ttt atg gtc tat ggt aat aag atc aag att aga ttt agt Ala Gly Ala Phe Met Val Tyr Gly Asn Lys Ile Lys Ile Arg Phe Ser 530 535 540			1632
aac ggc atc ggt tca gct tgg gca aca tat tct act tca atc cca ggt Asn Gly Ile Gly Ser Ala Trp Ala Thr Tyr Ser Thr Ser Ile Pro Gly 545 550 555 560			1680
atg gca ttc cgt gaa gaa aag cca aag gaa cct act gta cct gag cca Met Ala Phe Arg Glu Glu Lys Pro Lys Glu Pro Thr Val Pro Glu Pro 565 570 575			1728
cct aag tta gat ctt act tac acg cca ggt cat att gaa tta tcc aaa Pro Lys Leu Asp Leu Thr Tyr Thr Pro Gly His Ile Glu Leu Ser Lys 580 585 590			1776
tct aac gtc cat att cac tat gtt gat gtt cat gat act gca cag gct Ser Asn Val His Ile His Tyr Val Asp Val His Asp Thr Ala Gln Ala 595 600 605			1824
ggt aaa aat gat agc ttt gtt cct gat gat ggt ata gag ctt gat gat Gly Lys Asn Asp Ser Phe Val Pro Asp Asp Gly Ile Glu Leu Asp Asp 610 615 620			1872
cat gtt gat cat caa tta gat tta tta atc ggt acc ggt tat aac cac His Val Asp His Gln Leu Asp Leu Leu Ile Gly Thr Gly Tyr Asn His 625 630 635 640			1920
gac tta tgg aat ttc gaa gat gcc gga tat att ttg gca gaa gaa atc Asp Leu Trp Asn Phe Glu Asp Ala Gly Tyr Ile Leu Ala Glu Glu Ile 645 650 655			1968

aaa gat ggt gtg caa aat ggt acg gtt att aaa gac gat caa cac cat	2016
Lys Asp Gly Val Gln Asn Gly Thr Val Ile Lys Asp Asp Gln His His	
660 665 670	
tat gtt tac ttg aag cat aaa ttt att ccg aca acg gat gaa gag aat	2064
Tyr Val Tyr Leu Lys His Lys Phe Ile Pro Thr Thr Asp Glu Glu Asn	
675 680 685	
gaa aag aaa gat gta aat caa gtc att cat tat gta tat gat gca act	2112
Glu Lys Lys Asp Val Asn Gln Val Ile His Tyr Val Tyr Asp Ala Thr	
690 695 700	
ggt gaa acg gct tat aag gac tat cac gca gtt acg ctt cac ttc att	2160
Gly Glu Thr Ala Tyr Lys Asp Tyr His Ala Val Thr Leu His Phe Ile	
705 710 715 720	
aag agt gga caa aaa gat gtt gtg aac ggc aat att att tgg ggc aat	2208
Lys Ser Gly Gln Lys Asp Val Val Asn Gly Asn Ile Ile Trp Gly Asn	
725 730 735	
tgg aca ctt gca caa gac ttt gca ggt gtg aag agt ccg tca att gaa	2256
Trp Thr Leu Ala Gln Asp Phe Ala Gly Val Lys Ser Pro Ser Ile Glu	
740 745 750	
ggt tat cat ctc aag gat aaa aat gac gat gta gtt ggt cca tac acg	2304
Gly Tyr His Leu Lys Asp Lys Asn Asp Asp Val Val Gly Pro Tyr Thr	
755 760 765	
att gaa gta acg gag aaa aat tac caa aat aat ctt gat gta gaa tac	2352
Ile Glu Val Thr Glu Lys Asn Tyr Gln Asn Asn Leu Asp Val Glu Tyr	
770 775 780	
acg gta aga tac gta gct aat gct act caa gag ctt aac ctc aag aaa	2400
Thr Val Arg Tyr Val Ala Asn Ala Thr Gln Glu Leu Asn Leu Lys Lys	
785 790 795 800	
gaa gtt aac caa gtc atc cat tac att tac gaa aat ggt acg aaa gct	2448
Glu Val Asn Gln Val Ile His Tyr Ile Tyr Glu Asn Gly Thr Lys Ala	
805 810 815	
cat gat gat tat cat gca ttg act cta ctc ttt gag aaa aaa ggt atc	2496
His Asp Asp Tyr His Ala Leu Thr Leu Leu Phe Glu Lys Lys Gly Ile	
820 825 830	
aaa gac tta gaa act gga gaa gaa act tgg ggt gaa tgg act aag aca	2544
Lys Asp Leu Glu Thr Gly Glu Glu Thr Trp Gly Glu Trp Thr Lys Thr	
835 840 845	
cag aca ttc gta gtg gta aag agt cct gat att caa aat tac att gcg	2592
Gln Thr Phe Val Val Val Lys Ser Pro Asp Ile Gln Asn Tyr Ile Ala	
850 855 860	
gat aga cta gaa gtt ggt cca tat gaa atc act gtg act gat gaa aat	2640
Asp Arg Leu Glu Val Gly Pro Tyr Glu Ile Thr Val Thr Asp Glu Asn	
865 870 875 880	

tac aag act aac tta gat aaa gac gac att gta atc tac aga gct aga	2688
Tyr Lys Thr Asn Leu Asp Lys Asp Asp Ile Val Ile Tyr Arg Ala Arg	
885 890 895	
atc gaa gaa gtt aca cgt gat aag gta gtt aac caa gtc att cac tat	2736
Ile Glu Glu Val Thr Arg Asp Lys Val Val Asn Gln Val Ile His Tyr	
900 905 910	
att tac gaa gat ggt agt aca gct aga cca gac cat gtg agt gta aaa	2784
Ile Tyr Glu Asp Gly Ser Thr Ala Arg Pro Asp His Val Ser Val Lys	
915 920 925	
ctt gtc ttc acc caa aca gga gta aag aac ttg gct act aat act acg	2832
Leu Val Phe Thr Gln Thr Gly Val Lys Asn Leu Ala Thr Asn Thr Thr	
930 935 940	
aat tgg aat ggt gaa tgg act aag aca cag acc ttt gtc gta gtg aag	2880
Asn Trp Asn Gly Glu Trp Thr Lys Thr Gln Thr Phe Val Val Val Lys	
945 950 955 960	
agt ccg gag att gaa ggc tac act gca gat cgc gaa gaa gta ggc cca	2928
Ser Pro Glu Ile Glu Gly Tyr Thr Ala Asp Arg Glu Glu Val Gly Pro	
965 970 975	
tat gat att act gta acg aat gaa aac tac aac gat aaa tta gat aaa	2976
Tyr Asp Ile Thr Val Thr Asn Glu Asn Tyr Asn Asp Lys Leu Asp Lys	
980 985 990	
gag gat act gta att tat aga gca aat act aat gtt ccg gat aac cca	3024
Glu Asp Thr Val Ile Tyr Arg Ala Asn Thr Asn Val Pro Asp Asn Pro	
995 1000 1005	
gat cca gat aat cca act ccg gat aat cca gat cca gat aat cca act	3072
Asp Pro Asp Asn Pro Thr Pro Asp Asn Pro Asp Pro Asp Asn Pro Thr	
1010 1015 1020	
cca gac act cca acc cct gat cca act cca ggc gat gat gaa gaa att	3120
Pro Asp Thr Pro Thr Pro Asp Pro Thr Pro Gly Asp Asp Glu Glu Ile	
1025 1030 1035 1040	
gcc acg cca cct ctt cca gag gat gaa att ggt aat tac cca tct caa	3168
Ala Thr Pro Pro Leu Pro Glu Asp Glu Ile Gly Asn Tyr Pro Ser Gln	
1045 1050 1055	
tca gac gaa gat gat gaa gaa gag cgc aca gct cca cat gct aca gga	3216
Ser Asp Glu Asp Asp Glu Glu Glu Arg Thr Ala Pro His Ala Thr Gly	
1060 1065 1070	
aaa gaa aca aga tca gga acc aac aaa aac aat gct aga gta att tct	3264
Lys Glu Thr Arg Ser Gly Thr Asn Lys Asn Asn Ala Arg Val Ile Ser	
1075 1080 1085	
ctt gaa aat gca gga agt gat gat tca gta act cca gaa aat gtt tca	3312
Leu Glu Asn Ala Gly Ser Asp Asp Ser Val Thr Pro Glu Asn Val Ser	
1090 1095 1100	
act gaa gca acg gat aaa act gat gaa aaa caa act act gtt aac tca	3360

Thr Glu Ala Thr Asp Lys Thr Asp Glu Lys Gln Thr Thr Val Asn Ser
 1105 1110 1115 1120
 aca aat gaa aag act tta cca gca act ggt gaa gaa aaa gat gat ttt 3408
 Thr Asn Glu Lys Thr Leu Pro Ala Thr Gly Glu Glu Lys Asp Asp Phe
 1125 1130 1135
 gct aaa gtg atg agt ggg tta gca gct gca tta gga att aca gga tta 3456
 Ala Lys Val Met Ser Gly Leu Ala Ala Ala Leu Gly Ile Thr Gly Leu
 1140 1145 1150
 gct gta act tct aag aga cgc aaa gct act gca aaa cgc agc aag aaa 3504
 Ala Val Thr Ser Lys Arg Arg Lys Ala Thr Ala Lys Arg Ser Lys Lys
 1155 1160 1165
 gat aaa aag aac ggt aaa 3522
 Asp Lys Lys Asn Gly Lys
 1170

<210> 22

<211> 1174

<212> PRT

<213> Lactobacillus acidophilus

<400> 22

Met Val His Glu Lys Lys Lys Met Arg Lys Asn His Lys Lys Ile Thr
 1 5 10 15
 His Lys Gly Lys Lys Ile Thr Thr Gly Ala Ala Ser Val Leu Leu Gly
 20 25 30
 Ala Gly Ile Val Val Gly Ala Asn Ala Arg Pro Val Lys Ala Thr Ser
 35 40 45
 Ser Arg Glu Asp Glu Ile Thr Glu Val Asp Thr Ile Asn Val Ile Ser
 50 55 60
 Ser Glu Thr Glu Lys Ala Asp Val Glu Gln Arg Thr Asp Thr Thr Glu
 65 70 75 80
 Thr Val Glu Thr Glu Gly Asn Val Asp Asn Thr Asn Thr Glu Val Ser
 85 90 95
 Val Pro Ile Asp Glu Thr Ile Asn Thr Glu Ala Gln Ala Ala Asn Asn
 100 105 110
 Thr Thr Gln Val Glu Ser Thr Val Glu Asp Thr Thr Gln Glu Glu Thr
 115 120 125
 Thr Glu Thr Gln Gln Asn Pro Ser Val Asp Asn Gln Glu Pro Val Leu
 130 135 140
 Ser Asp Pro Pro Ser Val Glu Ser Pro Glu Asp Ser Ala Thr Glu Val
 145 150 155 160
 Thr Thr Thr Lys Thr Asp Glu Val Lys Asn Ala Ala Asp Glu Ala
 165 170 175
 Asn Lys Glu Asn Lys Asp Lys Leu Asp Ala Glu Ile Asn Lys Ala Glu
 180 185 190
 Asp Asn Gly His Thr Val Thr Gln Asp Gly Asp Lys Val Tyr Lys Ala
 195 200 205
 Asp Ala Thr Asn Ile Asp Lys Ile Ile Glu Asp Leu Asn Gln Phe Thr
 210 215 220
 Ala Asp Gln Ile Thr Asp Ile Glu Thr Lys Leu Ala Lys Tyr Lys Glu
 225 230 235 240
 Glu Leu Glu Ala Tyr Lys Ala Asp Gln Val Arg Tyr Glu Ala Glu Leu

- 89 -

Gly Glu Thr Ala Tyr Lys Asp Tyr His Ala Val Thr Leu His Phe Ile
 705 710 715 720
 Lys Ser Gly Gln Lys Asp Val Val Asn Gly Asn Ile Ile Trp Gly Asn
 725 730 735
 Trp Thr Leu Ala Gln Asp Phe Ala Gly Val Lys Ser Pro Ser Ile Glu
 740 745 750
 Gly Tyr His Leu Lys Asp Lys Asn Asp Asp Val Val Gly Pro Tyr Thr
 755 760 765
 Ile Glu Val Thr Glu Lys Asn Tyr Gln Asn Asn Leu Asp Val Glu Tyr
 770 775 780
 Thr Val Arg Tyr Val Ala Asn Ala Thr Gln Glu Leu Asn Leu Lys Lys
 785 790 795 800
 Glu Val Asn Gln Val Ile His Tyr Ile Tyr Glu Asn Gly Thr Lys Ala
 805 810 815
 His Asp Asp Tyr His Ala Leu Thr Leu Leu Phe Glu Lys Lys Gly Ile
 820 825 830
 Lys Asp Leu Glu Thr Gly Glu Glu Thr Trp Gly Glu Trp Thr Lys Thr
 835 840 845
 Gln Thr Phe Val Val Val Lys Ser Pro Asp Ile Gln Asn Tyr Ile Ala
 850 855 860
 Asp Arg Leu Glu Val Gly Pro Tyr Glu Ile Thr Val Thr Asp Glu Asn
 865 870 875 880
 Tyr Lys Thr Asn Leu Asp Lys Asp Asp Ile Val Ile Tyr Arg Ala Arg
 885 890 895
 Ile Glu Glu Val Thr Arg Asp Lys Val Val Asn Gln Val Ile His Tyr
 900 905 910
 Ile Tyr Glu Asp Gly Ser Thr Ala Arg Pro Asp His Val Ser Val Lys
 915 920 925
 Leu Val Phe Thr Gln Thr Gly Val Lys Asn Leu Ala Thr Asn Thr Thr
 930 935 940
 Asn Trp Asn Gly Glu Trp Thr Lys Thr Gln Thr Phe Val Val Val Lys
 945 950 955 960
 Ser Pro Glu Ile Glu Gly Tyr Thr Ala Asp Arg Glu Glu Val Gly Pro
 965 970 975
 Tyr Asp Ile Thr Val Thr Asn Glu Asn Tyr Asn Asp Lys Leu Asp Lys
 980 985 990
 Glu Asp Thr Val Ile Tyr Arg Ala Asn Thr Asn Val Pro Asp Asn Pro
 995 1000 1005
 Asp Pro Asp Asn Pro Thr Pro Asp Asn Pro Asp Pro Asp Asn Pro Thr
 1010 1015 1020
 Pro Asp Thr Pro Thr Pro Asp Pro Thr Pro Gly Asp Asp Glu Glu Ile
 1025 1030 1035 1040
 Ala Thr Pro Pro Leu Pro Glu Asp Glu Ile Gly Asn Tyr Pro Ser Gln
 1045 1050 1055
 Ser Asp Glu Asp Asp Glu Glu Glu Arg Thr Ala Pro His Ala Thr Gly
 1060 1065 1070
 Lys Glu Thr Arg Ser Gly Thr Asn Lys Asn Asn Ala Arg Val Ile Ser
 1075 1080 1085
 Leu Glu Asn Ala Gly Ser Asp Asp Ser Val Thr Pro Glu Asn Val Ser
 1090 1095 1100
 Thr Glu Ala Thr Asp Lys Thr Asp Glu Lys Gln Thr Thr Val Asn Ser
 1105 1110 1115 1120
 Thr Asn Glu Lys Thr Leu Pro Ala Thr Gly Glu Glu Lys Asp Asp Phe
 1125 1130 1135
 Ala Lys Val Met Ser Gly Leu Ala Ala Ala Leu Gly Ile Thr Gly Leu
 1140 1145 1150
 Ala Val Thr Ser Lys Arg Arg Lys Ala Thr Ala Lys Arg Ser Lys Lys

1155
Asp Lys Lys Asn Gly Lys
1170

1160

1165

<210> 23
<211> 2091
<212> DNA
<213> Lactobacillus acidophilus

<220>
<221> misc_feature
<222> (0)...(0)
<223> ORF 1218 - mucus binding protein precursor
/

<220>
<221> CDS
<222> (1)...(2091)

<400> 23
atg tat aat gct gct aat caa caa gtt tcc tat aat gat ttt gta aat 48
Met Tyr Asn Ala Ala Asn Gln Gln Val Ser Tyr Asn Asp Phe Val Asn
1 5 10 15
gcc agc aaa caa aat cag cca att cct gta gta aat aca att aaa ttc 96
Ala Ser Lys Gln Asn Gln Pro Ile Pro Val Val Asn Thr Ile Lys Phe
20 25 30
aat gaa aat ggt aaa ttt ggc gat ggc tca aat gac tgg agt aaa aat 144
Asn Glu Asn Gly Lys Phe Gly Asp Gly Ser Asn Asp Trp Ser Lys Asn
35 40 45
ggc ggg act aac gga gaa aac aac aat aat acc gtt ata cat aat cca 192
Gly Gly Thr Asn Gly Glu Asn Asn Asn Thr Val Ile His Asn Pro
50 55 60
cat agt aca ttt ttg att caa atg gat aca ctt ctt cca acc aat att 240
His Ser Thr Phe Leu Ile Gln Met Asp Thr Leu Leu Pro Thr Asn Ile
65 70 75 80
cct aca aat tgg act aaa cca ggc aac ggt cca tct tct act att act 288
Pro Thr Asn Trp Thr Lys Pro Gly Asn Gly Pro Ser Ser Thr Ile Thr
85 90 95
atc cca aat aat cct cat gca gta gtt act tct gat tcc aca act ggt 336
Ile Pro Asn Asn Pro His Ala Val Val Thr Ser Asp Ser Thr Thr Gly
100 105 110
aat aca tca act tat att ggc ttc aat aat ggt ggt agc gga ttt ata 384
Asn Thr Ser Thr Tyr Ile Gly Phe Asn Asn Gly Gly Ser Gly Phe Ile
115 120 125
aac aat aca aaa ttt act gct gat tta tat ttt gct gat gtc act aaa 432
Asn Asn Thr Lys Phe Thr Ala Asp Leu Tyr Phe Ala Asp Val Thr Lys
130 135 140

cat gag agt ata aaa gat tta ggt gga caa aat aat att cct tta aca	480
His Glu Ser Ile Lys Asp Leu Gly Gly Gln Asn Asn Ile Pro Leu Thr	
145 150 155 160	
ggt aag ggt gta aat gaa gag agt gca acg cta agc aca cta ata aga	528
Val Lys Gly Val Asn Glu Glu Ser Ala Thr Leu Ser Thr Leu Ile Arg	
165 170 175	
ttt aat aat att gag agc ttt att aag aat tta aat aag agt gga tac	576
Phe Asn Asn Ile Glu Ser Phe Ile Lys Asn Leu Asn Lys Ser Gly Tyr	
180 185 190	
gct ttt gtt ggt gct tct act gga aag cac gtt tct ggt aag tat act	624
Ala Phe Val Gly Ala Ser Thr Gly Lys His Val Ser Gly Lys Tyr Thr	
195 200 205	
aat tca act tta tat tct tct aaa aat tat gaa gat aat aaa tat ggt	672
Asn Ser Thr Leu Tyr Ser Ser Lys Asn Tyr Glu Asp Asn Lys Tyr Gly	
210 215 220	
aat tat gat tgg gaa ggt aag gaa ttt aca cta aat ttt gta aaa tta	720
Asn Tyr Asp Trp Glu Gly Lys Glu Phe Thr Leu Asn Phe Val Lys Leu	
225 230 235 240	
agt tct caa aat aag agt gtt agc gat tca gtt aaa tat att tat gaa	768
Ser Ser Gln Asn Lys Ser Val Ser Asp Ser Val Lys Tyr Ile Tyr Glu	
245 250 255	
aat gga cct aag aag gga caa gaa gtt gaa tct gaa tat gct aaa cct	816
Asn Gly Pro Lys Lys Gly Gln Glu Val Glu Ser Glu Tyr Ala Lys Pro	
260 265 270	
agt tct caa tct ttg acg ttt aat caa act cag ata gtg gac gat aac	864
Ser Ser Gln Ser Leu Thr Phe Asn Gln Thr Gln Ile Val Asp Asp Asn	
275 280 285	
ggc aat gtc gta tat cct tca aca tgg ctt gct gaa aat aat aat ggt	912
Gly Asn Val Val Tyr Pro Ser Thr Trp Leu Ala Glu Asn Asn Asn Gly	
290 295 300	
aaa ttc gat gta atc aat att cca act aat gtt aat ggt aat acg aaa	960
Lys Phe Asp Val Ile Asn Ile Pro Thr Asn Val Asn Gly Asn Thr Lys	
305 310 315 320	
tat agt att gat tat gat aat atc act ttg aat aat gaa aag ttg tcg	1008
Tyr Ser Ile Asp Tyr Asp Asn Ile Thr Leu Asn Asn Glu Lys Leu Ser	
325 330 335	
gca tta gac aaa agt gta agt gtt gac cga aag aaa aat ata atc act	1056
Ala Leu Asp Lys Ser Val Ser Val Asp Arg Lys Lys Asn Ile Ile Thr	
340 345 350	
att aca att gat aaa gac aca att cca gaa aaa aca cgt ttt gat tta	1104
Ile Thr Ile Asp Lys Asp Thr Ile Pro Glu Lys Thr Arg Phe Asp Leu	
355 360 365	
gtt att cca tat aaa tta att gaa aat att cgt gtt cat tat att gat	1152

Val	Ile	Pro	Tyr	Lys	Leu	Ile	Glu	Asn	Ile	Arg	Val	His	Tyr	Ile	Asp	
370						375					380					
gaa	gat	ata	aaa	ggg	ggg	agt	gaa	att	aac	cat	gct	tta	aat	att	aaa	1200
Glu	Asp	Ile	Lys	Gly	Gly	Ser	Glu	Ile	Asn	His	Ala	Leu	Asn	Ile	Lys	
385					390				395						400	
gta	gac	gat	tct	aaa	ttg	cat	act	ttt	tat	agt	ggg	gat	cct	gaa	act	1248
Val	Asp	Asp	Ser	Lys	Leu	His	Thr	Phe	Tyr	Ser	Gly	Asp	Pro	Glu	Thr	
				405					410					415		
aca	act	gcc	aat	ttg	act	cat	gat	act	att	aac	tat	ctt	gaa	acg	cta	1296
Thr	Thr	Ala	Asn	Leu	Thr	His	Asp	Thr	Ile	Asn	Tyr	Leu	Glu	Thr	Leu	
			420					425					430			
aat	tat	att	tta	gat	att	gat	gct	aca	aat	ggg	gga	aaa	gct	tat	aca	1344
Asn	Tyr	Ile	Leu	Asp	Ile	Asp	Ala	Thr	Asn	Gly	Gly	Lys	Ala	Tyr	Thr	
	435					440					445					
tct	ata	cct	aat	tat	gat	tca	agt	aag	ttg	aac	ttt	aat	gat	caa	gtt	1392
Ser	Ile	Pro	Asn	Tyr	Asp	Ser	Ser	Lys	Leu	Asn	Phe	Asn	Asp	Gln	Val	
	450					455					460					
aac	aag	tat	acc	agt	gat	aag	ttg	aca	ttt	gat	gat	gac	gaa	aat	cct	1440
Asn	Lys	Tyr	Thr	Ser	Asp	Lys	Leu	Thr	Phe	Asp	Asp	Asp	Glu	Asn	Pro	
465					470				475						480	
aat	gat	tat	tat	gtt	tac	ttg	tat	cac	aag	ata	aag	gaa	gat	aag	ata	1488
Asn	Asp	Tyr	Tyr	Val	Tyr	Leu	Tyr	His	Lys	Ile	Lys	Glu	Asp	Lys	Ile	
				485					490					495		
cgt	gtt	caa	cag	aaa	caa	att	gaa	gaa	gtg	att	cat	tat	gtt	gat	gaa	1536
Arg	Val	Gln	Gln	Lys	Gln	Ile	Glu	Glu	Val	Ile	His	Tyr	Val	Asp	Glu	
		500					505						510			
gat	gat	gct	tat	gat	aaa	caa	ggg	aat	tta	aaa	gat	tta	gct	acg	ccg	1584
Asp	Asp	Ala	Tyr	Asp	Lys	Gln	Gly	Asn	Leu	Lys	Asp	Leu	Ala	Thr	Pro	
		515					520					525				
tat	att	tct	gat	act	tta	aca	ttt	agt	agg	gat	gca	aat	gta	gat	caa	1632
Tyr	Ile	Ser	Asp	Thr	Leu	Thr	Phe	Ser	Arg	Asp	Ala	Asn	Val	Asp	Gln	
	530					535					540					
gtg	act	ggg	aaa	aca	gtc	agt	tgg	aat	aat	tgg	tca	att	gga	act	ttt	1680
Val	Thr	Gly	Lys	Thr	Val	Ser	Trp	Asn	Asn	Trp	Ser	Ile	Gly	Thr	Phe	
545					550					555					560	
gat	tca	cat	aag	aat	gca	agt	att	tcc	aat	tat	aca	att	gac	ctt	gag	1728
Asp	Ser	His	Lys	Asn	Ala	Ser	Ile	Ser	Asn	Tyr	Thr	Ile	Asp	Leu	Glu	
				565					570					575		
tca	aag	att	ttt	agt	caa	aaa	cta	aat	ggg	aaa	gct	aca	cat	ttg	gct	1776
Ser	Lys	Ile	Phe	Ser	Gln	Lys	Leu	Asn	Gly	Lys	Ala	Thr	His	Leu	Ala	
			580					585					590			
gac	att	act	tca	gat	caa	gtt	agt	gca	ata	aat	gca	ttt	gca	aat	aaa	1824
Asp	Ile	Thr	Ser	Asp	Gln	Val	Ser	Ala	Ile	Asn	Ala	Phe	Ala	Asn	Lys	

595	600	605	
gat gcc caa aaa gaa att gat gct ttg cct aaa ggt aag tca ctt att Asp Ala Gln Lys Glu Ile Asp Ala Leu Pro Lys Gly Lys Ser Leu Ile 610 615 620			1872
gaa ata gta att cca tat aag cat aat gct caa aag cct gaa cct cca Glu Ile Val Ile Pro Tyr Lys His Asn Ala Gln Lys Pro Glu Pro Pro 625 630 635 640			1920
aaa aat cca gga gat aca cca tca act cct acg aat gta cct gat act Lys Asn Pro Gly Asp Thr Pro Ser Thr Pro Thr Asn Val Pro Asp Thr 645 650 655			1968
ccg cca gca cca agt aat cca gta att cct tca acg tca act cct tct Pro Pro Ala Pro Ser Asn Pro Val Ile Pro Ser Thr Ser Thr Pro Ser 660 665 670			2016
gat aat cca ata act cct aat att cca tct gtt tct aat tct aag aaa Asp Asn Pro Ile Thr Pro Asn Ile Pro Ser Val Ser Asn Ser Lys Lys 675 680 685			2064
aca aat aat aag aca act gat cta agt Thr Asn Asn Lys Thr Thr Asp Leu Ser 690 695			2091

<210> 24

<211> 697

<212> PRT

<213> Lactobacillus acidophilus

<400> 24

Met Tyr Asn Ala Ala Asn Gln Gln Val Ser Tyr Asn Asp Phe Val Asn 1 5 10 15	
Ala Ser Lys Gln Asn Gln Pro Ile Pro Val Val Asn Thr Ile Lys Phe 20 25 30	
Asn Glu Asn Gly Lys Phe Gly Asp Gly Ser Asn Asp Trp Ser Lys Asn 35 40 45	
Gly Gly Thr Asn Gly Glu Asn Asn Asn Thr Val Ile His Asn Pro 50 55 60	
His Ser Thr Phe Leu Ile Gln Met Asp Thr Leu Leu Pro Thr Asn Ile 65 70 75 80	
Pro Thr Asn Trp Thr Lys Pro Gly Asn Gly Pro Ser Ser Thr Ile Thr 85 90 95	
Ile Pro Asn Asn Pro His Ala Val Val Thr Ser Asp Ser Thr Thr Gly 100 105 110	
Asn Thr Ser Thr Tyr Ile Gly Phe Asn Asn Gly Gly Ser Gly Phe Ile 115 120 125	
Asn Asn Thr Lys Phe Thr Ala Asp Leu Tyr Phe Ala Asp Val Thr Lys 130 135 140	
His Glu Ser Ile Lys Asp Leu Gly Gly Gln Asn Asn Ile Pro Leu Thr 145 150 155 160	
Val Lys Gly Val Asn Glu Glu Ser Ala Thr Leu Ser Thr Leu Ile Arg 165 170 175	
Phe Asn Asn Ile Glu Ser Phe Ile Lys Asn Leu Asn Lys Ser Gly Tyr 180 185 190	

- 95 -

```

        645                650                655
Pro Pro Ala Pro Ser Asn Pro Val Ile Pro Ser Thr Ser Thr Pro Ser
        660                665                670
Asp Asn Pro Ile Thr Pro Asn Ile Pro Ser Val Ser Asn Ser Lys Lys
        675                680                685
Thr Asn Asn Lys Thr Thr Asp Leu Ser
        690                695

```

<210> 25

<211> 6957

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1020 - Mucus binding protein

<220>

<221> CDS

<222> (1)...(6957)

<400> 25

```

atg tat aga aat agg ggg aca cga gac atg gtt tct aag aat aac cgc   48
Met Tyr Arg Asn Arg Gly Thr Arg Asp Met Val Ser Lys Asn Asn Arg
 1                5                10                15

gat aag aag atg gaa gcg gta gcc gaa cgt aag cca cac ttt gct att   96
Asp Lys Lys Met Glu Ala Val Ala Glu Arg Lys Pro His Phe Ala Ile
        20                25                30

aga aag ttg act ata ggt gca gct tca gtt ctt cta ggt aca agt tta   144
Arg Lys Leu Thr Ile Gly Ala Ala Ser Val Leu Leu Gly Thr Ser Leu
        35                40                45

tgg atg agt act tct act agt acg gtt cat gct gat gaa act gac aat   192
Trp Met Ser Thr Ser Thr Ser Thr Val His Ala Asp Glu Thr Asp Asn
        50                55                60

aat gac agt gat gct aag aca aat tta gaa agt aat cag tct gct tca   240
Asn Asp Ser Asp Ala Lys Thr Asn Leu Glu Ser Asn Gln Ser Ala Ser
        65                70                75                80

act ggt cat gtt gaa aag gtt gtt gtt gaa caa aat caa aca gca aat   288
Thr Gly His Val Glu Lys Val Val Val Glu Gln Asn Gln Thr Ala Asn
        85                90                95

gaa aat aca gat gat agt act aaa act aac aat gta tcc gca caa aat   336
Glu Asn Thr Asp Asp Ser Thr Lys Thr Asn Asn Val Ser Ala Gln Asn
        100                105                110

act caa gaa agt gtt gat gag tca agt gat ata tct tca gat aat gca   384
Thr Gln Glu Ser Val Asp Glu Ser Ser Asp Ile Ser Ser Asp Asn Ala
        115                120                125

```

caa caa aat aaa gct ata act tct gaa gaa caa aat tct gat gct gca	432
Gln Gln Asn Lys Ala Ile Thr Ser Glu Glu Gln Asn Ser Asp Ala Ala	
130 135 140	
gta act att gat aat aat caa gca gca gat gag aat aag gct gag act	480
Val Thr Ile Asp Asn Asn Gln Ala Ala Asp Glu Asn Lys Ala Glu Thr	
145 150 155 160	
caa aag gta act gat aag act act aaa act aag caa gat gat aat aag	528
Gln Lys Val Thr Asp Lys Thr Thr Lys Thr Lys Gln Asp Asp Asn Lys	
165 170 175	
agt agt caa act att gat aat aaa aag tcg tca gaa aaa gct gct aca	576
Ser Ser Gln Thr Ile Asp Asn Lys Lys Ser Ser Glu Lys Ala Ala Thr	
180 185 190	
gat act agt aat aaa aac aat gta gaa caa agt gct aat tct gta gaa	624
Asp Thr Ser Asn Lys Asn Asn Val Glu Gln Ser Ala Asn Ser Val Glu	
195 200 205	
aat aat gct aat ata gac aat tcc att gcg gca aac act caa aca gat	672
Asn Asn Ala Asn Ile Asp Asn Ser Ile Ala Ala Asn Thr Gln Thr Asp	
210 215 220	
ata act aaa tca aat ata caa ctt aat gaa agt ttg cct tca ata gct	720
Ile Thr Lys Ser Asn Ile Gln Leu Asn Glu Ser Leu Pro Ser Ile Ala	
225 230 235 240	
caa gct ggt caa aac ggt aag act att gtt aaa gat aat gat aca act	768
Gln Ala Gly Gln Asn Gly Lys Thr Ile Val Lys Asp Asn Asp Thr Thr	
245 250 255	
act caa gaa tta aag att ggt gat ctt tca tca gac ttg agt gga gat	816
Thr Gln Glu Leu Lys Ile Gly Asp Leu Ser Ser Asp Leu Ser Gly Asp	
260 265 270	
gcc tta aaa gct aat tta act aag gga aat caa gta tta tta aac caa	864
Ala Leu Lys Ala Asn Leu Thr Lys Gly Asn Gln Val Leu Leu Asn Gln	
275 280 285	
tct aat tct agt gaa gtt gta gta ggt aaa aat gta gat cct act aag	912
Ser Asn Ser Ser Glu Val Val Val Gly Lys Asn Val Asp Pro Thr Lys	
290 295 300	
caa ttg caa gca atg gca aga act gct atg ttt gct gca gta aat cct	960
Gln Leu Gln Ala Met Ala Arg Thr Ala Met Phe Ala Ala Val Asn Pro	
305 310 315 320	
aat gca gct gat aac tac act act gtt agt gac ttt aat gct ctt caa	1008
Asn Ala Ala Asp Asn Tyr Thr Thr Val Ser Asp Phe Asn Ala Leu Gln	
325 330 335	
caa gct gtt aat gat tac agt gtc agt ggt gta aat atc agt ggt aac	1056
Gln Ala Val Asn Asp Tyr Ser Val Ser Gly Val Asn Ile Ser Gly Asn	
340 345 350	
att act gca tat ggc gat tta aac att aat cgt aca ttt act att aag	1104

Ile Thr Ala Tyr Gly Asp Leu Asn Ile Asn Arg Thr Phe Thr Ile Lys	
355 360 365	
ggt gct gac aat aat gct aca tta agt ctt ggt caa aac aag att aat	1152
Gly Ala Asp Asn Asn Ala Thr Leu Ser Leu Gly Gln Asn Lys Ile Asn	
370 375 380	
aat aat ggt caa tta act ctt gat gac att act gtt aat ggt tca atc	1200
Asn Asn Gly Gln Leu Thr Leu Asp Asp Ile Thr Val Asn Gly Ser Ile	
385 390 395 400	
ctt ggt aat ggt act gta aat att aag ggt act gtt act tca aat gta	1248
Leu Gly Asn Gly Thr Val Asn Ile Lys Gly Thr Val Thr Ser Asn Val	
405 410 415	
aat agt gtt aac tca tct gtt cca aca cag gat caa ttt aaa gct caa	1296
Asn Ser Val Asn Ser Ser Val Pro Thr Gln Asp Gln Phe Lys Ala Gln	
420 425 430	
aat tat act ggt aat aga aat aac ttt aag aat tct aac att gct ggt	1344
Asn Tyr Thr Gly Asn Arg Asn Asn Phe Lys Asn Ser Asn Ile Ala Gly	
435 440 445	
aat agt gta aat att gaa aac ggt gca tca tta act att aat agt tct	1392
Asn Ser Val Asn Ile Glu Asn Gly Ala Ser Leu Thr Ile Asn Ser Ser	
450 455 460	
gaa att aat gat ggt att aat tta act gac ggt ggg aca gtt cgt gtt	1440
Glu Ile Asn Asp Gly Ile Asn Leu Thr Asp Gly Gly Thr Val Arg Val	
465 470 475 480	
ggc gat aac gct acc tta aat gtt aat tta act aac gct tca act act	1488
Gly Asp Asn Ala Thr Leu Asn Val Asn Leu Thr Asn Ala Ser Thr Thr	
485 490 495	
gct act cgt tac cat gta gcc ggt gta ttt gca aaa aat ggc ggt aac	1536
Ala Thr Arg Tyr His Val Ala Gly Val Phe Ala Lys Asn Gly Gly Asn	
500 505 510	
ttt att agt ggt tac aag tca aac gtc aac ttt aat act ggt tta gga	1584
Phe Ile Ser Gly Tyr Lys Ser Asn Val Asn Phe Asn Thr Gly Leu Gly	
515 520 525	
caa gct att gct att ggc gct act cga cca act ggt act gat tca gat	1632
Gln Ala Ile Ala Ile Gly Ala Thr Arg Pro Thr Gly Thr Asp Ser Asp	
530 535 540	
cga ttt ggt gga tat ggt gca cgt tca aga aat gat gga cca aca tta	1680
Arg Phe Gly Gly Tyr Gly Ala Arg Ser Arg Asn Asp Gly Pro Thr Leu	
545 550 555 560	
gtt caa cta ggt gat tca tcg aca ttt aat ttc act ggt cgt gac ggt	1728
Val Gln Leu Gly Asp Ser Ser Thr Phe Asn Phe Thr Gly Arg Asp Gly	
565 570 575	
att atc tta ggt aat aac gcc aac ttt att tct ggt gaa aat tca aat	1776
Ile Ile Leu Gly Asn Asn Ala Asn Phe Ile Ser Gly Glu Asn Ser Asn	

580	585	590	
gtt cat ttt gaa aat aag ggt cgt ggg gtt gcc tta gat tta gct gct Val His Phe Glu Asn Lys Gly Arg Gly Val Ala Leu Asp Leu Ala Ala 595 600 605			1824
aac tca aat atc gaa att tct aag cac tct act aca tat ttc cat tct Asn Ser Asn Ile Glu Ile Ser Lys His Ser Thr Thr Tyr Phe His Ser 610 615 620			1872
gtc ggt aag act gga acg tca ggt agt tat gat ggt tac aac tac att Val Gly Lys Thr Gly Thr Ser Gly Ser Tyr Asp Gly Tyr Asn Tyr Ile 625 630 635 640			1920
ggg gtt aac gaa ggc ggt aat att act gtt gat gag tac gct aca ttc Gly Val Asn Glu Gly Gly Asn Ile Thr Val Asp Glu Tyr Ala Thr Phe 645 650 655			1968
cgt gta att ctt gaa ggt cgt ggc gat aac cca tgg gac gat gtt gtt Arg Val Ile Leu Glu Gly Arg Gly Asp Asn Pro Trp Asp Asp Val Val 660 665 670			2016
tca ctt gat tca caa aat gcg aat act act gct gcc ttt act tca aag Ser Leu Asp Ser Gln Asn Ala Asn Thr Thr Ala Ala Phe Thr Ser Lys 675 680 685			2064
aaa ggt gcg att gtc gat att cgt gat gat aat acc aac ttc tat gct Lys Gly Ala Ile Val Asp Ile Arg Asp Asp Asn Thr Asn Phe Tyr Ala 690 695 700			2112
gaa tta att tcc ttc cca tta ggt gga tct aat tca cgc att gat atc Glu Leu Ile Ser Phe Pro Leu Gly Gly Ser Asn Ser Arg Ile Asp Ile 705 710 715 720			2160
caa gat cca ttg atg ctt aac ttg caa cgt tat tct aaa ggc gga gca Gln Asp Pro Leu Met Leu Asn Leu Gln Arg Tyr Ser Lys Gly Gly Ala 725 730 735			2208
act act ggt tgg atg cca acc ggt ggt gac atg att aac acc act tca Thr Thr Gly Trp Met Pro Thr Gly Gly Asp Met Ile Asn Thr Thr Ser 740 745 750			2256
gca gaa tat act tcc aat ttg att tat atg tct ggt aac aaa gga gta Ala Glu Tyr Thr Ser Asn Leu Ile Tyr Met Ser Gly Asn Lys Gly Val 755 760 765			2304
ttt agt gtt agt ggt ggc gac tat gat cca tca aat cct aat agt tca Phe Ser Val Ser Gly Gly Asp Tyr Asp Pro Ser Asn Pro Asn Ser Ser 770 775 780			2352
ggg ttt gtt gtt tac caa cgt att aag tca gat ggt tca aag caa att Gly Phe Val Val Tyr Gln Arg Ile Lys Ser Asp Gly Ser Lys Gln Ile 785 790 795 800			2400
tggt ctt aat gta aat gat gta aat att cca atg aat gga ttc cag act Trp Leu Asn Val Asn Asp Val Asn Ile Pro Met Asn Gly Phe Gln Thr 805 810 815			2448

aag gat att tgg aat aat cag gca aac cca gat gta tca att acg ggt	2496
Lys Asp Ile Trp Asn Asn Gln Ala Asn Pro Asp Val Ser Ile Thr Gly	
820 825 830	
aat ggc tta act ggt ggt att aga gct aac caa gtt cat aac tat aat	2544
Asn Gly Leu Thr Gly Gly Ile Arg Ala Asn Gln Val His Asn Tyr Asn	
835 840 845	
ggg tct cca tta aca ggt aaa gat gca cca tat tat ggt att tct act	2592
Gly Ser Pro Leu Thr Gly Lys Asp Ala Pro Tyr Tyr Gly Ile Ser Thr	
850 855 860	
cag cgt gcg agc caa caa att tgg att cct cat aga aca ccg ttg gaa	2640
Gln Arg Ala Ser Gln Gln Ile Trp Ile Pro His Arg Thr Pro Leu Glu	
865 870 875 880	
ata act ggt aat cat aca aat act att aag tat gtt gat gaa caa ggg	2688
Ile Thr Gly Asn His Thr Asn Thr Ile Lys Tyr Val Asp Glu Gln Gly	
885 890 895	
aat gaa att ttc cca gaa aat acc tca tcc tta aat ttg aag cgt aat	2736
Asn Glu Ile Phe Pro Glu Asn Thr Ser Ser Leu Asn Leu Lys Arg Asn	
900 905 910	
att atc ctt gat att aca caa gac caa att aag aaa att caa gat tat	2784
Ile Ile Leu Asp Ile Thr Gln Asp Gln Ile Lys Lys Ile Gln Asp Tyr	
915 920 925	
gca ttg aac cat aca gct gat gaa aca tta gag tat ata aag aat agc	2832
Ala Leu Asn His Thr Ala Asp Glu Thr Leu Glu Tyr Ile Lys Asn Ser	
930 935 940	
caa tca gtt gct caa gat tca gga tgg aaa ttt act aac ggt agc ggt	2880
Gln Ser Val Ala Gln Asp Ser Gly Trp Lys Phe Thr Asn Gly Ser Gly	
945 950 955 960	
cag aca gtg aca gat cca tat gct acc gta gaa tca cct aaa ctg gat	2928
Gln Thr Val Thr Asp Pro Tyr Ala Thr Val Glu Ser Pro Lys Leu Asp	
965 970 975	
ggc tat act gct act att caa tca act aat gtt caa ggt tta aag gtt	2976
Gly Tyr Thr Ala Thr Ile Gln Ser Thr Asn Val Gln Gly Leu Lys Val	
980 985 990	
gga gaa gac gcc tct tct gta act gct aaa ttt gca gta aat cca tcc	3024
Gly Glu Asp Ala Ser Ser Val Thr Ala Lys Phe Ala Val Asn Pro Ser	
995 1000 1005	
gaa gat ata gtt caa aat ggt gaa ttg aca gat agc tat aag aat gac	3072
Glu Asp Ile Val Gln Asn Gly Glu Leu Thr Asp Ser Tyr Lys Asn Asp	
1010 1015 1020	
ggg att act ggc ata cct gat aat tat gtt act gtt gtt gtc tac aaa	3120
Gly Ile Thr Gly Ile Pro Asp Asn Tyr Val Thr Val Val Val Tyr Lys	
1025 1030 1035 1040	

aaa gca gtt gaa aaa ggt tca gta aaa gtt gtt tac cac gat gat act	3168
Lys Ala Val Glu Lys Gly Ser Val Lys Val Val Tyr His Asp Asp Thr	
1045 1050 1055	
act aac act gag att cca aat act gaa tac aat act ggt tca gta gac	3216
Thr Asn Thr Glu Ile Pro Asn Thr Glu Tyr Asn Thr Gly Ser Val Asp	
1060 1065 1070	
gct ggt act aaa gtg gac tac aca act aca act act atc acc aat ctt	3264
Ala Gly Thr Lys Val Asp Tyr Thr Thr Thr Thr Ile Thr Asn Leu	
1075 1080 1085	
gaa aat caa gga tat gta tat gta tca aca gat ggt act ata cct tca	3312
Glu Asn Gln Gly Tyr Val Tyr Val Ser Thr Asp Gly Thr Ile Pro Ser	
1090 1095 1100	
aca att gaa gga aat caa aac gta gta gta act gta cat atg aag cat	3360
Thr Ile Glu Gly Asn Gln Asn Val Val Val Thr Val His Met Lys His	
1105 1110 1115 1120	
ggt gtg caa cca gta act cca gat aca cca act cca gat gta cca aag	3408
Gly Val Gln Pro Val Thr Pro Asp Thr Pro Thr Pro Asp Val Pro Lys	
1125 1130 1135	
aat act cca gca gaa gca caa cct gat caa tta act aaa aag gtt aac	3456
Asn Thr Pro Ala Glu Ala Gln Pro Asp Gln Leu Thr Lys Lys Val Asn	
1140 1145 1150	
tta act gtt aac tac gta aat agc gat ggt tca acc ttt act gct act	3504
Leu Thr Val Asn Tyr Val Asn Ser Asp Gly Ser Thr Phe Thr Ala Thr	
1155 1160 1165	
gtt cct gca aat gct aag caa act gtt acc ttc act gga act gct tat	3552
Val Pro Ala Asn Ala Lys Gln Thr Val Thr Phe Thr Gly Thr Ala Tyr	
1170 1175 1180	
gta gat aaa gtt act ggt caa ttg gtt aac gct act caa caa aat ggt	3600
Val Asp Lys Val Thr Gly Gln Leu Val Asn Ala Thr Gln Gln Asn Gly	
1185 1190 1195 1200	
cag tgg gta atc gat gag aat aat act gca act cca caa atc acg tgg	3648
Gln Trp Val Ile Asp Glu Asn Asn Thr Ala Thr Pro Gln Ile Thr Trp	
1205 1210 1215	
act agc gat aag acc tca ttt gat aag gtt gtt tct cca gta gaa caa	3696
Thr Ser Asp Lys Thr Ser Phe Asp Lys Val Val Ser Pro Val Glu Gln	
1220 1225 1230	
aat tac cat tta atc agt att tct gat cat caa gat ggc aac gat gtt	3744
Asn Tyr His Leu Ile Ser Ile Ser Asp His Gln Asp Gly Asn Asp Val	
1235 1240 1245	
gcc aca att act ggt ctg act aaa gat agt gga gat att acc gta act	3792
Ala Thr Ile Thr Gly Leu Thr Lys Asp Ser Gly Asp Ile Thr Val Thr	
1250 1255 1260	
gta act tat gct cct aat ggt aag atc atc cca gtt gat cca tca ggg	3840

- 102 -

1490	1495	1500	
tca gca gtt aaa tct cca gtt gtt tct gga tat cac ttg gta agt gtt			4560
Ser Ala Val Lys Ser Pro Val Val Ser Gly Tyr His Leu Val Ser Val			
1505	1510	1515	1520
gat cgt gat caa gat ggt aat aat gta aag gat gta act ctt act cat			4608
Asp Arg Asp Gln Asp Gly Asn Asn Val Lys Asp Val Thr Leu Thr His			
1525	1530	1535	
gat gat aat agt tac ata gtg act gtg cgt tat gct aag aac ggt aag			4656
Asp Asp Asn Ser Tyr Ile Val Thr Val Arg Tyr Ala Lys Asn Gly Lys			
1540	1545	1550	
att att cca gta gat cca aat ggc cac cca att cca aat gta cca cag			4704
Ile Ile Pro Val Asp Pro Asn Gly His Pro Ile Pro Asn Val Pro Gln			
1555	1560	1565	
cca caa tat cca acc gat cca aat aat cca gct aag gta aca ccg gat			4752
Pro Gln Tyr Pro Thr Asp Pro Asn Asn Pro Ala Lys Val Thr Pro Asp			
1570	1575	1580	
gag cca gtg cca aat att cct ggt atg act cca agt gtt cca aca gtg			4800
Glu Pro Val Pro Asn Ile Pro Gly Met Thr Pro Ser Val Pro Thr Val			
1585	1590	1595	1600
aca ccg act gat cca ggt aaa gat act cca gtt ccg tat act cca gta			4848
Thr Pro Thr Asp Pro Gly Lys Asp Thr Pro Val Pro Tyr Thr Pro Val			
1605	1610	1615	
gca cca gct aag gat caa gtt gct caa gta att tac cgt gat gta aat			4896
Ala Pro Ala Lys Asp Gln Val Ala Gln Val Ile Tyr Arg Asp Val Asn			
1620	1625	1630	
gat cca aac aag gta act caa ctt gca act tca ggt gat ctt act ggt			4944
Asp Pro Asn Lys Val Thr Gln Leu Ala Thr Ser Gly Asp Leu Thr Gly			
1635	1640	1645	
aaa gct ggt tcc gag atc gat tac aat gca caa tct gaa atc gat aac			4992
Lys Ala Gly Ser Glu Ile Asp Tyr Asn Ala Gln Ser Glu Ile Asp Asn			
1650	1655	1660	
ttg att aat aag ggt tat gtg ctt aag aac aat ggc ttc cca gca ggt			5040
Leu Ile Asn Lys Gly Tyr Val Leu Lys Asn Asn Gly Phe Pro Ala Gly			
1665	1670	1675	1680
gct gtg ttt gat aat gat gac aat aag aca cag acc ttc tat att gac			5088
Ala Val Phe Asp Asn Asp Asp Asn Lys Thr Gln Thr Phe Tyr Ile Asp			
1685	1690	1695	
ttt gtt cat ggt act gtt cca gta acg cca act gat cca ggt aag cca			5136
Phe Val His Gly Thr Val Pro Val Thr Pro Thr Asp Pro Gly Lys Pro			
1700	1705	1710	
ggt gaa cca att aac cct aat gat cca gat gga cct aag tgg cca gat			5184
Gly Glu Pro Ile Asn Pro Asn Asp Pro Asp Gly Pro Lys Trp Pro Asp			
1715	1720	1725	

ggt act agt gaa gat agt ttg aag aaa tca ggt aca caa aca att cac	5232
Gly Thr Ser Glu Asp Ser Leu Lys Lys Ser Gly Thr Gln Thr Ile His	
1730 1735 1740	
tac gta tac tca gat gga agc aag gct aag gat gac aat gta caa agc	5280
Tyr Val Tyr Ser Asp Gly Ser Lys Ala Lys Asp Asp Asn Val Gln Ser	
1745 1750 1755 1760	
ttt gat ttt act aag agt gca gta gtt gat aaa gta acc ggt gaa atc	5328
Phe Asp Phe Thr Lys Ser Ala Val Val Asp Lys Val Thr Gly Glu Ile	
1765 1770 1775	
att agt caa act ggt tgg aat gta gat agt cat aca ttt ggc aat gta	5376
Ile Ser Gln Thr Gly Trp Asn Val Asp Ser His Thr Phe Gly Asn Val	
1780 1785 1790	
gat act cca gta att gat ggc tac cat gca gac aag cgt act gca ggt	5424
Asp Thr Pro Val Ile Asp Gly Tyr His Ala Asp Lys Arg Thr Ala Gly	
1795 1800 1805	
ggt acc aca att act cca gat gat ttg aac aag gaa gta act gta act	5472
Gly Thr Thr Ile Thr Pro Asp Asp Leu Asn Lys Glu Val Thr Val Thr	
1810 1815 1820	
tac aca cca aac ggt aag att att cca gta gat cca aat ggt aac cca	5520
Tyr Thr Pro Asn Gly Lys Ile Ile Pro Val Asp Pro Asn Gly Asn Pro	
1825 1830 1835 1840	
att cca aat gta cca aca cca cag tat cca acc gat cca act gat ccg	5568
Ile Pro Asn Val Pro Thr Pro Gln Tyr Pro Thr Asp Pro Thr Asp Pro	
1845 1850 1855	
act aag gta aca cca gat gaa ccg gta cca aat atc cct ggt ttg act	5616
Thr Lys Val Thr Pro Asp Glu Pro Val Pro Asn Ile Pro Gly Leu Thr	
1860 1865 1870	
cca agt gtt cca aca gta act cca acc gat cca ggt aag gat aca ccg	5664
Pro Ser Val Pro Thr Val Thr Pro Thr Asp Pro Gly Lys Asp Thr Pro	
1875 1880 1885	
gtt cca tac aac cca gta gtt cca gct aag gat cag gca gct gta gta	5712
Val Pro Tyr Asn Pro Val Val Pro Ala Lys Asp Gln Ala Ala Val Val	
1890 1895 1900	
aac tac gtt gat gct gat gaa gat aat aag tta atc act agt tca ggt	5760
Asn Tyr Val Asp Ala Asp Glu Asp Asn Lys Leu Ile Thr Ser Ser Gly	
1905 1910 1915 1920	
gac tta aca ggc aag gct ggc gaa act att aac tat agt act gcc gat	5808
Asp Leu Thr Gly Lys Ala Gly Glu Thr Ile Asn Tyr Ser Thr Ala Asp	
1925 1930 1935	
aca att aaa gat ctt gaa aac aag gga tat gta ttg gta aat gat ggc	5856
Thr Ile Lys Asp Leu Glu Asn Lys Gly Tyr Val Leu Val Asn Asp Gly	
1940 1945 1950	

ttc cca gca ggt gca aaa tat gac agt gat gac aac act act cag att Phe Pro Ala Gly Ala Lys Tyr Asp Ser Asp Asp Asn Thr Thr Gln Ile 1955 1960 1965	5904
tac acc gtt gtc ttg aag cat ggt aca act act att act cca gat aag Tyr Thr Val Val Leu Lys His Gly Thr Thr Thr Ile Thr Pro Asp Lys 1970 1975 1980	5952
cca ggt aag ccg ggt gaa cca att aat cct aac gat cca gat gga cct Pro Gly Lys Pro Gly Glu Pro Ile Asn Pro Asn Asp Pro Asp Gly Pro 1985 1990 1995 2000	6000
aag tgg cca gac aat agt ggt gaa aac aat tta tct aag act ggt aca Lys Trp Pro Asp Asn Ser Gly Glu Asn Asn Leu Ser Lys Thr Gly Thr 2005 2010 2015	6048
caa act att cac tac act ggc gca ggt gac aag act cct gaa gac aac Gln Thr Ile His Tyr Thr Gly Ala Gly Asp Lys Thr Pro Glu Asp Asn 2020 2025 2030	6096
aaa caa gag ttc act ttc act aag aca atg gta gtg gat aac gta act Lys Gln Glu Phe Thr Phe Thr Lys Thr Met Val Val Asp Asn Val Thr 2035 2040 2045	6144
ggc aag gta att act gat ggt gct tgg aat gta act agt cat aca ttt Gly Lys Val Ile Thr Asp Gly Ala Trp Asn Val Thr Ser His Thr Phe 2050 2055 2060	6192
ggg aat gtt gat act cca gta att gat ggt tac cat gca gac aag cgt Gly Asn Val Asp Thr Pro Val Ile Asp Gly Tyr His Ala Asp Lys Arg 2065 2070 2075 2080	6240
act gca ggt ggt acc aca att act cca gat gac ttg aat aag act gta Thr Ala Gly Gly Thr Thr Ile Thr Pro Asp Asp Leu Asn Lys Thr Val 2085 2090 2095	6288
act gta aac tac aca cca aac gga aag att att cca gta gat cca aat Thr Val Asn Tyr Thr Pro Asn Gly Lys Ile Ile Pro Val Asp Pro Asn 2100 2105 2110	6336
ggg aac cca att cca aat gta cca aca cca caa tat cca act gat cca Gly Asn Pro Ile Pro Asn Val Pro Thr Pro Gln Tyr Pro Thr Asp Pro 2115 2120 2125	6384
act gat cca act aag gta aca cca gat gaa cca gta ccg act att cca Thr Asp Pro Thr Lys Val Thr Pro Asp Glu Pro Val Pro Thr Ile Pro 2130 2135 2140	6432
ggg tac act cca tcg acc cca aca gta aca cca acc gat cca ggt aag Gly Tyr Thr Pro Ser Thr Pro Thr Val Thr Pro Thr Asp Pro Gly Lys 2145 2150 2155 2160	6480
gat aca ccg gtt cca tat aac cca gta gtt cca gct aag gat caa aag Asp Thr Pro Val Pro Tyr Asn Pro Val Val Pro Ala Lys Asp Gln Lys 2165 2170 2175	6528
gct gta gta aac tac gtt gat gct gat gaa gat aat aag tta atc act	6576

Ala Val Val Asn Tyr Val Asp Ala Asp Glu Asp Asn Lys Leu Ile Thr
2180 2185 2190

agt tca ggt gac cta aca ggt aag gcc ggc aaa aag att gac tac tca 6624
Ser Ser Gly Asp Leu Thr Gly Lys Ala Gly Lys Lys Ile Asp Tyr Ser
2195 2200 2205

acc agt tca act atc gaa gat ctt att aac aag gga tat gta tta gta 6672
Thr Ser Ser Thr Ile Glu Asp Leu Ile Asn Lys Gly Tyr Val Leu Val
2210 2215 2220

aac gat ggt ttc cct aag gat gct acg tac gac aat gac gac aat act 6720
Asn Asp Gly Phe Pro Lys Asp Ala Thr Tyr Asp Asn Asp Asp Asn Thr
2225 2230 2235 2240

act caa act tat aca gta gta ttc aaa cac ggc act gtt cca gta aca 6768
Thr Gln Thr Tyr Thr Val Val Phe Lys His Gly Thr Val Pro Val Thr
2245 2250 2255

cca acc aat cca ggt aag cca ggt gaa cca atc aat cct aat gat cca 6816
Pro Thr Asn Pro Gly Lys Pro Gly Glu Pro Ile Asn Pro Asn Asp Pro
2260 2265 2270

gat gga cct aag tgg cca gat ggc aca ggt gaa aac agt att gat aag 6864
Asp Gly Pro Lys Trp Pro Asp Gly Thr Gly Glu Asn Ser Ile Asp Lys
2275 2280 2285

act gta act cgt acc att act ttc gta gat agc aat ggt aag gaa gtt 6912
Thr Val Thr Arg Thr Ile Thr Phe Val Asp Ser Asn Gly Lys Glu Val
2290 2295 2300

tca agt cct gta gaa caa agt gtt cac ttt act gca gtg aaa gat 6957
Ser Ser Pro Val Glu Gln Ser Val His Phe Thr Ala Val Lys Asp
2305 2310 2315

<210> 26

<211> 2319

<212> PRT

<213> Lactobacillus acidophilus

<400> 26

Met Tyr Arg Asn Arg Gly Thr Arg Asp Met Val Ser Lys Asn Asn Arg
1 5 10 15
Asp Lys Lys Met Glu Ala Val Ala Glu Arg Lys Pro His Phe Ala Ile
20 25 30
Arg Lys Leu Thr Ile Gly Ala Ala Ser Val Leu Leu Gly Thr Ser Leu
35 40 45
Trp Met Ser Thr Ser Thr Ser Thr Val His Ala Asp Glu Thr Asp Asn
50 55 60
Asn Asp Ser Asp Ala Lys Thr Asn Leu Glu Ser Asn Gln Ser Ala Ser
65 70 75 80
Thr Gly His Val Glu Lys Val Val Val Glu Gln Asn Gln Thr Ala Asn
85 90 95
Glu Asn Thr Asp Asp Ser Thr Lys Thr Asn Asn Val Ser Ala Gln Asn
100 105 110

```

Thr Gln Glu Ser Val Asp Glu Ser Ser Asp Ile Ser Ser Asp Asn Ala
      115                      120                      125
Gln Gln Asn Lys Ala Ile Thr Ser Glu Glu Gln Asn Ser Asp Ala Ala
      130                      135                      140
Val Thr Ile Asp Asn Asn Gln Ala Ala Asp Glu Asn Lys Ala Glu Thr
145                      150                      155                      160
Gln Lys Val Thr Asp Lys Thr Thr Lys Thr Lys Gln Asp Asp Asn Lys
      165                      170                      175
Ser Ser Gln Thr Ile Asp Asn Lys Lys Ser Ser Glu Lys Ala Ala Thr
      180                      185                      190
Asp Thr Ser Asn Lys Asn Asn Val Glu Gln Ser Ala Asn Ser Val Glu
      195                      200                      205
Asn Asn Ala Asn Ile Asp Asn Ser Ile Ala Ala Asn Thr Gln Thr Asp
210                      215                      220
Ile Thr Lys Ser Asn Ile Gln Leu Asn Glu Ser Leu Pro Ser Ile Ala
225                      230                      235                      240
Gln Ala Gly Gln Asn Gly Lys Thr Ile Val Lys Asp Asn Asp Thr Thr
      245                      250                      255
Thr Gln Glu Leu Lys Ile Gly Asp Leu Ser Ser Asp Leu Ser Gly Asp
      260                      265                      270
Ala Leu Lys Ala Asn Leu Thr Lys Gly Asn Gln Val Leu Leu Asn Gln
      275                      280                      285
Ser Asn Ser Ser Glu Val Val Val Gly Lys Asn Val Asp Pro Thr Lys
290                      295                      300
Gln Leu Gln Ala Met Ala Arg Thr Ala Met Phe Ala Ala Val Asn Pro
305                      310                      315                      320
Asn Ala Ala Asp Asn Tyr Thr Thr Val Ser Asp Phe Asn Ala Leu Gln
      325                      330                      335
Gln Ala Val Asn Asp Tyr Ser Val Ser Gly Val Asn Ile Ser Gly Asn
      340                      345                      350
Ile Thr Ala Tyr Gly Asp Leu Asn Ile Asn Arg Thr Phe Thr Ile Lys
      355                      360                      365
Gly Ala Asp Asn Asn Ala Thr Leu Ser Leu Gly Gln Asn Lys Ile Asn
370                      375                      380
Asn Asn Gly Gln Leu Thr Leu Asp Asp Ile Thr Val Asn Gly Ser Ile
385                      390                      395                      400
Leu Gly Asn Gly Thr Val Asn Ile Lys Gly Thr Val Thr Ser Asn Val
      405                      410                      415
Asn Ser Val Asn Ser Ser Val Pro Thr Gln Asp Gln Phe Lys Ala Gln
420                      425                      430
Asn Tyr Thr Gly Asn Arg Asn Asn Phe Lys Asn Ser Asn Ile Ala Gly
435                      440                      445
Asn Ser Val Asn Ile Glu Asn Gly Ala Ser Leu Thr Ile Asn Ser Ser
450                      455                      460
Glu Ile Asn Asp Gly Ile Asn Leu Thr Asp Gly Gly Thr Val Arg Val
465                      470                      475                      480
Gly Asp Asn Ala Thr Leu Asn Val Asn Leu Thr Asn Ala Ser Thr Thr
      485                      490                      495
Ala Thr Arg Tyr His Val Ala Gly Val Phe Ala Lys Asn Gly Gly Asn
      500                      505                      510
Phe Ile Ser Gly Tyr Lys Ser Asn Val Asn Phe Asn Thr Gly Leu Gly
515                      520                      525
Gln Ala Ile Ala Ile Gly Ala Thr Arg Pro Thr Gly Thr Asp Ser Asp
530                      535                      540
Arg Phe Gly Gly Tyr Gly Ala Arg Ser Arg Asn Asp Gly Pro Thr Leu
545                      550                      555                      560
Val Gln Leu Gly Asp Ser Ser Thr Phe Asn Phe Thr Gly Arg Asp Gly

```

- 108 -

Gly Ile Thr Gly Ile Pro Asp Asn Tyr Val Thr Val Val Val Tyr Lys
 1025 1030 1035 1040
 Lys Ala Val Glu Lys Gly Ser Val Lys Val Val Tyr His Asp Asp Thr
 1045 1050 1055
 Thr Asn Thr Glu Ile Pro Asn Thr Glu Tyr Asn Thr Gly Ser Val Asp
 1060 1065 1070
 Ala Gly Thr Lys Val Asp Tyr Thr Thr Thr Thr Ile Thr Asn Leu
 1075 1080 1085
 Glu Asn Gln Gly Tyr Val Tyr Val Ser Thr Asp Gly Thr Ile Pro Ser
 1090 1095 1100
 Thr Ile Glu Gly Asn Gln Asn Val Val Val Val His Met Lys His
 1105 1110 1115 1120
 Gly Val Gln Pro Val Thr Pro Asp Thr Pro Thr Pro Asp Val Pro Lys
 1125 1130 1135
 Asn Thr Pro Ala Glu Ala Gln Pro Asp Gln Leu Thr Lys Lys Val Asn
 1140 1145 1150
 Leu Thr Val Asn Tyr Val Asn Ser Asp Gly Ser Thr Phe Thr Ala Thr
 1155 1160 1165
 Val Pro Ala Asn Ala Lys Gln Thr Val Thr Phe Thr Gly Thr Ala Tyr
 1170 1175 1180
 Val Asp Lys Val Thr Gly Gln Leu Val Asn Ala Thr Gln Gln Asn Gly
 1185 1190 1195 1200
 Gln Trp Val Ile Asp Glu Asn Asn Thr Ala Thr Pro Gln Ile Thr Trp
 1205 1210 1215
 Thr Ser Asp Lys Thr Ser Phe Asp Lys Val Val Ser Pro Val Glu Gln
 1220 1225 1230
 Asn Tyr His Leu Ile Ser Ile Ser Asp His Gln Asp Gly Asn Asp Val
 1235 1240 1245
 Ala Thr Ile Thr Gly Leu Thr Lys Asp Ser Gly Asp Ile Thr Val Thr
 1250 1255 1260
 Val Thr Tyr Ala Pro Asn Gly Lys Ile Ile Pro Val Asp Pro Ser Gly
 1265 1270 1275 1280
 Asn Pro Ile Pro Asp Ala Pro Thr Pro Gln Tyr Pro Thr Asp Pro Thr
 1285 1290 1295
 Asp Pro Ser Lys Val Thr Pro Asn Glu Pro Val Pro Asn Val Pro Gly
 1300 1305 1310
 Tyr Thr Pro Ser Val Pro Thr Val Thr Pro Ile Asp Pro Gly Lys Asp
 1315 1320 1325
 Thr Pro Val Pro Tyr Thr Pro Glu Thr Pro Ala Lys Asp Gln Lys Ala
 1330 1335 1340
 Val Val Asn Tyr Val Asp Ala Asp Glu Asp Asn Lys Leu Ile Thr Ser
 1345 1350 1355 1360
 Ser Gly Asp Leu Thr Gly Lys Ala Gly Thr Lys Ile Asp Tyr Ser Thr
 1365 1370 1375
 Asn Ser Thr Ile Glu Asp Leu Thr Asn Lys Gly Tyr Val Leu Val Asn
 1380 1385 1390
 Asp Gly Phe Pro Lys Asp Ala Thr Tyr Asp Asn Asp Asp Asn Thr Thr
 1395 1400 1405
 Gln Thr Tyr Thr Val Val Leu Arg His Gly Thr Gln Pro Val Asn Pro
 1410 1415 1420
 Thr Asn Pro Gly Lys Pro Gly Glu Pro Ile Asn Pro Asn Asp Pro Asp
 1425 1430 1435 1440
 Gly Pro Lys Tyr Pro Thr Gly Ser Asn Glu Val Thr Lys Thr Val Thr
 1445 1450 1455
 Arg Thr Ile Gln Tyr Leu Asp Glu Asp Gly Asn Lys Val Ser Asp Ser
 1460 1465 1470
 Val Glu Gln Pro Val Asn Phe Thr Glu Ser Gly Val Leu Asp Lys Val

1475	1480	1485
Thr Gly Glu Trp Thr Thr Pro Leu Thr Trp Ser Val Asp Gln Thr Val		
1490	1495	1500
Ser Ala Val Lys Ser Pro Val Val Ser Gly Tyr His Leu Val Ser Val		
1505	1510	1515
Asp Arg Asp Gln Asp Gly Asn Asn Val Lys Asp Val Thr Leu Thr His		
1525	1530	1535
Asp Asp Asn Ser Tyr Ile Val Thr Val Arg Tyr Ala Lys Asn Gly Lys		
1540	1545	1550
Ile Ile Pro Val Asp Pro Asn Gly His Pro Ile Pro Asn Val Pro Gln		
1555	1560	1565
Pro Gln Tyr Pro Thr Asp Pro Asn Asn Pro Ala Lys Val Thr Pro Asp		
1570	1575	1580
Glu Pro Val Pro Asn Ile Pro Gly Met Thr Pro Ser Val Pro Thr Val		
1585	1590	1595
Thr Pro Thr Asp Pro Gly Lys Asp Thr Pro Val Pro Tyr Thr Pro Val		
1605	1610	1615
Ala Pro Ala Lys Asp Gln Val Ala Gln Val Ile Tyr Arg Asp Val Asn		
1620	1625	1630
Asp Pro Asn Lys Val Thr Gln Leu Ala Thr Ser Gly Asp Leu Thr Gly		
1635	1640	1645
Lys Ala Gly Ser Glu Ile Asp Tyr Asn Ala Gln Ser Glu Ile Asp Asn		
1650	1655	1660
Leu Ile Asn Lys Gly Tyr Val Leu Lys Asn Asn Gly Phe Pro Ala Gly		
1665	1670	1675
Ala Val Phe Asp Asn Asp Asn Lys Thr Gln Thr Phe Tyr Ile Asp		
1685	1690	1695
Phe Val His Gly Thr Val Pro Val Thr Pro Thr Asp Pro Gly Lys Pro		
1700	1705	1710
Gly Glu Pro Ile Asn Pro Asn Asp Pro Asp Gly Pro Lys Trp Pro Asp		
1715	1720	1725
Gly Thr Ser Glu Asp Ser Leu Lys Lys Ser Gly Thr Gln Thr Ile His		
1730	1735	1740
Tyr Val Tyr Ser Asp Gly Ser Lys Ala Lys Asp Asp Asn Val Gln Ser		
1745	1750	1755
Phe Asp Phe Thr Lys Ser Ala Val Val Asp Lys Val Thr Gly Glu Ile		
1765	1770	1775
Ile Ser Gln Thr Gly Trp Asn Val Asp Ser His Thr Phe Gly Asn Val		
1780	1785	1790
Asp Thr Pro Val Ile Asp Gly Tyr His Ala Asp Lys Arg Thr Ala Gly		
1795	1800	1805
Gly Thr Thr Ile Thr Pro Asp Asp Leu Asn Lys Glu Val Thr Val Thr		
1810	1815	1820
Tyr Thr Pro Asn Gly Lys Ile Ile Pro Val Asp Pro Asn Gly Asn Pro		
1825	1830	1835
Ile Pro Asn Val Pro Thr Pro Gln Tyr Pro Thr Asp Pro Thr Asp Pro		
1845	1850	1855
Thr Lys Val Thr Pro Asp Glu Pro Val Pro Asn Ile Pro Gly Leu Thr		
1860	1865	1870
Pro Ser Val Pro Thr Val Thr Pro Thr Asp Pro Gly Lys Asp Thr Pro		
1875	1880	1885
Val Pro Tyr Asn Pro Val Val Pro Ala Lys Asp Gln Ala Ala Val Val		
1890	1895	1900
Asn Tyr Val Asp Ala Asp Glu Asp Asn Lys Leu Ile Thr Ser Ser Gly		
1905	1910	1915
Asp Leu Thr Gly Lys Ala Gly Glu Thr Ile Asn Tyr Ser Thr Ala Asp		
1925	1930	1935

Thr Ile Lys Asp Leu Glu Asn Lys Gly Tyr Val Leu Val Asn Asp Gly
 1940 1945 1950
 Phe Pro Ala Gly Ala Lys Tyr Asp Ser Asp Asp Asn Thr Thr Gln Ile
 1955 1960 1965
 Tyr Thr Val Val Leu Lys His Gly Thr Thr Thr Ile Thr Pro Asp Lys
 1970 1975 1980
 Pro Gly Lys Pro Gly Glu Pro Ile Asn Pro Asn Asp Pro Asp Gly Pro
 1985 1990 1995 2000
 Lys Trp Pro Asp Asn Ser Gly Glu Asn Asn Leu Ser Lys Thr Gly Thr
 2005 2010 2015
 Gln Thr Ile His Tyr Thr Gly Ala Gly Asp Lys Thr Pro Glu Asp Asn
 2020 2025 2030
 Lys Gln Glu Phe Thr Phe Thr Lys Thr Met Val Val Asp Asn Val Thr
 2035 2040 2045
 Gly Lys Val Ile Thr Asp Gly Ala Trp Asn Val Thr Ser His Thr Phe
 2050 2055 2060
 Gly Asn Val Asp Thr Pro Val Ile Asp Gly Tyr His Ala Asp Lys Arg
 2065 2070 2075 2080
 Thr Ala Gly Gly Thr Thr Ile Thr Pro Asp Asp Leu Asn Lys Thr Val
 2085 2090 2095
 Thr Val Asn Tyr Thr Pro Asn Gly Lys Ile Ile Pro Val Asp Pro Asn
 2100 2105 2110
 Gly Asn Pro Ile Pro Asn Val Pro Thr Pro Gln Tyr Pro Thr Asp Pro
 2115 2120 2125
 Thr Asp Pro Thr Lys Val Thr Pro Asp Glu Pro Val Pro Thr Ile Pro
 2130 2135 2140
 Gly Tyr Thr Pro Ser Thr Pro Thr Val Thr Pro Thr Asp Pro Gly Lys
 2145 2150 2155 2160
 Asp Thr Pro Val Pro Tyr Asn Pro Val Val Pro Ala Lys Asp Gln Lys
 2165 2170 2175
 Ala Val Val Asn Tyr Val Asp Ala Asp Glu Asp Asn Lys Leu Ile Thr
 2180 2185 2190
 Ser Ser Gly Asp Leu Thr Gly Lys Ala Gly Lys Lys Ile Asp Tyr Ser
 2195 2200 2205
 Thr Ser Ser Thr Ile Glu Asp Leu Ile Asn Lys Gly Tyr Val Leu Val
 2210 2215 2220
 Asn Asp Gly Phe Pro Lys Asp Ala Thr Tyr Asp Asn Asp Asp Asn Thr
 2225 2230 2235 2240
 Thr Gln Thr Tyr Thr Val Val Phe Lys His Gly Thr Val Pro Val Thr
 2245 2250 2255
 Pro Thr Asn Pro Gly Lys Pro Gly Glu Pro Ile Asn Pro Asn Asp Pro
 2260 2265 2270
 Asp Gly Pro Lys Trp Pro Asp Gly Thr Gly Glu Asn Ser Ile Asp Lys
 2275 2280 2285
 Thr Val Thr Arg Thr Ile Thr Phe Val Asp Ser Asn Gly Lys Glu Val
 2290 2295 2300
 Ser Ser Pro Val Glu Gln Ser Val His Phe Thr Ala Val Lys Asp
 2305 2310 2315

<210> 27

<211> 7950

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1019 - mucus binding protein

<220>

<221> CDS

<222> (1)...(7950)

<400> 27

```

atg att tct aaa aat aat cgc att aag aga atg gaa gca act tca gag      48
Met Ile Ser Lys Asn Asn Arg Ile Lys Arg Met Glu Ala Thr Ser Glu
  1             5             10             15

cgc aaa cag cat cat ggg att cgt aca cta tct gtt ggt gcc gtt tca      96
Arg Lys Gln His His Gly Ile Arg Thr Leu Ser Val Gly Ala Val Ser
             20             25             30

gtt ctt tta gga act act ttg tgg att agt att cct act agc aca gtt      144
Val Leu Leu Gly Thr Thr Leu Trp Ile Ser Ile Pro Thr Ser Thr Val
             35             40             45

cat gct gat gaa att aat att gat gac aat caa cct aaa aca aat tta      192
His Ala Asp Glu Ile Asn Ile Asp Asp Asn Gln Pro Lys Thr Asn Leu
             50             55             60

gaa agt aat gaa tcc gct tca act gat cat gta gaa aaa gtg att gtt      240
Glu Ser Asn Glu Ser Ala Ser Thr Asp His Val Glu Lys Val Ile Val
             65             70             75             80

gaa caa aat caa tca tca agt gaa ggt gct caa caa gat att aat gca      288
Glu Gln Asn Gln Ser Ser Ser Glu Gly Ala Gln Gln Asp Ile Asn Ala
             85             90             95

gca aat gat gta tct gca caa aat gat caa aaa agt gtt aat aaa ata      336
Ala Asn Asp Val Ser Ala Gln Asn Asp Gln Lys Ser Val Asn Lys Ile
             100            105            110

aat gat gaa att ata aaa aat gaa aat gta gac gct gat att aaa aca      384
Asn Asp Glu Ile Ile Lys Asn Glu Asn Val Asp Ala Asp Ile Lys Thr
             115            120            125

aac act gat aac agt cat gct gaa aca tct tat ggt caa act gaa tca      432
Asn Thr Asp Asn Ser His Ala Glu Thr Ser Tyr Gly Gln Thr Glu Ser
             130            135            140

caa gaa ata att gaa aat aaa caa aaa aca gat gtt gaa aaa aat aaa      480
Gln Glu Ile Ile Glu Asn Lys Gln Lys Thr Asp Val Glu Lys Asn Lys
             145            150            155            160

act caa aca aca gat aat att aca cca gtt gag caa act ggc aat tca      528
Thr Gln Thr Thr Asp Asn Ile Thr Pro Val Glu Gln Thr Gly Asn Ser
             165            170            175

tca gaa aat aca tct acg aat gta acc act caa agc cct gta gat aat      576
Ser Glu Asn Thr Ser Thr Asn Val Thr Thr Gln Ser Pro Val Asp Asn
             180            185            190

```

agt act aat aat gat gtt aat gta aat aat tct aat tta gct gat aca	624
Ser Thr Asn Asn Asp Val Asn Val Asn Asn Ser Asn Leu Ala Asp Thr	
195 200 205	
caa gca gaa tta att gat tca aat aca cag ttt tat gaa agt tcg cct	672
Gln Ala Glu Leu Ile Asp Ser Asn Thr Gln Phe Tyr Glu Ser Ser Pro	
210 215 220	
tta att gat caa att ggt cag caa gga aaa act acg gtt aat tct agt	720
Leu Ile Asp Gln Ile Gly Gln Gln Gly Lys Thr Thr Val Asn Ser Ser	
225 230 235 240	
aac aat act agt tct aaa tta aat att gat gat ctt tca cca gat tta	768
Asn Asn Thr Ser Ser Lys Leu Asn Ile Asp Asp Leu Ser Pro Asp Leu	
245 250 255	
agc gat gaa gta tta aag gct aat tta act caa ggt aat caa ata ttg	816
Ser Asp Glu Val Leu Lys Ala Asn Leu Thr Gln Gly Asn Gln Ile Leu	
260 265 270	
cta aat caa tct aat tct agc gat aca atg gca ggt aaa aat gct gat	864
Leu Asn Gln Ser Asn Ser Ser Asp Thr Met Ala Gly Lys Asn Ala Asp	
275 280 285	
cct act aaa caa tta gag gca atg gct agg aca gct acc ctt gtt gca	912
Pro Thr Lys Gln Leu Glu Ala Met Ala Arg Thr Ala Thr Leu Val Ala	
290 295 300	
gcg agt cca aat gca gat aat tac act act gtt aat aac tat aat gat	960
Ala Ser Pro Asn Ala Asp Asn Tyr Thr Thr Val Asn Asn Tyr Asn Asp	
305 310 315 320	
ctt caa aga gct gtt agc aat tat agt gta agc gga gta aat atc gat	1008
Leu Gln Arg Ala Val Ser Asn Tyr Ser Val Ser Gly Val Asn Ile Asp	
325 330 335	
ggg gat att tat gtt ttt ggt aat tta act att aat cgt gct ttt act	1056
Gly Asp Ile Tyr Val Phe Gly Asn Leu Thr Ile Asn Arg Ala Phe Thr	
340 345 350	
att aag gga act aat aat gca aag tta aat tta aat caa aat gca att	1104
Ile Lys Gly Thr Asn Asn Ala Lys Leu Asn Leu Asn Gln Asn Ala Ile	
355 360 365	
att aat aat tct act tta act ctt gag gat att act gtt aat ggt tca	1152
Ile Asn Asn Ser Thr Leu Thr Leu Glu Asp Ile Thr Val Asn Gly Ser	
370 375 380	
att atg ggt aat gga aca gta aat att aaa ggg gat gtt att tct aat	1200
Ile Met Gly Asn Gly Thr Val Asn Ile Lys Gly Asp Val Ile Ser Asn	
385 390 395 400	
gtt aat gaa tct aat ggt tat acg ctt acc aat tct gaa aaa gca act	1248
Val Asn Glu Ser Asn Gly Tyr Thr Leu Thr Asn Ser Glu Lys Ala Thr	
405 410 415	
cct ggt gtt aag gtg aat tgg act caa act aaa gga tat aac att caa	1296

Pro Gly Val Lys Val Asn Trp Thr Gln Thr Lys Gly Tyr Asn Ile Gln	
420 425 430	
tca agt act gtt aat gtc gat gat aat gct tca cta aca att aat cgc 1344	
Ser Ser Thr Val Asn Val Asp Asp Asn Ala Ser Leu Thr Ile Asn Arg	
435 440 445	
tca tct gtt ggc gat ggt atc cat ttg tta agt aat ggt att gtt aat 1392	
Ser Ser Val Gly Asp Gly Ile His Leu Leu Ser Asn Gly Ile Val Asn	
450 455 460	
ggt ggt aat tat agc caa tta act att aat atg aat act aat aat gaa 1440	
Val Gly Asn Tyr Ser Gln Leu Thr Ile Asn Met Asn Thr Asn Asn Glu	
465 470 475 480	
ttg ggc aca gga gct act gct cgt tac cat gat gca ggt att ttt gct 1488	
Leu Gly Thr Gly Ala Thr Ala Arg Tyr His Asp Ala Gly Ile Phe Ala	
485 490 495	
gaa agt aat ggt agt ttt act aca gga tat aag tct gta gtg act cta 1536	
Glu Ser Asn Gly Ser Phe Thr Thr Gly Tyr Lys Ser Val Val Thr Leu	
500 505 510	
aac acc agt att ggt caa gga att gcg atg aca ggt ctg aga cct aac 1584	
Asn Thr Ser Ile Gly Gln Gly Ile Ala Met Thr Gly Leu Arg Pro Asn	
515 520 525	
gta aca gat aat gat cgt ttt ggt gga tat act cgt gat cgc gcg aat 1632	
Val Thr Asp Asn Asp Arg Phe Gly Gly Tyr Thr Arg Asp Arg Ala Asn	
530 535 540	
ggt gcg ggt caa att aat ttg ggt caa tac tct act tta aac ttt acc 1680	
Gly Ala Gly Gln Ile Asn Leu Gly Gln Tyr Ser Thr Leu Asn Phe Thr	
545 550 555 560	
ggt cgt gat gga gtt att ttg ggt aat aat tct aat ttt aac gtt ggt 1728	
Gly Arg Asp Gly Val Ile Leu Gly Asn Asn Ser Asn Phe Asn Val Gly	
565 570 575	
gaa tat gcc aat gtc cac ttt gaa aat aaa gga cgt ggt gtt gct ctt 1776	
Glu Tyr Ala Asn Val His Phe Glu Asn Lys Gly Arg Gly Val Ala Leu	
580 585 590	
gat cta gca aat aat agt aat att aat att gct gat cat gca gta acg 1824	
Asp Leu Ala Asn Asn Ser Asn Ile Asn Ile Ala Asp His Ala Val Thr	
595 600 605	
tat ttc cat tca gta ggt aag aat acc act aat gct att ggt gtt gta 1872	
Tyr Phe His Ser Val Gly Lys Asn Thr Thr Asn Ala Ile Gly Val Val	
610 615 620	
ggt ggt cca tca ggt agt tat gag ggt tat aac tat att ggt gta aat 1920	
Val Gly Pro Ser Gly Ser Tyr Glu Gly Tyr Asn Tyr Ile Gly Val Asn	
625 630 635 640	
gaa gca gga aat att act att ggt gaa gat gca act ttt aga gta atc 1968	
Glu Ala Gly Asn Ile Thr Ile Gly Glu Asp Ala Thr Phe Arg Val Ile	

645										650										655										
atg gaa aat cgt ggc gac aat gct tgg gat gat gtt att tct tta gat	2016																													
Met Glu Asn Arg Gly Asp Asn Ala Trp Asp Asp Val Ile Ser Leu Asp																														
660 665 670																														
tca cag ttg gca aca aca aat gct gcc ttt act tcc aaa aaa ggt gct	2064																													
Ser Gln Leu Ala Thr Thr Asn Ala Ala Phe Thr Ser Lys Lys Gly Ala																														
675 680 685																														
att att gac att cgt gat gat aac act aac ttc tat gca gaa ttg att	2112																													
Ile Ile Asp Ile Arg Asp Asn Thr Asn Phe Tyr Ala Glu Leu Ile																														
690 695 700																														
tcc ttc cca tta gga gct gca aat tca cgg att gat att caa gat ccg	2160																													
Ser Phe Pro Leu Gly Ala Ala Asn Ser Arg Ile Asp Ile Gln Asp Pro																														
705 710 715 720																														
ctg ctt ctt aac cta caa cgt tat tca gct ggt ggt gag act act ggc	2208																													
Leu Leu Leu Asn Leu Gln Arg Tyr Ser Ala Gly Gly Glu Thr Thr Gly																														
725 730 735																														
tgg atg gct gga gtt ggt ggg gta gct att aat tct act tct gaa aaa	2256																													
Trp Met Ala Gly Val Gly Gly Val Ala Ile Asn Ser Thr Ser Glu Lys																														
740 745 750																														
tat act gct aac ttg att tat atg ggt ggt act aaa ggt gtt tta agt	2304																													
Tyr Thr Ala Asn Leu Ile Tyr Met Gly Gly Thr Lys Gly Val Leu Ser																														
755 760 765																														
att ggt ggt act aac tat gtt gtt tac caa cag att aaa tca gat ggt	2352																													
Ile Gly Gly Thr Asn Tyr Val Val Tyr Gln Gln Ile Lys Ser Asp Gly																														
770 775 780																														
gcc caa caa att tgg act gat gta gat agt gta gaa ttc cat aaa aat	2400																													
Ala Gln Gln Ile Trp Thr Asp Val Asp Ser Val Glu Phe His Lys Asn																														
785 790 795 800																														
ggg ttt gct tca caa gat att ttc aat aat gga gct aat tct gat gtt	2448																													
Gly Phe Ala Ser Gln Asp Ile Phe Asn Asn Gly Ala Asn Ser Asp Val																														
805 810 815																														
tca att agc ggt aat ggt ttc aca agt gga att cgt gct aac caa atc	2496																													
Ser Ile Ser Gly Asn Gly Phe Thr Ser Gly Ile Arg Ala Asn Gln Ile																														
820 825 830																														
cgt gac aat cag act gat ccg act tta gtg aac tta caa aat agt cct	2544																													
Arg Asp Asn Gln Thr Asp Pro Thr Leu Val Asn Leu Gln Asn Ser Pro																														
835 840 845																														
gct tac ggt att tca act atg cgt gca agt cat caa att tgg att cca	2592																													
Ala Tyr Gly Ile Ser Thr Met Arg Ala Ser His Gln Ile Trp Ile Pro																														
850 855 860																														
cat gaa act tct act cag att aag gga aca cat act aat act att agt	2640																													
His Glu Thr Ser Thr Gln Ile Lys Gly Thr His Thr Asn Thr Ile Ser																														
865 870 875 880																														

tat gta tat gaa gat gga aca cca gtt atg ggt gcc gat agt caa cca	2688
Tyr Val Tyr Glu Asp Gly Thr Pro Val Met Gly Ala Asp Ser Gln Pro	
885 890 895	
tta gtt gtg act caa aac ttg aat tta gca cgt gat tta act ctt gat	2736
Leu Val Val Thr Gln Asn Leu Asn Leu Ala Arg Asp Leu Thr Leu Asp	
900 905 910	
cta act tct gaa caa att aaa aca att caa gac tat gcc tta gga cat	2784
Leu Thr Ser Glu Gln Ile Lys Thr Ile Gln Asp Tyr Ala Leu Gly His	
915 920 925	
act gct gat gag acc ttg aat tat att aga agt ggc tac tca gta act	2832
Thr Ala Asp Glu Thr Leu Asn Tyr Ile Arg Ser Gly Tyr Ser Val Thr	
930 935 940	
caa gat tct ggt tgg acg tac act aat gat caa gga caa aaa gtg act	2880
Gln Asp Ser Gly Trp Thr Tyr Thr Asn Asp Gln Gly Gln Lys Val Thr	
945 950 955 960	
gat cca tat gca tct gtg act tcc cca gta aaa gaa gga tat att att	2928
Asp Pro Tyr Ala Ser Val Thr Ser Pro Val Lys Glu Gly Tyr Ile Ile	
965 970 975	
act att caa tca act aat gca ccg ggt gta act tta ggt gct gat ggt	2976
Thr Ile Gln Ser Thr Asn Ala Pro Gly Val Thr Leu Gly Ala Asp Gly	
980 985 990	
caa act gta aaa gct aat ttt gtg ttt gat gca gcc aat gat gtg gtg	3024
Gln Thr Val Lys Ala Asn Phe Val Phe Asp Ala Ala Asn Asp Val Val	
995 1000 1005	
caa aat ggt caa ttg tca gct ggg tat aga aat caa ggt att act ggt	3072
Gln Asn Gly Gln Leu Ser Ala Gly Tyr Arg Asn Gln Gly Ile Thr Gly	
1010 1015 1020	
att ccg gac aat tat caa acg atc gtt gtt tac aag aaa gca gaa aag	3120
Ile Pro Asp Asn Tyr Gln Thr Ile Val Val Tyr Lys Lys Ala Glu Lys	
1025 1030 1035 1040	
ggt tct gtt caa gta atc ttt tac gat gat acg act aac gat gct atc	3168
Gly Ser Val Gln Val Ile Phe Tyr Asp Asp Thr Thr Asn Asp Ala Ile	
1045 1050 1055	
cca agt gtt ggt ttt aat tca ggg aca gag gaa gca gga aca cca gtt	3216
Pro Ser Val Gly Phe Asn Ser Gly Thr Glu Glu Ala Gly Thr Pro Val	
1060 1065 1070	
aca tat aca act gca caa aat att agt gat tta gaa aaa caa gga tat	3264
Thr Tyr Thr Thr Ala Gln Asn Ile Ser Asp Leu Glu Lys Gln Gly Tyr	
1075 1080 1085	
gta tat gta agt aca gat ggt gtg att cca aca act ata cct aat aat	3312
Val Tyr Val Ser Thr Asp Gly Val Ile Pro Thr Thr Ile Pro Asn Asn	
1090 1095 1100	

gca acc cta att act gtt cat atg aag cat ggt acc aat cca gtc aac	3360
Ala Thr Leu Ile Thr Val His Met Lys His Gly Thr Asn Pro Val Asn	
1105 1110 1115 1120	
cct gat cag cca act gat aag tat act aag gaa gat ttg caa aag aca	3408
Pro Asp Gln Pro Thr Asp Lys Tyr Thr Lys Glu Asp Leu Gln Lys Thr	
1125 1130 1135	
gta act cgg aca atc aat tat att gac act gct ggc aat ata att gct	3456
Val Thr Arg Thr Ile Asn Tyr Ile Asp Thr Ala Gly Asn Ile Ile Ala	
1140 1145 1150	
gac tct gtt act tcg acg gtt gtc ttt aca ggt tca ggc aca att gat	3504
Asp Ser Val Thr Ser Thr Val Val Phe Thr Gly Ser Gly Thr Ile Asp	
1155 1160 1165	
aca gtg aca ggt aac tta gta acc gtt gat gca agt ggt aat att gta	3552
Thr Val Thr Gly Asn Leu Val Thr Val Asp Ala Ser Gly Asn Ile Val	
1170 1175 1180	
gat caa aac ggt caa ctc act tgg act tat tca gta gat ggc gat agt	3600
Asp Gln Asn Gly Gln Leu Thr Trp Thr Tyr Ser Val Asp Gly Asp Ser	
1185 1190 1195 1200	
gct caa agt ggt aat tct tat aca ttt gct gaa act gct gcc aaa cca	3648
Ala Gln Ser Gly Asn Ser Tyr Thr Phe Ala Glu Thr Ala Ala Lys Pro	
1205 1210 1215	
tca att gat tat aat gga tct aca tat aac ttt gtt tca gta act cct	3696
Ser Ile Asp Tyr Asn Gly Ser Thr Tyr Asn Phe Val Ser Val Thr Pro	
1220 1225 1230	
ggt aac tat agt gcc ggt aat ggt agt gtg acg agt tat gaa gta aac	3744
Gly Asn Tyr Ser Ala Gly Asn Gly Ser Val Thr Ser Tyr Glu Val Asn	
1235 1240 1245	
act aat aat tca cat gac tta aca gtt gat gtt att tac aat gag gga	3792
Thr Asn Asn Ser His Asp Leu Thr Val Asp Val Ile Tyr Asn Glu Gly	
1250 1255 1260	
gca act tat cat aca ggc aag act gat act aaa aat gta act aga ata	3840
Ala Thr Tyr His Thr Gly Lys Thr Asp Thr Lys Asn Val Thr Arg Ile	
1265 1270 1275 1280	
att aat tat tta gat ggt aaa aca gat gaa aaa atc cca atc aac ttg	3888
Ile Asn Tyr Leu Asp Gly Lys Thr Asp Glu Lys Ile Pro Ile Asn Leu	
1285 1290 1295	
atc cta gct aat cca gtt gaa caa act gta agt atg tat cga act gaa	3936
Ile Leu Ala Asn Pro Val Glu Gln Thr Val Ser Met Tyr Arg Thr Glu	
1300 1305 1310	
att ttg gat tca act ggc aag gtg att ggc tat ggt aca gtg agc caa	3984
Ile Leu Asp Ser Thr Gly Lys Val Ile Gly Tyr Gly Thr Val Ser Gln	
1315 1320 1325	
gat ggt aag atg tac act ctt aat aat aat tgg att att gat gga att	4032

Asp Gly Lys Met Tyr Thr Leu Asn Asn Asn Trp Ile Ile Asp Gly Ile	
1330 1335 1340	
tgg gaa agt gtg aat tca cct gat tta act aca aat gga tat aag gca	4080
Trp Glu Ser Val Asn Ser Pro Asp Leu Thr Thr Asn Gly Tyr Lys Ala	
1345 1350 1355 1360	
cca cgg ttc gaa gat agt agt tta gct gca att gta gct gaa tat att	4128
Pro Arg Phe Glu Asp Ser Ser Leu Ala Ala Ile Val Ala Glu Tyr Ile	
1365 1370 1375	
gtt aat gct gat act aaa aat gca acg gta aat gta tac tat gat cac	4176
Val Asn Ala Asp Thr Lys Asn Ala Thr Val Asn Val Tyr Tyr Asp His	
1380 1385 1390	
caa gtg att cca att gga ccg gat act cca gac aaa cat ggt gta gat	4224
Gln Val Ile Pro Ile Gly Pro Asp Thr Pro Asp Lys His Gly Val Asp	
1395 1400 1405	
ata aat caa gtt gaa aag gtt gtt aaa gaa acg gtt cat tat gtt ggc	4272
Ile Asn Gln Val Glu Lys Val Val Lys Glu Thr Val His Tyr Val Gly	
1410 1415 1420	
gcg ggt gat aag act cct gct gat caa gtt caa act tct aaa tgg att	4320
Ala Gly Asp Lys Thr Pro Ala Asp Gln Val Gln Thr Ser Lys Trp Ile	
1425 1430 1435 1440	
cgt act gtt act gtg gat gtc gtg act aat gaa gtt gtt cca gat gga	4368
Arg Thr Val Thr Val Asp Val Val Thr Asn Glu Val Val Pro Asp Gly	
1445 1450 1455	
gaa ttt act act gat tgg aca att cca agt gat gaa aaa agc act tac	4416
Glu Phe Thr Thr Asp Trp Thr Ile Pro Ser Asp Glu Lys Ser Thr Tyr	
1460 1465 1470	
gat caa gta gat act cca gta gtg aat ggc tac tat gct gat caa gct	4464
Asp Gln Val Asp Thr Pro Val Val Asn Gly Tyr Tyr Ala Asp Gln Ala	
1475 1480 1485	
aat gtt ccg gca act gct gta act caa aat gat att gaa aag act att	4512
Asn Val Pro Ala Thr Ala Val Thr Gln Asn Asp Ile Glu Lys Thr Ile	
1490 1495 1500	
act tat aaa caa att ggt aaa gta ata cca gtt gat cca tca ggg aat	4560
Thr Tyr Lys Gln Ile Gly Lys Val Ile Pro Val Asp Pro Ser Gly Asn	
1505 1510 1515 1520	
cag att ccg ggt att gat act cca cat ttc cct aac gat cca aat gat	4608
Gln Ile Pro Gly Ile Asp Thr Pro His Phe Pro Asn Asp Pro Asn Asp	
1525 1530 1535	
cca act aag gta att cca gga gaa aag cca tat gta cca gga tat cat	4656
Pro Thr Lys Val Ile Pro Gly Glu Lys Pro Tyr Val Pro Gly Tyr His	
1540 1545 1550	
cct gaa act gga aaa cca ggt gac gca gtt gat cca gct cca ggt gat	4704
Pro Glu Thr Gly Lys Pro Gly Asp Ala Val Asp Pro Ala Pro Gly Asp	

1555	1560	1565	
ccg agt aaa gat gtt gaa gtt cca tat act	ccg gaa act cca att gta	4752	
Pro Ser Lys Asp Val Glu Val Pro Tyr Thr	Pro Glu Thr Pro Ile Val		
1570	1580		
gat caa aaa gca gta gta aat tat att gat tct gat gaa gaa aac aaa	4800		
Asp Gln Lys Ala Val Val Asn Tyr Ile Asp Ser Asp Glu Glu Asn Lys			
1585	1590	1595	1600
gtg atc act tct tca ggt gat tta att gga aaa cca ggt gag cag att	4848		
Val Ile Thr Ser Ser Gly Asp Leu Ile Gly Lys Pro Gly Glu Gln Ile			
1605	1610	1615	
gat tat aca act ata cca aca att aca gat ctt act aat aaa gga tat	4896		
Asp Tyr Thr Thr Ile Pro Thr Ile Thr Asp Leu Thr Asn Lys Gly Tyr			
1620	1625	1630	
gtg ttg att tat gat ggc ttt cca act aga gta act ttt gat gat gat	4944		
Val Leu Ile Tyr Asp Gly Phe Pro Thr Arg Val Thr Phe Asp Asp Asp			
1635	1640	1645	
gat ggt att act caa ata ttc acg gtg gta tta aaa cat ggt aca caa	4992		
Asp Gly Ile Thr Gln Ile Phe Thr Val Val Leu Lys His Gly Thr Gln			
1650	1655	1660	
act gta acc cca gaa aaa cca gga ata cca ggc gat ccc att aat ccg	5040		
Thr Val Thr Pro Glu Lys Pro Gly Ile Pro Gly Asp Pro Ile Asn Pro			
1665	1670	1675	1680
aat gat cca gat gga cct aag tgg tca gat gaa act gga aaa gat agc	5088		
Asn Asp Pro Asp Gly Pro Lys Trp Ser Asp Glu Thr Gly Lys Asp Ser			
1685	1690	1695	
ttg att aag act ggt act caa aca att cat tat gaa gga gca ggt agt	5136		
Leu Ile Lys Thr Gly Thr Gln Thr Ile His Tyr Glu Gly Ala Gly Ser			
1700	1705	1710	
aaa act cca aca gat aac gtg caa aac ttc gag ttt act aga acc gct	5184		
Lys Thr Pro Thr Asp Asn Val Gln Asn Phe Glu Phe Thr Arg Thr Ala			
1715	1720	1725	
gtg att gac aaa gta act ggt gaa gta att agc act agt ggt tgg aat	5232		
Val Ile Asp Lys Val Thr Gly Glu Val Ile Ser Thr Ser Gly Trp Asn			
1730	1735	1740	
gta act agt tat aca ttt ggt aat gtt gat act cca ata gtt gag ggc	5280		
Val Thr Ser Tyr Thr Phe Gly Asn Val Asp Thr Pro Ile Val Glu Gly			
1745	1750	1755	1760
tat cat gca gat aaa cgg aat gct ggt ggt aca acg att aca cca gat	5328		
Tyr His Ala Asp Lys Arg Asn Ala Gly Gly Thr Thr Ile Thr Pro Asp			
1765	1770	1775	
gat ttg aac aag atg ctg gta gta aga tac aca cca aat ggt aaa att	5376		
Asp Leu Asn Lys Met Leu Val Val Arg Tyr Thr Pro Asn Gly Lys Ile			
1780	1785	1790	

att cca gtt gat cca gct ggc aat cca att ccg aat gta cca acg ccg Ile Pro Val Asp Pro Ala Gly Asn Pro Ile Pro Asn Val Pro Thr Pro 1795 1800 1805	5424
cag tac cca aca gat cca aca gat cca acg aag gta gtg ccg gat gaa Gln Tyr Pro Thr Asp Pro Thr Asp Pro Thr Lys Val Val Pro Asp Glu 1810 1815 1820	5472
cca gtg cca gct att cct ggc tat aga cca agc acg cca ata gtt aca Pro Val Pro Ala Ile Pro Gly Tyr Arg Pro Ser Thr Pro Ile Val Thr 1825 1830 1835 1840	5520
cca aca gat cct gat aaa gat act ccg gtt cca tat gct cca att caa Pro Thr Asp Pro Asp Lys Asp Thr Pro Val Pro Tyr Ala Pro Ile Gln 1845 1850 1855	5568
ggg tca ata caa gta att ttc cac gat gac acc agt aat caa act att Gly Ser Ile Gln Val Ile Phe His Asp Asp Thr Ser Asn Gln Thr Ile 1860 1865 1870	5616
cca gat gtt ggt tat aac tct gga gta caa gat gaa ggt act agg atc Pro Asp Val Gly Tyr Asn Ser Gly Val Gln Asp Glu Gly Thr Arg Ile 1875 1880 1885	5664
gat tac acg act aac aaa aat att acc gac ttg att aat aag ggg tat Asp Tyr Thr Thr Asn Lys Asn Ile Thr Asp Leu Ile Asn Lys Gly Tyr 1890 1895 1900	5712
gta tat gta gga aca gat ggt aat gtc cca gca gaa att gtt gct gat Val Tyr Val Gly Thr Asp Gly Asn Val Pro Ala Glu Ile Val Ala Asp 1905 1910 1915 1920	5760
caa aat att act ata aca gtc cac atg aag cat gga aca acc acg att Gln Asn Ile Thr Ile Thr Val His Met Lys His Gly Thr Thr Thr Ile 1925 1930 1935	5808
act cct gat cag cct ggt aag cca ggt gaa cca att aat cca aat gat Thr Pro Asp Gln Pro Gly Lys Pro Gly Glu Pro Ile Asn Pro Asn Asp 1940 1945 1950	5856
ccc aac ggg cct aag tgg cca agc gat act gac act aag gga ttg act Pro Asn Gly Pro Lys Trp Pro Ser Asp Thr Asp Thr Lys Gly Leu Thr 1955 1960 1965	5904
aaa caa ggt aat caa act att cat tac gtt tac gtt gat gga aat aag Lys Gln Gly Asn Gln Thr Ile His Tyr Val Tyr Val Asp Gly Asn Lys 1970 1975 1980	5952
gca gct gat gat aat gtt caa aat gtt aca ttt gtt cat aca ctt gta Ala Ala Asp Asp Asn Val Gln Asn Val Thr Phe Val His Thr Leu Val 1985 1990 1995 2000	6000
ttt gat aat gta act ggt caa gtg atc gat gat agg gga tgg act cct Phe Asp Asn Val Thr Gly Gln Val Ile Asp Asp Arg Gly Trp Thr Pro 2005 2010 2015	6048

gaa agt cat aag ttt aat aat gtg ttc tca cca acg att gat ggc cat	6096
Glu Ser His Lys Phe Asn Asn Val Phe Ser Pro Thr Ile Asp Gly His	
2020 2025 2030	
cat gca gat aaa atc gtg gtt gat ggt gtt aca gta act gtt gat aat	6144
His Ala Asp Lys Ile Val Val Asp Gly Val Thr Val Thr Val Asp Asn	
2035 2040 2045	
cca aca agc gaa act act gtg gtt tat gct aag aat ggt cag gtg att	6192
Pro Thr Ser Glu Thr Thr Val Val Tyr Ala Lys Asn Gly Gln Val Ile	
2050 2055 2060	
cgt gag cag caa gaa gtt aaa gct tcg cag atc gtt aag tat gta gat	6240
Arg Glu Gln Gln Glu Val Lys Ala Ser Gln Ile Val Lys Tyr Val Asp	
2065 2070 2075 2080	
gat gaa ggt aat gaa tta cat aaa tct gaa ttg caa gaa ttt aca ttt	6288
Asp Glu Gly Asn Glu Leu His Lys Ser Glu Leu Gln Glu Phe Thr Phe	
2085 2090 2095	
act tat aca ggt gat gct tat gat gaa gta act ggt gcg aag gtt caa	6336
Thr Tyr Thr Gly Asp Ala Tyr Asp Glu Val Thr Gly Ala Lys Val Gln	
2100 2105 2110	
act ggt act tgg aat gca ata agc aca gac ttt cct gtt gtt gat gtt	6384
Thr Gly Thr Trp Asn Ala Ile Ser Thr Asp Phe Pro Val Val Asp Val	
2115 2120 2125	
cca gta att acc ggt tac gta gct gtt tct ggc tat act aac aat aat	6432
Pro Val Ile Thr Gly Tyr Val Ala Val Ser Gly Tyr Thr Asn Asn Asn	
2130 2135 2140	
gga aaa tac atg gcc gga gga ttt act act act cgt gaa tct agt gaa	6480
Gly Lys Tyr Met Ala Gly Gly Phe Thr Thr Thr Arg Glu Ser Ser Glu	
2145 2150 2155 2160	
gat caa cgt aat cgt gta ttt aca gtt ctt tac aag aaa gtt ggt aat	6528
Asp Gln Arg Asn Arg Val Phe Thr Val Leu Tyr Lys Lys Val Gly Asn	
2165 2170 2175	
att gta ccg gta ggt cca gat ggt act aca cca att cca gat gca cca	6576
Ile Val Pro Val Gly Pro Asp Gly Thr Thr Pro Ile Pro Asp Ala Pro	
2180 2185 2190	
act ccg agt tac aag aat gat cca aca aat cca act aag gta ata cct	6624
Thr Pro Ser Tyr Lys Asn Asp Pro Thr Asn Pro Thr Lys Val Ile Pro	
2195 2200 2205	
gat gaa ccg gta cca aaa gtt cca gga tac aca cca aat act cca aca	6672
Asp Glu Pro Val Pro Lys Val Pro Gly Tyr Thr Pro Asn Thr Pro Thr	
2210 2215 2220	
gta aca cca gga gat cct act acg gat act cta gtt cca tat act cca	6720
Val Thr Pro Gly Asp Pro Thr Thr Asp Thr Leu Val Pro Tyr Thr Pro	
2225 2230 2235 2240	
gga aat cca att aca gat caa aaa gct gta gta aat tac att gat gct	6768

Gly Asn Pro Ile Thr Asp Gln Lys Ala Val Val Asn Tyr Ile Asp Ala	
2245 2250 2255	
gat gaa ggt aac aaa gta att att agt tca gga aat ttg att ggt aaa	6816
Asp Glu Gly Asn Lys Val Ile Ile Ser Ser Gly Asn Leu Ile Gly Lys	
2260 2265 2270	
gca gga gac aag gta gac tat aat act tct gat aca atc aaa aat ctt	6864
Ala Gly Asp Lys Val Asp Tyr Asn Thr Ser Asp Thr Ile Lys Asn Leu	
2275 2280 2285	
gaa aac aaa gga tat gta ttg gtt cat aat ggt ttt cca gat ggt gtg	6912
Glu Asn Lys Gly Tyr Val Leu Val His Asn Gly Phe Pro Asp Gly Val	
2290 2295 2300	
aca ttt gat aat gat gac agc acc att cag act tac aca gtt atc ttg	6960
Thr Phe Asp Asn Asp Asp Ser Thr Ile Gln Thr Tyr Thr Val Ile Leu	
2305 2310 2315 2320	
aag cat gga aca act act gta ata cct gat aaa cca ggt aag cca ggt	7008
Lys His Gly Thr Thr Thr Val Ile Pro Asp Lys Pro Gly Lys Pro Gly	
2325 2330 2335	
gaa cca att aac cct aac gat cca gat gga cct aag tgg cca gat aca	7056
Glu Pro Ile Asn Pro Asn Asp Pro Asp Gly Pro Lys Trp Pro Asp Thr	
2340 2345 2350	
acc ggt aag gat aac ttg agt aag act ggt act caa act att cat tat	7104
Thr Gly Lys Asp Asn Leu Ser Lys Thr Gly Thr Gln Thr Ile His Tyr	
2355 2360 2365	
act ggg gca gga aac aat act cct aag gat aat gta caa agc ttt acc	7152
Thr Gly Ala Gly Asn Asn Thr Pro Lys Asp Asn Val Gln Ser Phe Thr	
2370 2375 2380	
ttt act aga aca gct gta gtt gat aat gta act ggt aag gta att agt	7200
Phe Thr Arg Thr Ala Val Val Asp Asn Val Thr Gly Lys Val Ile Ser	
2385 2390 2395 2400	
acc ggt gct tgg aat gta acc agt cat aca ttt ggc aat gta gat acc	7248
Thr Gly Ala Trp Asn Val Thr Ser His Thr Phe Gly Asn Val Asp Thr	
2405 2410 2415	
cca gtg gtt gag ggc tac cat gca gat aag cgt act gca ggt aat act	7296
Pro Val Val Glu Gly Tyr His Ala Asp Lys Arg Thr Ala Gly Asn Thr	
2420 2425 2430	
aca att acc cca gag gac ttg aat aag atc gta act gta aac tac aca	7344
Thr Ile Thr Pro Glu Asp Leu Asn Lys Ile Val Thr Val Asn Tyr Thr	
2435 2440 2445	
gcc aac gga aag att att cca gta gat cca aat ggt aag cca ata cca	7392
Ala Asn Gly Lys Ile Ile Pro Val Asp Pro Asn Gly Lys Pro Ile Pro	
2450 2455 2460	
aac gta cca acg cca acc tac cca acc gat ccg aat gat cca act aag	7440
Asn Val Pro Thr Pro Thr Tyr Pro Thr Asp Pro Asn Asp Pro Thr Lys	

2465	2470	2475	2480	
gta gtg cca aat gaa ccg gta cca act atc cca ggt tac aag cca agt				7488
Val Val Pro Asn Glu Pro Val Pro Thr Ile Pro Gly Tyr Lys Pro Ser				
	2485	2490	2495	
gtg cca acg gtg act cca agc gat cca ggc aag gat acg cca gta cca				7536
Val Pro Thr Val Thr Pro Ser Asp Pro Gly Lys Asp Thr Pro Val Pro				
	2500	2505	2510	
tac gca cca caa act acg cca gta acg ccg aat ata ccg gta act cca				7584
Tyr Ala Pro Gln Thr Thr Pro Val Thr Pro Asn Ile Pro Val Thr Pro				
	2515	2520	2525	
aat gag cca agt act cca aca aca cca gat aca tca gct cca aca ccg				7632
Asn Glu Pro Ser Thr Pro Thr Thr Pro Asp Thr Ser Ala Pro Thr Pro				
	2530	2535	2540	
cac gga gaa gat gta ccg gta aca ccg aat gag cca gat aca ccg gct				7680
His Gly Glu Asp Val Pro Val Thr Pro Asn Glu Pro Asp Thr Pro Ala				
	2545	2550	2555	2560
cca gca cca cat ggt gaa aag ccg gaa gaa cca gac aga cca gct cca				7728
Pro Ala Pro His Gly Glu Lys Pro Glu Glu Pro Asp Arg Pro Ala Pro				
	2565	2570	2575	
gct cca cat gca cca aag gca cct act gct aag ggc aat aac act cca				7776
Ala Pro His Ala Pro Lys Ala Pro Thr Ala Lys Gly Asn Asn Thr Pro				
	2580	2585	2590	
gaa aag gaa gat aag act gtt cca act gca gct gct gta gtt aag aat				7824
Glu Lys Glu Asp Lys Thr Val Pro Thr Ala Ala Ala Val Val Lys Asn				
	2595	2600	2605	
gaa caa act cct gaa gca gag ctt cca caa aca ggt gaa aag aat gac				7872
Glu Gln Thr Pro Glu Ala Glu Leu Pro Gln Thr Gly Glu Lys Asn Asp				
	2610	2615	2620	
agt gca gct gca att cta gga gca acg gca gga atg ata ggt tta atc				7920
Ser Ala Ala Ala Ile Leu Gly Ala Thr Ala Gly Met Ile Gly Leu Ile				
	2625	2630	2635	2640
gga tta tca ggt gtt aag aag aaa aaa tca				7950
Gly Leu Ser Gly Val Lys Lys Lys Lys Ser				
	2645	2650		

<210> 28

<211> 2650

<212> PRT

<213> Lactobacillus acidophilus

<400> 28

Met Ile Ser Lys Asn Asn Arg Ile Lys Arg Met Glu Ala Thr Ser Glu

1

5

10

15

Arg Lys Gln His His Gly Ile Arg Thr Leu Ser Val Gly Ala Val Ser

20

25

30

Val Leu Leu Gly Thr Thr Leu Trp Ile Ser Ile Pro Thr Ser Thr Val
 35 40 45
 His Ala Asp Glu Ile Asn Ile Asp Asp Asn Gln Pro Lys Thr Asn Leu
 50 55 60
 Glu Ser Asn Glu Ser Ala Ser Thr Asp His Val Glu Lys Val Ile Val
 65 70 75 80
 Glu Gln Asn Gln Ser Ser Ser Glu Gly Ala Gln Gln Asp Ile Asn Ala
 85 90 95
 Ala Asn Asp Val Ser Ala Gln Asn Asp Gln Lys Ser Val Asn Lys Ile
 100 105 110
 Asn Asp Glu Ile Ile Lys Asn Glu Asn Val Asp Ala Asp Ile Lys Thr
 115 120 125
 Asn Thr Asp Asn Ser His Ala Glu Thr Ser Tyr Gly Gln Thr Glu Ser
 130 135 140
 Gln Glu Ile Ile Glu Asn Lys Gln Lys Thr Asp Val Glu Lys Asn Lys
 145 150 155 160
 Thr Gln Thr Thr Asp Asn Ile Thr Pro Val Glu Gln Thr Gly Asn Ser
 165 170 175
 Ser Glu Asn Thr Ser Thr Asn Val Thr Thr Gln Ser Pro Val Asp Asn
 180 185 190
 Ser Thr Asn Asn Asp Val Asn Val Asn Asn Ser Asn Leu Ala Asp Thr
 195 200 205
 Gln Ala Glu Leu Ile Asp Ser Asn Thr Gln Phe Tyr Glu Ser Ser Pro
 210 215 220
 Leu Ile Asp Gln Ile Gly Gln Gln Gly Lys Thr Thr Val Asn Ser Ser
 225 230 235 240
 Asn Asn Thr Ser Ser Lys Leu Asn Ile Asp Asp Leu Ser Pro Asp Leu
 245 250 255
 Ser Asp Glu Val Leu Lys Ala Asn Leu Thr Gln Gly Asn Gln Ile Leu
 260 265 270
 Leu Asn Gln Ser Asn Ser Ser Asp Thr Met Ala Gly Lys Asn Ala Asp
 275 280 285
 Pro Thr Lys Gln Leu Glu Ala Met Ala Arg Thr Ala Thr Leu Val Ala
 290 295 300
 Ala Ser Pro Asn Ala Asp Asn Tyr Thr Thr Val Asn Asn Tyr Asn Asp
 305 310 315 320
 Leu Gln Arg Ala Val Ser Asn Tyr Ser Val Ser Gly Val Asn Ile Asp
 325 330 335
 Gly Asp Ile Tyr Val Phe Gly Asn Leu Thr Ile Asn Arg Ala Phe Thr
 340 345 350
 Ile Lys Gly Thr Asn Asn Ala Lys Leu Asn Leu Asn Gln Asn Ala Ile
 355 360 365
 Ile Asn Asn Ser Thr Leu Thr Leu Glu Asp Ile Thr Val Asn Gly Ser
 370 375 380
 Ile Met Gly Asn Gly Thr Val Asn Ile Lys Gly Asp Val Ile Ser Asn
 385 390 395 400
 Val Asn Glu Ser Asn Gly Tyr Thr Leu Thr Asn Ser Glu Lys Ala Thr
 405 410 415
 Pro Gly Val Lys Val Asn Trp Thr Gln Thr Lys Gly Tyr Asn Ile Gln
 420 425 430
 Ser Ser Thr Val Asn Val Asp Asp Asn Ala Ser Leu Thr Ile Asn Arg
 435 440 445
 Ser Ser Val Gly Asp Gly Ile His Leu Leu Ser Asn Gly Ile Val Asn
 450 455 460
 Val Gly Asn Tyr Ser Gln Leu Thr Ile Asn Met Asn Thr Asn Asn Glu
 465 470 475 480
 Leu Gly Thr Gly Ala Thr Ala Arg Tyr His Asp Ala Gly Ile Phe Ala

- 125 -

Gln Asp Ser Gly Trp Thr Tyr Thr Asn Asp Gln Gly Gln Lys Val Thr
 945 950 955 960
 Asp Pro Tyr Ala Ser Val Thr Ser Pro Val Lys Glu Gly Tyr Ile Ile
 965 970 975
 Thr Ile Gln Ser Thr Asn Ala Pro Gly Val Thr Leu Gly Ala Asp Gly
 980 985 990
 Gln Thr Val Lys Ala Asn Phe Val Phe Asp Ala Ala Asn Asp Val Val
 995 1000 1005
 Gln Asn Gly Gln Leu Ser Ala Gly Tyr Arg Asn Gln Gly Ile Thr Gly
 1010 1015 1020
 Ile Pro Asp Asn Tyr Gln Thr Ile Val Val Tyr Lys Lys Ala Glu Lys
 1025 1030 1035 1040
 Gly Ser Val Gln Val Ile Phe Tyr Asp Asp Thr Thr Asn Asp Ala Ile
 1045 1050 1055
 Pro Ser Val Gly Phe Asn Ser Gly Thr Glu Glu Ala Gly Thr Pro Val
 1060 1065 1070
 Thr Tyr Thr Thr Ala Gln Asn Ile Ser Asp Leu Glu Lys Gln Gly Tyr
 1075 1080 1085
 Val Tyr Val Ser Thr Asp Gly Val Ile Pro Thr Thr Ile Pro Asn Asn
 1090 1095 1100
 Ala Thr Leu Ile Thr Val His Met Lys His Gly Thr Asn Pro Val Asn
 1105 1110 1115 1120
 Pro Asp Gln Pro Thr Asp Lys Tyr Thr Lys Glu Asp Leu Gln Lys Thr
 1125 1130 1135
 Val Thr Arg Thr Ile Asn Tyr Ile Asp Thr Ala Gly Asn Ile Ile Ala
 1140 1145 1150
 Asp Ser Val Thr Ser Thr Val Val Phe Thr Gly Ser Gly Thr Ile Asp
 1155 1160 1165
 Thr Val Thr Gly Asn Leu Val Thr Val Asp Ala Ser Gly Asn Ile Val
 1170 1175 1180
 Asp Gln Asn Gly Gln Leu Thr Trp Thr Tyr Ser Val Asp Gly Asp Ser
 1185 1190 1195 1200
 Ala Gln Ser Gly Asn Ser Tyr Thr Phe Ala Glu Thr Ala Ala Lys Pro
 1205 1210 1215
 Ser Ile Asp Tyr Asn Gly Ser Thr Tyr Asn Phe Val Ser Val Thr Pro
 1220 1225 1230
 Gly Asn Tyr Ser Ala Gly Asn Gly Ser Val Thr Ser Tyr Glu Val Asn
 1235 1240 1245
 Thr Asn Asn Ser His Asp Leu Thr Val Asp Val Ile Tyr Asn Glu Gly
 1250 1255 1260
 Ala Thr Tyr His Thr Gly Lys Thr Asp Thr Lys Asn Val Thr Arg Ile
 1265 1270 1275 1280
 Ile Asn Tyr Leu Asp Gly Lys Thr Asp Glu Lys Ile Pro Ile Asn Leu
 1285 1290 1295
 Ile Leu Ala Asn Pro Val Glu Gln Thr Val Ser Met Tyr Arg Thr Glu
 1300 1305 1310
 Ile Leu Asp Ser Thr Gly Lys Val Ile Gly Tyr Gly Thr Val Ser Gln
 1315 1320 1325
 Asp Gly Lys Met Tyr Thr Leu Asn Asn Asn Trp Ile Ile Asp Gly Ile
 1330 1335 1340
 Trp Glu Ser Val Asn Ser Pro Asp Leu Thr Thr Asn Gly Tyr Lys Ala
 1345 1350 1355 1360
 Pro Arg Phe Glu Asp Ser Ser Leu Ala Ala Ile Val Ala Glu Tyr Ile
 1365 1370 1375
 Val Asn Ala Asp Thr Lys Asn Ala Thr Val Asn Val Tyr Tyr Asp His
 1380 1385 1390
 Gln Val Ile Pro Ile Gly Pro Asp Thr Pro Asp Lys His Gly Val Asp

- 127 -

Gly Ser Ile Gln Val Ile Phe His Asp Asp Thr Ser Asn Gln Thr Ile
 1860 1865 1870
 Pro Asp Val Gly Tyr Asn Ser Gly Val Gln Asp Glu Gly Thr Arg Ile
 1875 1880 1885
 Asp Tyr Thr Thr Asn Lys Asn Ile Thr Asp Leu Ile Asn Lys Gly Tyr
 1890 1895 1900
 Val Tyr Val Gly Thr Asp Gly Asn Val Pro Ala Glu Ile Val Ala Asp
 1905 1910 1915 1920
 Gln Asn Ile Thr Ile Thr Val His Met Lys His Gly Thr Thr Thr Ile
 1925 1930 1935
 Thr Pro Asp Gln Pro Gly Lys Pro Gly Glu Pro Ile Asn Pro Asn Asp
 1940 1945 1950
 Pro Asn Gly Pro Lys Trp Pro Ser Asp Thr Asp Thr Lys Gly Leu Thr
 1955 1960 1965
 Lys Gln Gly Asn Gln Thr Ile His Tyr Val Tyr Val Asp Gly Asn Lys
 1970 1975 1980
 Ala Ala Asp Asp Asn Val Gln Asn Val Thr Phe Val His Thr Leu Val
 1985 1990 1995 2000
 Phe Asp Asn Val Thr Gly Gln Val Ile Asp Asp Arg Gly Trp Thr Pro
 2005 2010 2015
 Glu Ser His Lys Phe Asn Asn Val Phe Ser Pro Thr Ile Asp Gly His
 2020 2025 2030
 His Ala Asp Lys Ile Val Val Asp Gly Val Thr Val Thr Val Asp Asn
 2035 2040 2045
 Pro Thr Ser Glu Thr Thr Val Val Tyr Ala Lys Asn Gly Gln Val Ile
 2050 2055 2060
 Arg Glu Gln Gln Glu Val Lys Ala Ser Gln Ile Val Lys Tyr Val Asp
 2065 2070 2075 2080
 Asp Glu Gly Asn Glu Leu His Lys Ser Glu Leu Gln Glu Phe Thr Phe
 2085 2090 2095
 Thr Tyr Thr Gly Asp Ala Tyr Asp Glu Val Thr Gly Ala Lys Val Gln
 2100 2105 2110
 Thr Gly Thr Trp Asn Ala Ile Ser Thr Asp Phe Pro Val Val Asp Val
 2115 2120 2125
 Pro Val Ile Thr Gly Tyr Val Ala Val Ser Gly Tyr Thr Asn Asn Asn
 2130 2135 2140
 Gly Lys Tyr Met Ala Gly Gly Phe Thr Thr Thr Arg Glu Ser Ser Glu
 2145 2150 2155 2160
 Asp Gln Arg Asn Arg Val Phe Thr Val Leu Tyr Lys Lys Val Gly Asn
 2165 2170 2175
 Ile Val Pro Val Gly Pro Asp Gly Thr Thr Pro Ile Pro Asp Ala Pro
 2180 2185 2190
 Thr Pro Ser Tyr Lys Asn Asp Pro Thr Asn Pro Thr Lys Val Ile Pro
 2195 2200 2205
 Asp Glu Pro Val Pro Lys Val Pro Gly Tyr Thr Pro Asn Thr Pro Thr
 2210 2215 2220
 Val Thr Pro Gly Asp Pro Thr Thr Asp Thr Leu Val Pro Tyr Thr Pro
 2225 2230 2235 2240
 Gly Asn Pro Ile Thr Asp Gln Lys Ala Val Val Asn Tyr Ile Asp Ala
 2245 2250 2255
 Asp Glu Gly Asn Lys Val Ile Ile Ser Ser Gly Asn Leu Ile Gly Lys
 2260 2265 2270
 Ala Gly Asp Lys Val Asp Tyr Asn Thr Ser Asp Thr Ile Lys Asn Leu
 2275 2280 2285
 Glu Asn Lys Gly Tyr Val Leu Val His Asn Gly Phe Pro Asp Gly Val
 2290 2295 2300
 Thr Phe Asp Asn Asp Asp Ser Thr Ile Gln Thr Tyr Thr Val Ile Leu

```

2305          2310          2315          2320
Lys His Gly Thr Thr Thr Val Ile Pro Asp Lys Pro Gly Lys Pro Gly
          2325          2330          2335
Glu Pro Ile Asn Pro Asn Asp Pro Asp Gly Pro Lys Trp Pro Asp Thr
          2340          2345          2350
Thr Gly Lys Asp Asn Leu Ser Lys Thr Gly Thr Gln Thr Ile His Tyr
          2355          2360          2365
Thr Gly Ala Gly Asn Asn Thr Pro Lys Asp Asn Val Gln Ser Phe Thr
          2370          2375          2380
Phe Thr Arg Thr Ala Val Val Asp Asn Val Thr Gly Lys Val Ile Ser
2385          2390          2395          2400
Thr Gly Ala Trp Asn Val Thr Ser His Thr Phe Gly Asn Val Asp Thr
          2405          2410          2415
Pro Val Val Glu Gly Tyr His Ala Asp Lys Arg Thr Ala Gly Asn Thr
          2420          2425          2430
Thr Ile Thr Pro Glu Asp Leu Asn Lys Ile Val Thr Val Asn Tyr Thr
          2435          2440          2445
Ala Asn Gly Lys Ile Ile Pro Val Asp Pro Asn Gly Lys Pro Ile Pro
2450          2455          2460
Asn Val Pro Thr Pro Thr Tyr Pro Thr Asp Pro Asn Asp Pro Thr Lys
2465          2470          2475          2480
Val Val Pro Asn Glu Pro Val Pro Thr Ile Pro Gly Tyr Lys Pro Ser
          2485          2490          2495
Val Pro Thr Val Thr Pro Ser Asp Pro Gly Lys Asp Thr Pro Val Pro
          2500          2505          2510
Tyr Ala Pro Gln Thr Thr Pro Val Thr Pro Asn Ile Pro Val Thr Pro
          2515          2520          2525
Asn Glu Pro Ser Thr Pro Thr Thr Pro Asp Thr Ser Ala Pro Thr Pro
2530          2535          2540
His Gly Glu Asp Val Pro Val Thr Pro Asn Glu Pro Asp Thr Pro Ala
2545          2550          2555          2560
Pro Ala Pro His Gly Glu Lys Pro Glu Glu Pro Asp Arg Pro Ala Pro
          2565          2570          2575
Ala Pro His Ala Pro Lys Ala Pro Thr Ala Lys Gly Asn Asn Thr Pro
          2580          2585          2590
Glu Lys Glu Asp Lys Thr Val Pro Thr Ala Ala Ala Val Val Lys Asn
          2595          2600          2605
Glu Gln Thr Pro Glu Ala Glu Leu Pro Gln Thr Gly Glu Lys Asn Asp
2610          2615          2620
Ser Ala Ala Ala Ile Leu Gly Ala Thr Ala Gly Met Ile Gly Leu Ile
2625          2630          2635          2640
Gly Leu Ser Gly Val Lys Lys Lys Lys Ser
          2645          2650

```

<210> 29

<211> 1038

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1018 - mucus binding protein

<220>

<221> CDS

<222> (1)...(1038)

<400> 29

ttg att caa tac gta ggt gaa aat ggt gaa gtt ata agt gaa gat act	48
Met Ile Gln Tyr Val Gly Glu Asn Gly Glu Val Ile Ser Glu Asp Thr	
1 5 10 15	
ttt gtt gga aaa gat caa gaa aaa caa gat gtt acc ata aat tat cca	96
Phe Val Gly Lys Asp Gln Glu Lys Gln Asp Val Thr Ile Asn Tyr Pro	
20 25 30	
aaa gga tgg att tta tca gat caa gaa gta cca act aaa atc caa att	144
Lys Gly Trp Ile Leu Ser Asp Gln Glu Val Pro Thr Lys Ile Gln Ile	
35 40 45	
aat ggt ggg att aca caa att cat att aaa cat gca aaa aca gtg gta	192
Asn Gly Ile Thr Gln Ile His Ile Lys His Ala Lys Thr Val Val	
50 55 60	
aaa gct gat gat cca aaa act act gat gat gtt tta cct cat aat act	240
Lys Ala Asp Asp Pro Lys Thr Thr Asp Asp Val Leu Pro His Asn Thr	
65 70 75 80	
gat gca cat tat cca gat gga gtg aaa aaa gaa gat ctg aat aaa act	288
Asp Ala His Tyr Pro Asp Gly Val Lys Lys Glu Asp Leu Asn Lys Thr	
85 90 95	
att aca aga aag atc att atc aat ttg cca aat ggt gaa gta aag act	336
Ile Thr Arg Lys Ile Ile Ile Asn Leu Pro Asn Gly Glu Val Lys Thr	
100 105 110	
agg gtg caa ata gct aat ttt act agg gat gcg gaa gtt gat gaa gct	384
Arg Val Gln Ile Ala Asn Phe Thr Arg Asp Ala Glu Val Asp Glu Ala	
115 120 125	
acc gga gat att cat tat ttg aag tgg aga ttg gat aaa aat ggg cta	432
Thr Gly Asp Ile His Tyr Leu Lys Trp Arg Leu Asp Lys Asn Gly Leu	
130 135 140	
aca gaa tat cta gtg cct aaa tat cag ggc tat aag gct aat ttg gaa	480
Thr Glu Tyr Leu Val Pro Lys Tyr Gln Gly Tyr Lys Ala Asn Leu Glu	
145 150 155 160	
aaa gtt aat tat gag ata cca aat gta aat agc cac tat gat gat tta	528
Lys Val Asn Tyr Glu Ile Pro Asn Val Asn Ser His Tyr Asp Asp Leu	
165 170 175	
gtg att gaa tat gtt gct gac aaa ctt tct gat gat tca cca acg gat	576
Val Ile Glu Tyr Val Ala Asp Lys Leu Ser Asp Asp Ser Pro Thr Asp	
180 185 190	
tca cat gac gat gtt att aat act aac tcg agt ctt gat aat ttt ctg	624
Ser His Asp Asp Val Ile Asn Thr Asn Ser Ser Leu Asp Asn Phe Leu	
195 200 205	
tca gaa aaa gat cga gaa gat aat aat agt caa tat gaa cga tta aat	672

```

Ser Glu Lys Asp Arg Glu Asp Asn Asn Ser Gln Tyr Glu Arg Leu Asn
210                215                220

caa aat gat gat ata ttt aat gca cca tta ggt aag gcg gaa gta cca 720
Gln Asn Asp Asp Ile Phe Asn Ala Pro Leu Gly Lys Ala Glu Val Pro
225                230                235                240

gat aaa cgg tca gat aag aag aca caa tca tat aaa aac cat cat aaa 768
Asp Lys Arg Ser Asp Lys Lys Thr Gln Ser Tyr Lys Asn His His Lys
245                250                255

gtg ata agt aat gcc aat att act cag ttt aac aaa tat gaa tct tcg 816
Val Ile Ser Asn Ala Asn Ile Thr Gln Phe Asn Lys Tyr Glu Ser Ser
260                265                270

aaa aaa tta ata aca aat gat cgg att cca aat agc act gag aaa gat 864
Lys Lys Leu Ile Thr Asn Asp Arg Ile Pro Asn Ser Thr Glu Lys Asp
275                280                285

aaa aaa gtt aat aaa gtt gaa aat ata aaa tta cgc cag aaa ata tca 912
Lys Lys Val Asn Lys Val Glu Asn Ile Lys Leu Arg Gln Lys Ile Ser
290                295                300

ttt aaa aat agt aca aaa ata tta cct gaa act ggt gaa aat aat caa 960
Phe Lys Asn Ser Thr Lys Ile Leu Pro Glu Thr Gly Glu Asn Asn Gln
305                310                315                320

tat cta cca tgg atg ggt att tta ctt tcc atg ttg ggg tta aat ggt 1008
Tyr Leu Pro Trp Met Gly Ile Leu Leu Ser Met Leu Gly Leu Asn Gly
325                330                335

tta gtc gtt aga cgt aaa aag aag atg aaa 1038
Leu Val Val Arg Arg Lys Lys Lys Met Lys
340                345

```

<210> 30

<211> 346

<212> PRT

<213> Lactobacillus acidophilus

<400> 30

```

Met Ile Gln Tyr Val Gly Glu Asn Gly Glu Val Ile Ser Glu Asp Thr
1          5          10          15
Phe Val Gly Lys Asp Gln Glu Lys Gln Asp Val Thr Ile Asn Tyr Pro
20          25          30
Lys Gly Trp Ile Leu Ser Asp Gln Glu Val Pro Thr Lys Ile Gln Ile
35          40          45
Asn Gly Gly Ile Thr Gln Ile His Ile Lys His Ala Lys Thr Val Val
50          55          60
Lys Ala Asp Asp Pro Lys Thr Thr Asp Asp Val Leu Pro His Asn Thr
65          70          75          80
Asp Ala His Tyr Pro Asp Gly Val Lys Lys Glu Asp Leu Asn Lys Thr
85          90          95
Ile Thr Arg Lys Ile Ile Ile Asn Leu Pro Asn Gly Glu Val Lys Thr
100         105         110
Arg Val Gln Ile Ala Asn Phe Thr Arg Asp Ala Glu Val Asp Glu Ala

```

```

      115      120      125
Thr Gly Asp Ile His Tyr Leu Lys Trp Arg Leu Asp Lys Asn Gly Leu
      130      135      140
Thr Glu Tyr Leu Val Pro Lys Tyr Gln Gly Tyr Lys Ala Asn Leu Glu
145      150      155      160
Lys Val Asn Tyr Glu Ile Pro Asn Val Asn Ser His Tyr Asp Asp Leu
      165      170      175
Val Ile Glu Tyr Val Ala Asp Lys Leu Ser Asp Asp Ser Pro Thr Asp
      180      185      190
Ser His Asp Asp Val Ile Asn Thr Asn Ser Ser Leu Asp Asn Phe Leu
      195      200      205
Ser Glu Lys Asp Arg Glu Asp Asn Asn Ser Gln Tyr Glu Arg Leu Asn
      210      215      220
Gln Asn Asp Asp Ile Phe Asn Ala Pro Leu Gly Lys Ala Glu Val Pro
225      230      235      240
Asp Lys Arg Ser Asp Lys Lys Thr Gln Ser Tyr Lys Asn His His Lys
      245      250      255
Val Ile Ser Asn Ala Asn Ile Thr Gln Phe Asn Lys Tyr Glu Ser Ser
      260      265      270
Lys Lys Leu Ile Thr Asn Asp Arg Ile Pro Asn Ser Thr Glu Lys Asp
      275      280      285
Lys Lys Val Asn Lys Val Glu Asn Ile Lys Leu Arg Gln Lys Ile Ser
      290      295      300
Phe Lys Asn Ser Thr Lys Ile Leu Pro Glu Thr Gly Glu Asn Asn Gln
305      310      315      320
Tyr Leu Pro Trp Met Gly Ile Leu Leu Ser Met Leu Gly Leu Asn Gly
      325      330      335
Leu Val Val Arg Arg Lys Lys Lys Met Lys
      340      345

```

```

<210> 31
<211> 882
<212> DNA
<213> Lactobacillus acidophilus

```

```

<220>
<221> misc_feature
<222> (0)...(0)
<223> ORF 1017 - mucus binding protein

```

```

<220>
<221> CDS
<222> (1)...(882)

```

```

<400> 31
atg att ggt caa aca gat caa aat ata gtc atc act tat agc gct aat 48
Met Ile Gly Gln Thr Asp Gln Asn Ile Val Ile Thr Tyr Ser Ala Asn
1 5 10 15

att caa caa gtt aaa att cta tat gtt gat gaa aaa ggt agt gaa gtt 96
Ile Gln Gln Val Lys Ile Leu Tyr Val Asp Glu Lys Gly Ser Glu Val
20 25 30

tca tca atg tta ttg aag ggg aat act gat caa aca gtt aat gtc agt 144
Ser Ser Met Leu Leu Lys Gly Asn Thr Asp Gln Thr Val Asn Val Ser

```

35	40	45	
tat tca gta cca gac cat	tgg ata gct atc tct	ggt caa gat agt cca	192
Tyr Ser Val Pro Asp His	Trp Ile Ala Ile Ser	Gly Gln Asp Ser Pro	
50	55	60	
ttg caa tat aca ttt aag	gca aaa gat aat aaa	aat att gta att aga	240
Leu Gln Tyr Thr Phe Lys	Ala Lys Asp Asn Lys	Asn Ile Val Ile Arg	
65	70	75	80
att ggt cat aag tta gaa	gat caa gaa aat gat	atc cat aaa ata att	288
Ile Gly His Lys Leu Glu	Asp Gln Glu Asn Asp	Ile His Lys Ile Ile	
85	90	95	
cgc aat gtt aat att gtg	aat ccc gat ggt agt	gta gct aaa gta tcg	336
Arg Asn Val Asn Ile Val	Asn Pro Asp Gly Ser	Val Ala Lys Val Ser	
100	105	110	
caa aca gct atc ttt aca	aga gtt cat caa cgt	gat gaa gta act ggg	384
Gln Thr Ala Ile Phe Thr	Arg Val His Gln Arg	Asp Glu Val Thr Gly	
115	120	125	
gaa gaa gtt tat ggt aac	tgg gat aag ata tcg	caa gat ttt aat gct	432
Glu Glu Val Tyr Gly Asn	Trp Asp Lys Ile Ser	Gln Asp Phe Asn Ala	
130	135	140	
ata gat ata ccc aaa ata	ttt ggt tat act gca	act tct tca gtt gga	480
Ile Asp Ile Pro Lys Ile	Phe Gly Tyr Thr Ala	Thr Ser Ser Val Gly	
145	150	155	160
aag atg act gta act ccg	gat tca cag agt gaa	aat ata act att act	528
Lys Met Thr Val Thr Pro	Asp Ser Gln Ser Glu	Asn Ile Thr Ile Thr	
165	170	175	
tat acg gct gat att caa	aat aat aaa att gtg	ata att gat gat gaa	576
Tyr Thr Ala Asp Ile Gln	Asn Asn Lys Ile Val	Ile Ile Asp Asp Glu	
180	185	190	
agc cat gga tcc caa att	aat aca gtt ggg ttt	act ggt aaa act ggg	624
Ser His Gly Ser Gln Ile	Asn Thr Val Gly Phe	Thr Gly Lys Thr Gly	
195	200	205	
aag agt att gca tgg caa	gta act ata cca gaa	aat tat gat tta gct	672
Lys Ser Ile Ala Trp Gln	Val Thr Ile Pro Glu	Asn Tyr Asp Leu Ala	
210	215	220	
gct ggt ggt aag ata tca	ggg aat tat act ttt	aat gct gtg aat caa	720
Ala Gly Gly Lys Ile Ser	Gly Asn Tyr Thr Phe	Asn Ala Val Asn Gln	
225	230	235	240
atc cca att gaa gtt cat	gtt cgg cat aag cat	gta caa gat gac gaa	768
Ile Pro Ile Glu Val His	Val Arg His Lys His	Val Gln Asp Asp Glu	
245	250	255	
tct aaa tca gtt aca cga	acc atc gtt act aac	ttg cca gga tta gat	816
Ser Lys Ser Val Thr Arg	Thr Ile Val Thr Asn	Leu Pro Gly Leu Asp	
260	265	270	

aaa tct gaa att gtt caa act gta aca ttt agt aga att ata gat aag 864
 Lys Ser Glu Ile Val Gln Thr Val Thr Phe Ser Arg Ile Ile Asp Lys
 275 280 285

gat tta gta gat ggt aat 882
 Asp Leu Val Asp Gly Asn
 290

<210> 32

<211> 294

<212> PRT

<213> Lactobacillus acidophilus

<400> 32

Met Ile Gly Gln Thr Asp Gln Asn Ile Val Ile Thr Tyr Ser Ala Asn
 1 5 10 15
 Ile Gln Gln Val Lys Ile Leu Tyr Val Asp Glu Lys Gly Ser Glu Val
 20 25 30
 Ser Ser Met Leu Leu Lys Gly Asn Thr Asp Gln Thr Val Asn Val Ser
 35 40 45
 Tyr Ser Val Pro Asp His Trp Ile Ala Ile Ser Gly Gln Asp Ser Pro
 50 55 60
 Leu Gln Tyr Thr Phe Lys Ala Lys Asp Asn Lys Asn Ile Val Ile Arg
 65 70 75 80
 Ile Gly His Lys Leu Glu Asp Gln Glu Asn Asp Ile His Lys Ile Ile
 85 90 95
 Arg Asn Val Asn Ile Val Asn Pro Asp Gly Ser Val Ala Lys Val Ser
 100 105 110
 Gln Thr Ala Ile Phe Thr Arg Val His Gln Arg Asp Glu Val Thr Gly
 115 120 125
 Glu Glu Val Tyr Gly Asn Trp Asp Lys Ile Ser Gln Asp Phe Asn Ala
 130 135 140
 Ile Asp Ile Pro Lys Ile Phe Gly Tyr Thr Ala Thr Ser Ser Val Gly
 145 150 155 160
 Lys Met Thr Val Thr Pro Asp Ser Gln Ser Glu Asn Ile Thr Ile Thr
 165 170 175
 Tyr Thr Ala Asp Ile Gln Asn Asn Lys Ile Val Ile Ile Asp Asp Glu
 180 185 190
 Ser His Gly Ser Gln Ile Asn Thr Val Gly Phe Thr Gly Lys Thr Gly
 195 200 205
 Lys Ser Ile Ala Trp Gln Val Thr Ile Pro Glu Asn Tyr Asp Leu Ala
 210 215 220
 Ala Gly Gly Lys Ile Ser Gly Asn Tyr Thr Phe Asn Ala Val Asn Gln
 225 230 235 240
 Ile Pro Ile Glu Val His Val Arg His Lys His Val Gln Asp Asp Glu
 245 250 255
 Ser Lys Ser Val Thr Arg Thr Ile Val Thr Asn Leu Pro Gly Leu Asp
 260 265 270
 Lys Ser Glu Ile Val Gln Thr Val Thr Phe Ser Arg Ile Ile Asp Lys
 275 280 285
 Asp Leu Val Asp Gly Asn
 290

<210> 33

<211> 555
 <212> DNA
 <213> Lactobacillus acidophilus

 <220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1016 - mucus binding protein

<220>
 <221> CDS
 <222> (1)...(555)

<400> 33
 atg atc ttt ggt gca gat aat aaa gta gct gca att aat gca gtt gaa 48
 Met Ile Phe Gly Ala Asp Asn Lys Val Ala Ala Ile Asn Ala Val Glu
 1 5 10 15

 gta act agt gat aca gct gat att gta gtt aat atc act tat gta gcc 96
 Val Thr Ser Asp Thr Ala Asp Ile Val Val Asn Ile Thr Tyr Val Ala
 20 25 30

 gat aat cag tat atg cat atc atc tat acg gat agg aat gat gaa gtg 144
 Asp Asn Gln Tyr Met His Ile Ile Tyr Thr Asp Arg Asn Asp Glu Val
 35 40 45

 gtt aga att gat aaa gtt agt agt caa aca gat caa act gta aat gtt 192
 Val Arg Ile Asp Lys Val Ser Ser Gln Thr Asp Gln Thr Val Asn Val
 50 55 60

 aat tct aat gta cct aat ggt tgg aaa ttg ctc gat aat gaa aaa att 240
 Asn Ser Asn Val Pro Asn Gly Trp Lys Leu Leu Asp Asn Glu Lys Ile
 65 70 75 80

 cca gca act att cac ttt act gga acg cca ata gct gat atc aag tta 288
 Pro Ala Thr Ile His Phe Thr Gly Thr Pro Ile Ala Asp Ile Lys Leu
 85 90 95

 aca att gaa cat agt ttt act aag gtt act cat gac aag cca gtt gag 336
 Thr Ile Glu His Ser Phe Thr Lys Val Thr His Asp Lys Pro Val Glu
 100 105 110

 tta aat agt aag act att aca ggt caa aca att agt ggt gct cat caa 384
 Leu Asn Ser Lys Thr Ile Thr Gly Gln Thr Ile Ser Gly Ala His Gln
 115 120 125

 aat gat ttg aat cag gtg atc act cgt aaa att aca ata tat gaa cct 432
 Asn Asp Leu Asn Gln Val Ile Thr Arg Lys Ile Thr Ile Tyr Glu Pro
 130 135 140

 gat aaa aag gta caa aca att aaa caa att gct aga att tac cgt aat 480
 Asp Lys Lys Val Gln Thr Ile Lys Gln Ile Ala Arg Ile Tyr Arg Asn
 145 150 155 160

 gcc atg ata gat aat gtt act ggt aaa gta aaa tat aat gat tgg tca 528
 Ala Met Ile Asp Asn Val Thr Gly Lys Val Lys Tyr Asn Asp Trp Ser

165 170 175 555
 aac aga tca aaa tat agt cat cac tta
 Asn Arg Ser Lys Tyr Ser His His Leu
 180 185

<210> 34
 <211> 185
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 34
 Met Ile Phe Gly Ala Asp Asn Lys Val Ala Ala Ile Asn Ala Val Glu
 1 5 10 15
 Val Thr Ser Asp Thr Ala Asp Ile Val Val Asn Ile Thr Tyr Val Ala
 20 25 30
 Asp Asn Gln Tyr Met His Ile Ile Tyr Thr Asp Arg Asn Asp Glu Val
 35 40 45
 Val Arg Ile Asp Lys Val Ser Ser Gln Thr Asp Gln Thr Val Asn Val
 50 55 60
 Asn Ser Asn Val Pro Asn Gly Trp Lys Leu Leu Asp Asn Glu Lys Ile
 65 70 75 80
 Pro Ala Thr Ile His Phe Thr Gly Thr Pro Ile Ala Asp Ile Lys Leu
 85 90 95
 Thr Ile Glu His Ser Phe Thr Lys Val Thr His Asp Lys Pro Val Glu
 100 105 110
 Leu Asn Ser Lys Thr Ile Thr Gly Gln Thr Ile Ser Gly Ala His Gln
 115 120 125
 Asn Asp Leu Asn Gln Val Ile Thr Arg Lys Ile Thr Ile Tyr Glu Pro
 130 135 140
 Asp Lys Lys Val Gln Thr Ile Lys Gln Ile Ala Arg Ile Tyr Arg Asn
 145 150 155 160
 Ala Met Ile Asp Asn Val Thr Gly Lys Val Lys Tyr Asn Asp Trp Ser
 165 170 175
 Asn Arg Ser Lys Tyr Ser His His Leu
 180 185

<210> 35
 <211> 1524
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 909 - mucus binding precursor

<220>
 <221> CDS
 <222> (1)...(1524)

<400> 35 48
 atg agc aaa ata aca ttt ttt tct aaa aca ata cat ata aaa att aag
 Met Ser Lys Ile Thr Phe Phe Ser Lys Thr Ile His Ile Lys Ile Lys

1	5	10	15	
ttt gtt gat atg gat aat tgg agt ccg atc ctt aag cct att gaa gtt				96
Phe Val Asp Met Asp Asn Trp Ser Pro Ile Leu Lys Pro Ile Glu Val				
	20	25	30	
aaa ggt aaa gaa gga aaa aca att gat tgt agt ata aat aat caa ctt				144
Lys Gly Lys Glu Gly Lys Thr Ile Asp Cys Ser Ile Asn Asn Gln Leu				
	35	40	45	
gaa gag gca aaa aaa caa gga tat gaa ctt gct agt aat gaa ctt gaa				192
Glu Glu Ala Lys Lys Gln Gly Tyr Glu Leu Ala Ser Asn Glu Leu Glu				
	50	55	60	
caa gat ggt cag aga aaa gaa ttt tct agt gat aat gat gaa tat ata				240
Gln Asp Gly Gln Arg Lys Glu Phe Ser Ser Asp Asn Asp Glu Tyr Ile				
	65	70	75	80
att ggc ttt cat cat ggt caa gct att att gat gct atg cat cct ggc				288
Ile Gly Phe His His Gly Gln Ala Ile Ile Asp Ala Met His Pro Gly				
	85	90	95	
tat gga tat aca aag ggt caa tta gag aaa aca att act caa ata gtt				336
Tyr Gly Tyr Thr Lys Gly Gln Leu Glu Lys Thr Ile Thr Gln Ile Val				
	100	105	110	
cat tat cag gga gca tca agt aag acg cca att gac aat aag atc tca				384
His Tyr Gln Gly Ala Ser Ser Lys Thr Pro Ile Asp Asn Lys Ile Ser				
	115	120	125	
aga gtt ctt agg cga aaa tta ata att gat aaa gta aat gga aag ata				432
Arg Val Leu Arg Arg Lys Leu Ile Ile Asp Lys Val Asn Gly Lys Ile				
	130	135	140	
att aat gat agt ggc tgg aat aat caa gga tat ttt aaa ttg att gct				480
Ile Asn Asp Ser Gly Trp Asn Asn Gln Gly Tyr Phe Lys Leu Ile Ala				
	145	150	155	160
act cct gtg gtc cct gga ttc aaa gca gat cat tta att gca ggt ggt				528
Thr Pro Val Val Pro Gly Phe Lys Ala Asp His Leu Ile Ala Gly Gly				
	165	170	175	
ggc aaa att gat cca cac aat ccg gtt caa aac tat gtg gta gag tat				576
Gly Lys Ile Asp Pro His Asn Pro Val Gln Asn Tyr Val Val Glu Tyr				
	180	185	190	
gct tta aat aat gag cca gtg tct gaa agg caa act gct aag att caa				624
Ala Leu Asn Asn Glu Pro Val Ser Glu Arg Gln Thr Ala Lys Ile Gln				
	195	200	205	
tac gtt gat ata tta aac aat aat cgg gta atc tta agt gat gaa gtg				672
Tyr Val Asp Ile Leu Asn Asn Asn Arg Val Ile Leu Ser Asp Glu Val				
	210	215	220	
gta gga aaa gca aat gat tgg att gaa tat gat cct cag aat aga atc				720
Val Gly Lys Ala Asn Asp Trp Ile Glu Tyr Asp Pro Gln Asn Arg Ile				
	225	230	235	240

act gag tta cga aaa aat gga tat gaa tta gtt gat aat gcg ttt aat	768
Thr Glu Leu Arg Lys Asn Gly Tyr Glu Leu Val Asp Asn Ala Phe Asn	
245 250 255	
gca aat gga aac gtt caa ttt ttt ggt gat agc aat gaa gaa ttt gtt	816
Ala Asn Gly Asn Val Gln Phe Phe Gly Asp Ser Asn Glu Glu Phe Val	
260 265 270	
ttc atc att aca atg aag cat acc ttt atc aat gtt gat att aag cat	864
Phe Ile Ile Thr Met Lys His Thr Phe Ile Asn Val Asp Ile Lys His	
275 280 285	
cct ttt gat aag ata ctt cct aaa cag tat ctt aaa gca gtt aat ttt	912
Pro Phe Asp Lys Ile Leu Pro Lys Gln Tyr Leu Lys Ala Val Asn Phe	
290 295 300	
aga gta gtt ttt caa ggg gca ggt att ttg act ccg gat gaa att acg	960
Arg Val Val Phe Gln Gly Ala Gly Ile Leu Thr Pro Asp Glu Ile Thr	
305 310 315 320	
caa aca gca att tta aat aga agt tta aag gta att cct gaa act gga	1008
Gln Thr Ala Ile Leu Asn Arg Ser Leu Lys Val Ile Pro Glu Thr Gly	
325 330 335	
aga gta tta tct aaa aca aga tgg ttt agt gat att gac tct ttt cat	1056
Arg Val Leu Ser Lys Thr Arg Trp Phe Ser Asp Ile Asp Ser Phe His	
340 345 350	
gat gtt aaa gtt cca gtt gtt gaa ggt ttc gta gct gat aaa cta aaa	1104
Asp Val Lys Val Pro Val Val Glu Gly Phe Val Ala Asp Lys Leu Lys	
355 360 365	
ata aag gca cca gaa atc gtg cca agt gat att ata gtt act gtc aat	1152
Ile Lys Ala Pro Glu Ile Val Pro Ser Asp Ile Ile Val Thr Val Asn	
370 375 380	
tat att gat gcg atg gtg gcc aag ctt aaa aaa gca gaa aaa aga ttg	1200
Tyr Ile Asp Ala Met Val Ala Lys Leu Lys Lys Ala Glu Lys Arg Leu	
385 390 395 400	
cag gaa caa aaa aag tta gaa atg gca atc ata act ttt att gat att	1248
Gln Glu Gln Lys Lys Leu Glu Met Ala Ile Ile Thr Phe Ile Asp Ile	
405 410 415	
gac aaa aat ggt aca caa att atg aca tct ggt gca ata act gga caa	1296
Asp Lys Asn Gly Thr Gln Ile Met Thr Ser Gly Ala Ile Thr Gly Gln	
420 425 430	
cct gga gaa agt att aat gat tct tat agt act aaa gaa cct tta aaa	1344
Pro Gly Glu Ser Ile Asn Asp Ser Tyr Ser Thr Lys Glu Pro Leu Lys	
435 440 445	
act ttg aag aat gaa ggg tat gaa gtt gtc ttt aat aat ttc gat att	1392
Thr Leu Lys Asn Glu Gly Tyr Glu Val Val Phe Asn Asn Phe Asp Ile	
450 455 460	

```

cca ggt atg gtt caa cgt ttt gat aat aat gat tta cag cca caa gta 1440
Pro Gly Met Val Gln Arg Phe Asp Asn Asn Asp Leu Gln Pro Gln Val
465                470                475                480

ttt aca att ggc tta aaa aaa gtg gct caa ata gaa tct aat ctt aaa 1488
Phe Thr Ile Gly Leu Lys Lys Val Ala Gln Ile Glu Ser Asn Leu Lys
485                490                495

att gtt aga gat aag tca gaa gcg acc ata att aaa 1524
Ile Val Arg Asp Lys Ser Glu Ala Thr Ile Ile Lys
500                505

```

<210> 36

<211> 508

<212> PRT

<213> Lactobacillus acidophilus

<400> 36

```

Met Ser Lys Ile Thr Phe Phe Ser Lys Thr Ile His Ile Lys Ile Lys
1      5      10      15
Phe Val Asp Met Asp Asn Trp Ser Pro Ile Leu Lys Pro Ile Glu Val
20     25     30
Lys Gly Lys Glu Gly Lys Thr Ile Asp Cys Ser Ile Asn Asn Gln Leu
35     40     45
Glu Glu Ala Lys Lys Gln Gly Tyr Glu Leu Ala Ser Asn Glu Leu Glu
50     55     60
Gln Asp Gly Gln Arg Lys Glu Phe Ser Ser Asp Asn Asp Glu Tyr Ile
65     70     75     80
Ile Gly Phe His His Gly Gln Ala Ile Ile Asp Ala Met His Pro Gly
85     90     95
Tyr Gly Tyr Thr Lys Gly Gln Leu Glu Lys Thr Ile Thr Gln Ile Val
100    105    110
His Tyr Gln Gly Ala Ser Ser Lys Thr Pro Ile Asp Asn Lys Ile Ser
115    120    125
Arg Val Leu Arg Arg Lys Leu Ile Ile Asp Lys Val Asn Gly Lys Ile
130    135    140
Ile Asn Asp Ser Gly Trp Asn Asn Gln Gly Tyr Phe Lys Leu Ile Ala
145    150    155    160
Thr Pro Val Val Pro Gly Phe Lys Ala Asp His Leu Ile Ala Gly Gly
165    170    175
Gly Lys Ile Asp Pro His Asn Pro Val Gln Asn Tyr Val Val Glu Tyr
180    185    190
Ala Leu Asn Asn Glu Pro Val Ser Glu Arg Gln Thr Ala Lys Ile Gln
195    200    205
Tyr Val Asp Ile Leu Asn Asn Arg Val Ile Leu Ser Asp Glu Val
210    215    220
Val Gly Lys Ala Asn Asp Trp Ile Glu Tyr Asp Pro Gln Asn Arg Ile
225    230    235    240
Thr Glu Leu Arg Lys Asn Gly Tyr Glu Leu Val Asp Asn Ala Phe Asn
245    250    255
Ala Asn Gly Asn Val Gln Phe Phe Gly Asp Ser Asn Glu Glu Phe Val
260    265    270
Phe Ile Ile Thr Met Lys His Thr Phe Ile Asn Val Asp Ile Lys His
275    280    285
Pro Phe Asp Lys Ile Leu Pro Lys Gln Tyr Leu Lys Ala Val Asn Phe
290    295    300

```

Arg Val Val Phe Gln Gly Ala Gly Ile Leu Thr Pro Asp Glu Ile Thr
 305 310 315 320
 Gln Thr Ala Ile Leu Asn Arg Ser Leu Lys Val Ile Pro Glu Thr Gly
 325 330 335
 Arg Val Leu Ser Lys Thr Arg Trp Phe Ser Asp Ile Asp Ser Phe His
 340 345 350
 Asp Val Lys Val Pro Val Val Glu Gly Phe Val Ala Asp Lys Leu Lys
 355 360 365
 Ile Lys Ala Pro Glu Ile Val Pro Ser Asp Ile Ile Val Thr Val Asn
 370 375 380
 Tyr Ile Asp Ala Met Val Ala Lys Leu Lys Lys Ala Glu Lys Arg Leu
 385 390 395 400
 Gln Glu Gln Lys Lys Leu Glu Met Ala Ile Ile Thr Phe Ile Asp Ile
 405 410 415
 Asp Lys Asn Gly Thr Gln Ile Met Thr Ser Gly Ala Ile Thr Gly Gln
 420 425 430
 Pro Gly Glu Ser Ile Asn Asp Ser Tyr Ser Thr Lys Glu Pro Leu Lys
 435 440 445
 Thr Leu Lys Asn Glu Gly Tyr Glu Val Val Phe Asn Asn Phe Asp Ile
 450 455 460
 Pro Gly Met Val Gln Arg Phe Asp Asn Asn Asp Leu Gln Pro Gln Val
 465 470 475 480
 Phe Thr Ile Gly Leu Lys Lys Val Ala Gln Ile Glu Ser Asn Leu Lys
 485 490 495
 Ile Val Arg Asp Lys Ser Glu Ala Thr Ile Ile Lys
 500 505

<210> 37

<211> 1017

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1460 - mucus binding protein precursor

<220>

<221> CDS

<222> (1)...(1017)

<400> 37

atg cca cat aaa aat acg aaa tct aat gta caa aaa att act gct agt 48
 Met Pro His Lys Asn Thr Lys Ser Asn Val Gln Lys Ile Thr Ala Ser
 1 5 10 15

gta gct tct gtg att gta agt act gga att gta atg aat tca agt aat 96
 Val Ala Ser Val Ile Val Ser Thr Gly Ile Val Met Asn Ser Ser Asn
 20 25 30

cgt aga gtt aaa gca act ggt aaa cga gaa gat gaa att gtt gaa gtt 144
 Arg Arg Val Lys Ala Thr Gly Lys Arg Glu Asp Glu Ile Val Glu Val
 35 40 45

gaa agt ttg aag aga gct gat act gaa acg acg aag gct gct gct gctg 192

Glu	Ser	Leu	Lys	Arg	Ala	Asp	Thr	Glu	Thr	Thr	Lys	Ala	Ala	Ala	Val		
50						55					60						
caa	act	cct	aaa	ata	aac	caa	act	aaa	aag	atg	agt	cat	cgt	act	caa	240	
Gln	Thr	Pro	Lys	Ile	Asn	Gln	Thr	Lys	Lys	Met	Ser	His	Arg	Thr	Gln	80	
65					70				75								
aag	gtt	aca	cag	atg	att	cac	tat	gta	gat	gaa	gat	gaa	aga	ccg	gtt	288	
Lys	Val	Thr	Gln	Met	Ile	His	Tyr	Val	Asp	Glu	Asp	Glu	Arg	Pro	Val	95	
			85					90									
tat	gat	gat	tac	acg	gct	agt	tta	att	ttt	gaa	caa	aca	gga	att	ctg	336	
Tyr	Asp	Asp	Tyr	Thr	Ala	Ser	Leu	Ile	Phe	Glu	Gln	Thr	Gly	Ile	Leu	110	
			100				105										
gat	aat	gtt	act	ggg	aag	cag	aca	tgg	aat	agc	aat	tgg	tta	cca	aag	384	
Asp	Asn	Val	Thr	Gly	Lys	Gln	Thr	Trp	Asn	Ser	Asn	Trp	Leu	Pro	Lys	125	
		115				120											
act	acg	gca	act	ttt	agt	gct	gta	gaa	cat	ccc	gtg	gta	aga	aat	cat	432	
Thr	Thr	Ala	Thr	Phe	Ser	Ala	Val	Glu	His	Pro	Val	Val	Arg	Asn	His	140	
		130				135											
cat	tta	gta	aat	cca	gag	ata	aat	gaa	gta	agt	gcg	tat	gat	gtt	gaa	480	
His	Leu	Val	Asn	Pro	Glu	Ile	Asn	Glu	Val	Ser	Ala	Tyr	Asp	Val	Glu	160	
		145			150				155								
gta	acg	gat	gat	act	ttt	aaa	aat	cct	ctt	ctt	aaa	gtt	cat	aaa	gtt	528	
Val	Thr	Asp	Asp	Thr	Phe	Lys	Asn	Pro	Leu	Leu	Lys	Val	His	Lys	Val	175	
				165				170									
gta	tat	gca	cat	gat	ata	gaa	cca	att	aaa	cgg	acg	cag	gta	gta	acg	576	
Val	Tyr	Ala	His	Asp	Ile	Glu	Pro	Ile	Lys	Arg	Thr	Gln	Val	Val	Thr	190	
			180				185										
caa	act	att	cat	tat	aga	tat	gaa	gat	ggg	gcg	gtt	gca	cat	gat	gat	624	
Gln	Thr	Ile	His	Tyr	Arg	Tyr	Glu	Asp	Gly	Ala	Val	Ala	His	Asp	Asp	205	
		195					200										
cat	gtt	gtg	tca	tta	ata	ttt	aca	cag	tca	ggg	aag	agg	gat	ttg	act	672	
His	Val	Val	Ser	Leu	Ile	Phe	Thr	Gln	Ser	Gly	Lys	Arg	Asp	Leu	Thr	220	
		210				215											
aat	ggg	aaa	gaa	att	tgg	gat	agt	aaa	tgg	tcg	ctg	act	caa	act	ttt	720	
Asn	Gly	Lys	Glu	Ile	Trp	Asp	Ser	Lys	Trp	Ser	Leu	Thr	Gln	Thr	Phe	240	
		225			230				235								
gaa	gct	ttg	cct	agc	cca	gtt	att	att	gga	tat	aca	gca	gat	aag	ccg	768	
Glu	Ala	Leu	Pro	Ser	Pro	Val	Ile	Ile	Gly	Tyr	Thr	Ala	Asp	Lys	Pro	255	
			245					250									
atg	gtt	ggg	cct	gat	gag	gtt	acg	gtt	gat	agt	aaa	aat	ttc	ctt	gat	816	
Met	Val	Gly	Pro	Asp	Glu	Val	Thr	Val	Asp	Ser	Lys	Asn	Phe	Leu	Asp	270	
			260				265										
aaa	caa	aat	aga	gaa	gaa	acc	gta	att	tat	agt	gcg	aat	act	att	acg	864	
Lys	Gln	Asn	Arg	Glu	Glu	Thr	Val	Ile	Tyr	Ser	Ala	Asn	Thr	Ile	Thr		

275	280	285	
caa aat aag aaa gat ggg att agt gaa gaa aag aat gta aat aat tct			912
Gln Asn Lys Lys Asp Gly Ile Ser Glu Glu Lys Asn Val Asn Asn Ser			
290	295	300	
ggt gct gtc gcg cca cta aaa agt gct gta atg att ggc gga gta ata			960
Val Ala Val Ala Pro Leu Lys Ser Ala Val Met Ile Gly Gly Val Ile			
305	310	315	320
tct att tta aaa ttt aaa aga tta atg gtt att ata aaa aac aag aag			1008
Ser Ile Leu Lys Phe Lys Arg Leu Met Val Ile Ile Lys Asn Lys Lys			
325	330	335	
gat cat aaa			1017
Asp His Lys			

<210> 38

<211> 339

<212> PRT

<213> Lactobacillus acidophilus

<400> 38

Met Pro His Lys Asn Thr Lys Ser Asn Val Gln Lys Ile Thr Ala Ser			
1	5	10	15
Val Ala Ser Val Ile Val Ser Thr Gly Ile Val Met Asn Ser Ser Asn			
20	25	30	
Arg Arg Val Lys Ala Thr Gly Lys Arg Glu Asp Glu Ile Val Glu Val			
35	40	45	
Glu Ser Leu Lys Arg Ala Asp Thr Glu Thr Thr Lys Ala Ala Ala Val			
50	55	60	
Gln Thr Pro Lys Ile Asn Gln Thr Lys Lys Met Ser His Arg Thr Gln			
65	70	75	80
Lys Val Thr Gln Met Ile His Tyr Val Asp Glu Asp Glu Arg Pro Val			
85	90	95	
Tyr Asp Asp Tyr Thr Ala Ser Leu Ile Phe Glu Gln Thr Gly Ile Leu			
100	105	110	
Asp Asn Val Thr Gly Lys Gln Thr Trp Asn Ser Asn Trp Leu Pro Lys			
115	120	125	
Thr Thr Ala Thr Phe Ser Ala Val Glu His Pro Val Val Arg Asn His			
130	135	140	
His Leu Val Asn Pro Glu Ile Asn Glu Val Ser Ala Tyr Asp Val Glu			
145	150	155	160
Val Thr Asp Asp Thr Phe Lys Asn Pro Leu Leu Lys Val His Lys Val			
165	170	175	
Val Tyr Ala His Asp Ile Glu Pro Ile Lys Arg Thr Gln Val Val Thr			
180	185	190	
Gln Thr Ile His Tyr Arg Tyr Glu Asp Gly Ala Val Ala His Asp Asp			
195	200	205	
His Val Val Ser Leu Ile Phe Thr Gln Ser Gly Lys Arg Asp Leu Thr			
210	215	220	
Asn Gly Lys Glu Ile Trp Asp Ser Lys Trp Ser Leu Thr Gln Thr Phe			
225	230	235	240
Glu Ala Leu Pro Ser Pro Val Ile Ile Gly Tyr Thr Ala Asp Lys Pro			
245	250	255	

```

Met Val Gly Pro Asp Glu Val Thr Val Asp Ser Lys Asn Phe Leu Asp
      260      265      270
Lys Gln Asn Arg Glu Glu Thr Val Ile Tyr Ser Ala Asn Thr Ile Thr
      275      280      285
Gln Asn Lys Lys Asp Gly Ile Ser Glu Glu Lys Asn Val Asn Asn Ser
      290      295      300
Val Ala Val Ala Pro Leu Lys Ser Ala Val Met Ile Gly Gly Val Ile
      305      310      315      320
Ser Ile Leu Lys Phe Lys Arg Leu Met Val Ile Ile Lys Asn Lys Lys
      325      330      335
Asp His Lys

```

<210> 39

<211> 228

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 66 - steroid binding protein

<220>

<221> CDS

<222> (1)...(228)

<400> 39

```

atg aaa caa ttt aca aaa gaa act ctg tca aat tat gat ggt aaa aac      48
Met Lys Gln Phe Thr Lys Glu Thr Leu Ser Asn Tyr Asp Gly Lys Asn
  1              5              10              15

ggc cga cct gct tat att gca gtt aat ggt atc gtt tat gac gta acc      96
Gly Arg Pro Ala Tyr Ile Ala Val Asn Gly Ile Val Tyr Asp Val Thr
              20              25              30

aac aat gct cat tgg gtt aac ggt gaa cac cac ggt ata aga gcc gga      144
Asn Asn Ala His Trp Val Asn Gly Glu His His Gly Ile Arg Ala Gly
              35              40              45

aaa gat gta agc ttt gac tta act aat aca tct cct cat gga gaa aaa      192
Lys Asp Val Ser Phe Asp Leu Thr Asn Thr Ser Pro His Gly Glu Lys
              50              55              60

gtc tta gtt aat gct aat caa gtt ggt gta tac aac      228
Val Leu Val Asn Ala Asn Gln Val Gly Val Tyr Asn
  65              70              75

```

<210> 40

<211> 76

<212> PRT

<213> Lactobacillus acidophilus

<400> 40

```

Met Lys Gln Phe Thr Lys Glu Thr Leu Ser Asn Tyr Asp Gly Lys Asn
 1           5           10           15
Gly Arg Pro Ala Tyr Ile Ala Val Asn Gly Ile Val Tyr Asp Val Thr
          20           25           30
Asn Asn Ala His Trp Val Asn Gly Glu His His Gly Ile Arg Ala Gly
          35           40           45
Lys Asp Val Ser Phe Asp Leu Thr Asn Thr Ser Pro His Gly Glu Lys
          50           55           60
Val Leu Val Asn Ala Asn Gln Val Gly Val Tyr Asn
65           70           75

```

<210> 41

<211> 1065

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 494 - surface exclusion protein

<220>

<221> CDS

<222> (1)...(1065)

<400> 41

```

atg tct aag aaa att ttt act aaa tta ctg acc agt att tgt tta atg      48
Met Ser Lys Lys Ile Phe Thr Lys Leu Leu Thr Ser Ile Cys Leu Met
 1           5           10           15

ggc cca att agc acc act att caa ata aca cca caa gta gtt caa gca      96
Gly Pro Ile Ser Thr Thr Ile Gln Ile Thr Pro Gln Val Val Gln Ala
          20           25           30

gcc agt aat aag gta caa gtc aaa gga agt aaa aag atc cgc ctt tat      144
Ala Ser Asn Lys Val Gln Val Lys Gly Ser Lys Lys Ile Arg Leu Tyr
          35           40           45

aat tca aaa ggt aaa aag acc aaa tat tat gct tat cca ggt aaa aga      192
Asn Ser Lys Gly Lys Lys Thr Lys Tyr Tyr Ala Tyr Pro Gly Lys Arg
          50           55           60

tat gct tat tct act aaa aag aaa tta aag att ggc aag aaa aca tat      240
Tyr Ala Tyr Ser Thr Lys Lys Lys Leu Lys Ile Gly Lys Lys Thr Tyr
          65           70           75           80

ttg gct tat aaa tta aat gct aat tca tat tgg cta ctt gct aaa aat      288
Leu Ala Tyr Lys Leu Asn Ala Asn Ser Tyr Trp Leu Leu Ala Lys Asn
          85           90           95

gct aaa gtt gta aaa aat act acc tca act gtt cct act tct tat tct      336
Ala Lys Val Val Lys Asn Thr Thr Ser Thr Val Pro Thr Ser Tyr Ser
          100           105           110

caa gct acg att aaa tta cca agc gga tat act tta tcc ggc ttg ctt      384

```

Gln	Ala	Thr	Ile	Lys	Leu	Pro	Ser	Gly	Tyr	Thr	Leu	Ser	Gly	Leu	Leu		
		115					120					125					
gag	gct	tat	aag	gga	gcg	cca	agt	gaa	agc	ttt	att	gat	gct	tca	atg	432	
Glu	Ala	Tyr	Lys	Gly	Ala	Pro	Ser	Glu	Ser	Phe	Ile	Asp	Ala	Ser	Met		
		130				135					140						
aag	gga	atg	gag	att	aat	aac	ttt	tca	cgt	ggt	gct	aaa	ggg	gaa	agc	480	
Lys	Gly	Met	Glu	Ile	Asn	Asn	Phe	Ser	Arg	Val	Ala	Lys	Gly	Glu	Ser		
		145				150				155					160		
agt	agt	gat	aaa	agg	gta	att	aat	cct	agc	aaa	ttg	aca	gct	agc	gat	528	
Ser	Ser	Asp	Lys	Arg	Val	Ile	Asn	Pro	Ser	Lys	Leu	Thr	Ala	Ser	Asp		
				165					170					175			
caa	aaa	gaa	ttg	act	gaa	ttt	gca	ctt	aaa	ata	att	aat	agt	gct	cgt	576	
Gln	Lys	Glu	Leu	Thr	Glu	Phe	Ala	Leu	Lys	Ile	Ile	Asn	Ser	Ala	Arg		
			180					185					190				
gag	caa	ctt	ggt	ttg	cat	cct	tgg	att	tat	agc	tca	gga	aca	caa	caa	624	
Glu	Gln	Leu	Gly	Leu	His	Pro	Trp	Ile	Tyr	Ser	Ser	Gly	Thr	Gln	Gln		
		195				200						205					
tta	gcc	aat	gat	att	gca	aaa	gaa	tat	caa	gat	aat	ggt	cgc	agt	att	672	
Leu	Ala	Asn	Asp	Ile	Ala	Lys	Glu	Tyr	Gln	Asp	Asn	Gly	Arg	Ser	Ile		
		210				215					220						
agt	gat	gga	gac	cat	tac	att	tca	gga	att	gtc	aga	gca	tgc	aaa	aag	720	
Ser	Asp	Gly	Asp	His	Tyr	Ile	Ser	Gly	Ile	Val	Arg	Ala	Cys	Lys	Lys		
		225			230					235					240		
aac	ggc	ttg	gac	ttg	gat	gac	aat	tac	gta	gag	gat	atg	gcc	ggt	ttc	768	
Asn	Gly	Leu	Asp	Leu	Asp	Asp	Asn	Tyr	Val	Glu	Asp	Met	Ala	Gly	Phe		
				245					250					255			
tca	att	aaa	aag	aca	act	atg	cct	atg	ggt	gaa	atg	aaa	aag	gat	att	816	
Ser	Ile	Lys	Lys	Thr	Thr	Met	Pro	Met	Gly	Glu	Met	Lys	Lys	Asp	Ile		
			260					265						270			
tac	ttc	ggt	tta	aag	caa	atg	ata	ttt	ggt	ttt	acc	ggt	tca	ggt	gaa	864	
Tyr	Phe	Gly	Leu	Lys	Gln	Met	Ile	Phe	Gly	Phe	Thr	Gly	Ser	Gly	Glu		
		275					280					285					
agc	act	agg	aat	aat	aag	tca	ttg	tat	cgt	gaa	tgg	gaa	cat	gcg	ggg	912	
Ser	Thr	Arg	Asn	Asn	Lys	Ser	Leu	Tyr	Arg	Glu	Trp	Glu	His	Ala	Gly		
		290				295					300						
gac	cta	ttt	aat	aca	cag	gat	tca	ggt	cac	gat	gga	gac	tat	aac	tat	960	
Asp	Leu	Phe	Asn	Thr	Gln	Asp	Ser	Val	His	Asp	Gly	Asp	Tyr	Asn	Tyr		
		305			310					315					320		
tat	ggc	ttc	agt	att	tca	aaa	aca	gga	aat	acg	tat	tca	atg	cat	ttt	1008	
Tyr	Gly	Phe	Ser	Ile	Ser	Lys	Thr	Gly	Asn	Thr	Tyr	Ser	Met	His	Phe		
				325					330					335			
att	agt	gtt	cca	aat	ttt	gtg	gtt	gaa	agt	agt	aaa	tat	aat	gtt	ggt	1056	
Ile	Ser	Val	Pro	Asn	Phe	Val	Val	Glu	Ser	Ser	Lys	Tyr	Asn	Val	Gly		

340 345 350 1065

ttt aaa cca
Phe Lys Pro
355

<210> 42
<211> 355
<212> PRT
<213> Lactobacillus acidophilus

<400> 42
Met Ser Lys Lys Ile Phe Thr Lys Leu Leu Thr Ser Ile Cys Leu Met
1 5 10 15
Gly Pro Ile Ser Thr Thr Ile Gln Ile Thr Pro Gln Val Val Gln Ala
20 25 30
Ala Ser Asn Lys Val Gln Val Lys Gly Ser Lys Lys Ile Arg Leu Tyr
35 40 45
Asn Ser Lys Gly Lys Lys Thr Lys Tyr Tyr Ala Tyr Pro Gly Lys Arg
50 55 60
Tyr Ala Tyr Ser Thr Lys Lys Lys Leu Lys Ile Gly Lys Lys Thr Tyr
65 70 75 80
Leu Ala Tyr Lys Leu Asn Ala Asn Ser Tyr Trp Leu Leu Ala Lys Asn
85 90 95
Ala Lys Val Val Lys Asn Thr Thr Ser Thr Val Pro Thr Ser Tyr Ser
100 105 110
Gln Ala Thr Ile Lys Leu Pro Ser Gly Tyr Thr Leu Ser Gly Leu Leu
115 120 125
Glu Ala Tyr Lys Gly Ala Pro Ser Glu Ser Phe Ile Asp Ala Ser Met
130 135 140
Lys Gly Met Glu Ile Asn Asn Phe Ser Arg Val Ala Lys Gly Glu Ser
145 150 155 160
Ser Ser Asp Lys Arg Val Ile Asn Pro Ser Lys Leu Thr Ala Ser Asp
165 170 175
Gln Lys Glu Leu Thr Glu Phe Ala Leu Lys Ile Ile Asn Ser Ala Arg
180 185 190
Glu Gln Leu Gly Leu His Pro Trp Ile Tyr Ser Ser Gly Thr Gln Gln
195 200 205
Leu Ala Asn Asp Ile Ala Lys Glu Tyr Gln Asp Asn Gly Arg Ser Ile
210 215 220
Ser Asp Gly Asp His Tyr Ile Ser Gly Ile Val Arg Ala Cys Lys Lys
225 230 235 240
Asn Gly Leu Asp Leu Asp Asp Asn Tyr Val Glu Asp Met Ala Gly Phe
245 250 255
Ser Ile Lys Lys Thr Thr Met Pro Met Gly Glu Met Lys Lys Asp Ile
260 265 270
Tyr Phe Gly Leu Lys Gln Met Ile Phe Gly Phe Thr Gly Ser Gly Glu
275 280 285
Ser Thr Arg Asn Asn Lys Ser Leu Tyr Arg Glu Trp Glu His Ala Gly
290 295 300
Asp Leu Phe Asn Thr Gln Asp Ser Val His Asp Gly Asp Tyr Asn Tyr
305 310 315 320
Tyr Gly Phe Ser Ile Ser Lys Thr Gly Asn Thr Tyr Ser Met His Phe
325 330 335
Ile Ser Val Pro Asn Phe Val Val Glu Ser Ser Lys Tyr Asn Val Gly
340 345 350

Phe Lys Pro
355

<210> 43

<211> 333

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1587 - tropomyosin-like protein

<220>

<221> CDS

<222> (1)...(333)

<400> 43

atg	aaa	cat	ttc	tta	tta	ggc	aca	gtt	ttt	ggt	gcc	gca	gca	gga	ttc	48
Met	Lys	His	Phe	Leu	Leu	Gly	Thr	Val	Phe	Gly	Ala	Ala	Ala	Gly	Phe	
1				5				10						15		
gta	ttt	tcc	tgc	tta	aca	gat	agt	gat	ggc	aac	cgt	ccc	ggc	aaa	cca	96
Val	Phe	Ser	Cys	Leu	Thr	Asp	Ser	Asp	Gly	Asn	Arg	Pro	Gly	Lys	Pro	
			20					25					30			
tta	aaa	gat	gaa	tat	gat	gct	att	aag	cat	gaa	ggc	gga	cgc	ttt	agt	144
Leu	Lys	Asp	Glu	Tyr	Asp	Ala	Ile	Lys	His	Glu	Gly	Gly	Arg	Phe	Ser	
		35					40					45				
gat	gca	tta	aaa	aag	gct	aaa	caa	gcc	agt	cac	gat	tta	aat	gaa	cat	192
Asp	Ala	Leu	Lys	Lys	Ala	Lys	Gln	Ala	Ser	His	Asp	Leu	Asn	Glu	His	
	50					55					60					
ctt	cct	gaa	gca	gaa	cgc	aca	att	agt	gat	atg	aat	gat	gat	ttt	gaa	240
Leu	Pro	Glu	Ala	Glu	Arg	Thr	Ile	Ser	Asp	Met	Asn	Asp	Asp	Phe	Glu	
65					70				75						80	
aaa	tat	tcc	aaa	cac	att	cag	cct	att	gtt	gaa	aaa	atg	caa	caa	aaa	288
Lys	Tyr	Ser	Lys	His	Ile	Gln	Pro	Ile	Val	Glu	Lys	Met	Gln	Gln	Lys	
				85				90						95		
agt	gat	gaa	tta	aac	caa	aat	ttg	aat	aat	tta	gat	aca	aag	gac		333
Ser	Asp	Glu	Leu	Asn	Gln	Asn	Leu	Asn	Asn	Leu	Asp	Thr	Lys	Asp		
			100				105						110			

<210> 44

<211> 111

<212> PRT

<213> Lactobacillus acidophilus

<400> 44

Met Lys His Phe Leu Leu Gly Thr Val Phe Gly Ala Ala Ala Gly Phe

```

      1           5           10           15
Val Phe Ser Cys Leu Thr Asp Ser Asp Gly Asn Arg Pro Gly Lys Pro
      20           25           30
Leu Lys Asp Glu Tyr Asp Ala Ile Lys His Glu Gly Gly Arg Phe Ser
      35           40           45
Asp Ala Leu Lys Lys Ala Lys Gln Ala Ser His Asp Leu Asn Glu His
      50           55           60
Leu Pro Glu Ala Glu Arg Thr Ile Ser Asp Met Asn Asp Asp Phe Glu
      65           70           75           80
Lys Tyr Ser Lys His Ile Gln Pro Ile Val Glu Lys Met Gln Gln Lys
      85           90           95
Ser Asp Glu Leu Asn Gln Asn Leu Asn Asn Leu Asp Thr Lys Asp
      100           105           110

```

<210> 45

<211> 198

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1378 - biofilm-associated surface protein

<220>

<221> CDS

<222> (1)...(198)

<400> 45

```

atg aga aga gac tta cat aat tta gac gta ggg gac gtt aaa gaa aaa 48
Met Arg Arg Asp Leu His Asn Leu Asp Val Gly Asp Val Lys Glu Lys
  1           5           10           15

```

```

caa cgt ttt tca att cgc aag tta act gta ggt act gct agt gta ttg 96
Gln Arg Phe Ser Ile Arg Lys Leu Thr Val Gly Thr Ala Ser Val Leu
      20           25           30

```

```

ctg ggt act aca ttc ttg ttt ggt gca ggt cag act gct tac gct gat 144
Leu Gly Thr Thr Phe Leu Phe Gly Ala Gly Gln Thr Ala Tyr Ala Asp
      35           40           45

```

```

act act gct tca ggt gct att act agt gaa gat tcc caa aac caa att 192
Thr Thr Ala Ser Gly Ala Ile Thr Ser Glu Asp Ser Gln Asn Gln Ile
      50           55           60

```

```

ggg ggg 198
Gly Gly
  65

```

<210> 46

<211> 66

<212> PRT

<213> Lactobacillus acidophilus

<400> 46

```

Met Arg Arg Asp Leu His Asn Leu Asp Val Gly Asp Val Lys Glu Lys
 1           5           10           15
Gln Arg Phe Ser Ile Arg Lys Leu Thr Val Gly Thr Ala Ser Val Leu
          20           25           30
Leu Gly Thr Thr Phe Leu Phe Gly Ala Gly Gln Thr Ala Tyr Ala Asp
          35           40           45
Thr Thr Ala Ser Gly Ala Ile Thr Ser Glu Asp Ser Gln Asn Gln Ile
          50           55           60
Gly Gly
65

```

<210> 47

<211> 693

<212> DNA

<213> *Lactobacillus acidophilus*

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 493 - aggregation promoting protein

<220>

<221> CDS

<222> (1)...(693)

<400> 47

```

ttg aaa atc aaa tct atc tta gtt aag tca att gca gta gct gct atg 48
Met Lys Ile Lys Ser Ile Leu Val Lys Ser Ile Ala Val Ala Ala Met
 1           5           10           15

tca gtt aca ggt gta gta gca gca aat aac gta act tca aac aat gca 96
Ser Val Thr Val Val Val Ala Ala Asn Asn Val Thr Ser Asn Asn Ala
          20           25           30

caa gct gct act gtt caa aat gat gct agc gta gtt aca gta aac tac 144
Gln Ala Ala Thr Val Gln Asn Asp Ala Ser Val Val Thr Val Asn Tyr
          35           40           45

gtt gca aac aac tca atc aac gta tac aac aat tac gaa aac cca gta 192
Val Ala Asn Asn Ser Ile Asn Val Tyr Asn Asn Tyr Glu Asn Pro Val
          50           55           60

gca aca ggt caa att tta gca agt aat act tca tgg aaa gtt att aag 240
Ala Thr Gly Gln Ile Leu Ala Ser Asn Thr Ser Trp Lys Val Ile Lys
          65           70           75           80

act gct tac gac tca aag ggt aac aaa tgg tac gac tta ggc aag aac 288
Thr Ala Tyr Asp Ser Lys Gly Asn Lys Trp Tyr Asp Leu Gly Lys Asn
          85           90           95

caa tgg gtt cgt gct agt caa gta acc gct gga tac act gct tca gca 336
Gln Trp Val Arg Ala Ser Gln Val Thr Ala Gly Tyr Thr Ala Ser Ala
          100           105           110

```

```

aca act act gca caa aca caa caa tca act act act caa gta gct aat 384
Thr Thr Thr Ala Gln Thr Gln Gln Ser Thr Thr Thr Gln Val Ala Asn
      115                      120                      125

act caa caa tca tca caa gta gca act caa tca caa act gca gct gct 432
Thr Gln Gln Ser Ser Gln Val Ala Thr Gln Ser Gln Thr Ala Ala Ala
      130                      135                      140

tca act act agt gct tca tca tat act tca agt gca tct ggt tca gaa 480
Ser Thr Thr Ser Ala Ser Ser Tyr Thr Ser Ser Ala Ser Gly Ser Glu
      145                      150                      155                      160

gct agt gct aag gct tgg att gct ggt aag gaa tca ggt ggc tca tac 528
Ala Ser Ala Lys Ala Trp Ile Ala Gly Lys Glu Ser Gly Gly Ser Tyr
      165                      170                      175

tca gct act aat ggt caa tac atc ggt aag tac caa ctt tca gca tca 576
Ser Ala Thr Asn Gly Gln Tyr Ile Gly Lys Tyr Gln Leu Ser Ala Ser
      180                      185                      190

tac ttg aat ggt gac tac tca gca gct aac caa gaa aga gta gct gat 624
Tyr Leu Asn Gly Asp Tyr Ser Ala Ala Asn Gln Glu Arg Val Ala Asp
      195                      200                      205

aat tac gta caa agt cgt tac ggt tca tgg act gct gct aag gca ttc 672
Asn Tyr Val Gln Ser Arg Tyr Gly Ser Trp Thr Ala Ala Lys Ala Phe
      210                      215                      220

tgg caa gca aac ggc tgg tac 693
Trp Gln Ala Asn Gly Trp Tyr
      225                      230

```

<210> 48

<211> 231

<212> PRT

<213> Lactobacillus acidophilus

<400> 48

```

Met Lys Ile Lys Ser Ile Leu Val Lys Ser Ile Ala Val Ala Ala Met
 1      5      10      15
Ser Val Thr Gly Val Val Ala Ala Asn Asn Val Thr Ser Asn Asn Ala
      20      25      30
Gln Ala Ala Thr Val Gln Asn Asp Ala Ser Val Val Thr Val Asn Tyr
      35      40      45
Val Ala Asn Asn Ser Ile Asn Val Tyr Asn Asn Tyr Glu Asn Pro Val
      50      55      60
Ala Thr Gly Gln Ile Leu Ala Ser Asn Thr Ser Trp Lys Val Ile Lys
      65      70      75      80
Thr Ala Tyr Asp Ser Lys Gly Asn Lys Trp Tyr Asp Leu Gly Lys Asn
      85      90      95
Gln Trp Val Arg Ala Ser Gln Val Thr Ala Gly Tyr Thr Ala Ser Ala
      100      105      110
Thr Thr Thr Ala Gln Thr Gln Gln Ser Thr Thr Thr Gln Val Ala Asn
      115      120      125
Thr Gln Gln Ser Ser Gln Val Ala Thr Gln Ser Gln Thr Ala Ala Ala
      130      135      140

```

```

Ser Thr Thr Ser Ala Ser Ser Tyr Thr Ser Ser Ala Ser Gly Ser Glu
145          150          155          160
Ala Ser Ala Lys Ala Trp Ile Ala Gly Lys Glu Ser Gly Gly Ser Tyr
          165          170          175
Ser Ala Thr Asn Gly Gln Tyr Ile Gly Lys Tyr Gln Leu Ser Ala Ser
          180          185          190
Tyr Leu Asn Gly Asp Tyr Ser Ala Ala Asn Gln Glu Arg Val Ala Asp
          195          200          205
Asn Tyr Val Gln Ser Arg Tyr Gly Ser Trp Thr Ala Ala Lys Ala Phe
          210          215          220
Trp Gln Ala Asn Gly Trp Tyr
225          230

```

```

<210> 49
<211> 360
<212> DNA
<213> Lactobacillus acidophilus

```

```

<220>
<221> misc_feature
<222> (0)...(0)
<223> ORF 1850 - lysM or aggregation promoting protein

```

```

<220>
<221> CDS
<222> (1)...(360)

```

```

<400> 49
atg agt aaa aac gtt aaa tct act ttg gtt aaa att ttt gca gct tta 48
Met Ser Lys Asn Val Lys Ser Thr Leu Val Lys Ile Phe Ala Ala Leu
  1          5          10          15

gca ctt gcc ttt gca tgt gtt act gtt gcc caa gct ttt tct acc act 96
Ala Leu Ala Phe Ala Cys Val Thr Val Ala Gln Ala Phe Ser Thr Thr
          20          25          30

tca aat aac caa act gta caa gcc gca act aga aag ctt tct aag aag 144
Ser Asn Asn Gln Thr Val Gln Ala Ala Thr Arg Lys Leu Ser Lys Lys
          35          40          45

gaa aag gca gct aag cgt tgg atc gca atg cgt gaa tca ggt ggt agc 192
Glu Lys Ala Ala Lys Arg Trp Ile Ala Met Arg Glu Ser Gly Gly Ser
          50          55          60

tac act gct aga aac ggt gtt tgt tac ggt aaa tat caa tta aat att 240
Tyr Thr Ala Arg Asn Gly Val Cys Tyr Gly Lys Tyr Gln Leu Asn Ile
          65          70          75          80

ggt tac tta aac ggt gat tta tca cct aag aat caa gaa cgt aca gct 288
Gly Tyr Leu Asn Gly Asp Leu Ser Pro Lys Asn Gln Glu Arg Thr Ala
          85          90          95

gat aat tac gtt tat ggt cgt tac ggt tca tgg gtt aat gcc aag aga 336
Asp Asn Tyr Val Tyr Gly Arg Tyr Gly Ser Trp Val Asn Ala Lys Arg
          100          105          110

```

ttt tgg cta gca cat aat tgg tat
 Phe Trp Leu Ala His Asn Trp Tyr
 115 120

360

<210> 50
 <211> 120
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 50
 Met Ser Lys Asn Val Lys Ser Thr Leu Val Lys Ile Phe Ala Ala Leu
 1 5 10 15
 Ala Leu Ala Phe Ala Cys Val Thr Val Ala Gln Ala Phe Ser Thr Thr
 20 25 30
 Ser Asn Asn Gln Thr Val Gln Ala Thr Arg Lys Leu Ser Lys Lys
 35 40 45
 Glu Lys Ala Ala Lys Arg Trp Ile Ala Met Arg Glu Ser Gly Gly Ser
 50 55 60
 Tyr Thr Ala Arg Asn Gly Val Cys Tyr Gly Lys Tyr Gln Leu Asn Ile
 65 70 75 80
 Gly Tyr Leu Asn Gly Asp Leu Ser Pro Lys Asn Gln Glu Arg Thr Ala
 85 90 95
 Asp Asn Tyr Val Tyr Gly Arg Tyr Gly Ser Trp Val Asn Ala Lys Arg
 100 105 110
 Phe Trp Leu Ala His Asn Trp Tyr
 115 120

<210> 51
 <211> 792
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1495 - fibrinogen-binding protein

<220>
 <221> CDS
 <222> (1)...(792)

<400> 51
 atg ttt aga gac aaa aaa aca caa ttt gct att aga aaa cta aca aca 48
 Met Phe Arg Asp Lys Lys Thr Gln Phe Ala Ile Arg Lys Leu Thr Thr
 1 5 10 15
 ggt act ggg atc ctg ttg tta agt gtt ggt atg ggg att aac tta tcc 96
 Gly Thr Gly Ile Leu Leu Leu Ser Val Gly Met Gly Ile Asn Leu Ser
 20 25 30
 tca aaa gaa gta tct gct tca gaa att gat cca gct caa act act gag 144
 Ser Lys Glu Val Ser Ala Ser Glu Ile Asp Pro Ala Gln Thr Thr Glu
 35 40 45

act gtt caa act gaa gct gcg aca gaa tta acc gcg gaa caa gaa cca	192
Thr Val Gln Thr Glu Ala Ala Thr Glu Leu Thr Ala Glu Gln Glu Pro	
50 55 60	
gct gtt gaa ttc tct gcc cca gtt caa gaa act gaa ggt acc tct aca	240
Ala Val Glu Phe Ser Ala Pro Val Gln Glu Thr Glu Gly Thr Ser Thr	
65 70 75 80	
gtt gaa tca aca cct aat gtt aag gaa gag act gtt aca gag ata cca	288
Val Glu Ser Thr Pro Asn Val Lys Glu Glu Thr Val Thr Glu Ile Pro	
85 90 95	
gca gaa act gtt act ggc aac act aat aat gaa aat aac ggc agt gta	336
Ala Glu Thr Val Thr Gly Asn Thr Asn Asn Glu Asn Asn Gly Ser Val	
100 105 110	
aac aca gga act caa tcc cct gct act caa cct gaa gct gaa aag cca	384
Asn Thr Gly Thr Gln Ser Pro Ala Thr Gln Pro Glu Ala Glu Lys Pro	
115 120 125	
ggt caa gac act acc gct act gac aat act aat aat gaa aat aaa gat	432
Gly Gln Asp Thr Thr Ala Thr Asp Asn Thr Asn Asn Glu Asn Lys Asp	
130 135 140	
gct gta aat aca gaa act caa aaa cca gag act act act cct gct acc	480
Ala Val Asn Thr Glu Thr Gln Lys Pro Glu Thr Thr Thr Pro Ala Thr	
145 150 155 160	
cag cct gaa act gat aaa gca gaa gaa ggt gaa aaa act cca gct aaa	528
Gln Pro Glu Thr Asp Lys Ala Glu Glu Gly Glu Lys Thr Pro Ala Lys	
165 170 175	
aac gaa act gac tct tca tca gaa aaa gaa gaa tcc aaa gct gat tca	576
Asn Glu Thr Asp Ser Ser Ser Glu Lys Glu Glu Ser Lys Ala Asp Ser	
180 185 190	
gat aaa aaa gat gaa gta gaa aaa aat gaa aat gag tta aat aaa gga	624
Asp Lys Lys Asp Glu Val Glu Lys Asn Glu Asn Glu Leu Asn Lys Gly	
195 200 205	
aac ata aaa gat gac gcc att aac att gat ggt tct atc ctt cct gac	672
Asn Ile Lys Asp Asp Ala Ile Asn Ile Asp Gly Ser Ile Leu Pro Asp	
210 215 220	
gca gct aag cct gat aaa gat aat att aat gag act tta tca att caa	720
Ala Ala Lys Pro Asp Lys Asp Asn Ile Asn Glu Thr Leu Ser Ile Gln	
225 230 235 240	
ttc ttt ctg atc cgg ata aac ttg cag aat ttg aag gaa aag cta att	768
Phe Phe Leu Ile Arg Ile Asn Leu Gln Asn Leu Lys Glu Lys Leu Ile	
245 250 255	
gga cag atg cta tat tgc aag gaa	792
Gly Gln Met Leu Tyr Cys Lys Glu	
260	

<210> 52
 <211> 264
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 52
 Met Phe Arg Asp Lys Lys Thr Gln Phe Ala Ile Arg Lys Leu Thr Thr
 1 5 10 15
 Gly Thr Gly Ile Leu Leu Leu Ser Val Gly Met Gly Ile Asn Leu Ser
 20 25 30
 Ser Lys Glu Val Ser Ala Ser Glu Ile Asp Pro Ala Gln Thr Thr Glu
 35 40 45
 Thr Val Gln Thr Glu Ala Ala Thr Glu Leu Thr Ala Glu Gln Glu Pro
 50 55 60
 Ala Val Glu Phe Ser Ala Pro Val Gln Glu Thr Glu Gly Thr Ser Thr
 65 70 75 80
 Val Glu Ser Thr Pro Asn Val Lys Glu Glu Thr Val Thr Glu Ile Pro
 85 90 95
 Ala Glu Thr Val Thr Gly Asn Thr Asn Asn Glu Asn Asn Gly Ser Val
 100 105 110
 Asn Thr Gly Thr Gln Ser Pro Ala Thr Gln Pro Glu Ala Glu Lys Pro
 115 120 125
 Gly Gln Asp Thr Thr Ala Thr Asp Asn Thr Asn Asn Glu Asn Lys Asp
 130 135 140
 Ala Val Asn Thr Glu Thr Gln Lys Pro Glu Thr Thr Thr Pro Ala Thr
 145 150 155 160
 Gln Pro Glu Thr Asp Lys Ala Glu Glu Gly Glu Lys Thr Pro Ala Lys
 165 170 175
 Asn Glu Thr Asp Ser Ser Ser Glu Lys Glu Glu Ser Lys Ala Asp Ser
 180 185 190
 Asp Lys Lys Asp Glu Val Glu Lys Asn Glu Asn Glu Leu Asn Lys Gly
 195 200 205
 Asn Ile Lys Asp Asp Ala Ile Asn Ile Asp Gly Ser Ile Leu Pro Asp
 210 215 220
 Ala Ala Lys Pro Asp Lys Asp Asn Ile Asn Glu Thr Leu Ser Ile Gln
 225 230 235 240
 Phe Phe Leu Ile Arg Ile Asn Leu Gln Asn Leu Lys Glu Lys Leu Ile
 245 250 255
 Gly Gln Met Leu Tyr Cys Lys Glu
 260

<210> 53
 <211> 2973
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1496 - fibrinogen-binding protein

<220>
 <221> CDS
 <222> (1)...(2973)

<400> 53

ttg caa gga ata att aag tgg ata gaa gat aat aga ctt tca tgg gat 48
 Met Gln Gly Ile Ile Lys Trp Ile Glu Asp Asn Arg Leu Ser Trp Asp
 1 5 10 15

cac att agt gat caa gaa aaa tac cct gga tgg gaa gat gtt ttt gat 96
 His Ile Ser Asp Gln Glu Lys Tyr Pro Gly Trp Glu Asp Val Phe Asp
 20 25 30

gaa agt tta aaa atc gac aga gtt gat cct ttt gat cat aaa aat ccc 144
 Glu Ser Leu Lys Ile Asp Arg Val Asp Pro Phe Asp His Lys Asn Pro
 35 40 45

caa tgg caa gca act gca aac aaa gaa att act att acc caa aca gta 192
 Gln Trp Gln Ala Thr Ala Asn Lys Glu Ile Thr Ile Thr Gln Thr Val
 50 55 60

aat aac ggt tca cag caa tcc aca caa caa atc aaa gtt aac tac gat 240
 Asn Asn Gly Ser Gln Gln Ser Thr Gln Gln Ile Lys Val Asn Tyr Asp
 65 70 75 80

gta gtc ata tat att gcg att gat cct aat atg agc gga tgg gat gca 288
 Val Val Ile Tyr Ile Ala Ile Asp Pro Asn Met Ser Gly Trp Asp Ala
 85 90 95

ctt ttt ggt aat tat aaa ttt ata att agc gat gta aaa gtc agc aac 336
 Leu Phe Gly Asn Tyr Lys Phe Ile Ile Ser Asp Val Lys Val Ser Asn
 100 105 110

att aat aaa gta gac cct gat act aat act ccg aaa gat gat ttt gat 384
 Ile Asn Lys Val Asp Pro Asp Thr Asn Thr Pro Lys Asp Asp Phe Asp
 115 120 125

gca gta aat att cct act gct cca gaa ggc ttt gaa aac aga gtc aca 432
 Ala Val Asn Ile Pro Thr Ala Pro Glu Gly Phe Glu Asn Arg Val Thr
 130 135 140

ggc aca att gaa gga ccc aaa ttt gat gat tac aat ata aac aat aat 480
 Gly Thr Ile Glu Gly Pro Lys Phe Asp Asp Tyr Asn Ile Asn Asn Asn
 145 150 155 160

atc agc ctt gaa gac aaa gta att aaa act aat tta gat agt atc ttc 528
 Ile Ser Leu Glu Asp Lys Val Ile Lys Thr Asn Leu Asp Ser Ile Phe
 165 170 175

aat acc atc cta caa aaa ggt aca gat gta acc ttt aaa tac gat att 576
 Asn Thr Ile Leu Gln Lys Gly Thr Asp Val Thr Phe Lys Tyr Asp Ile
 180 185 190

gaa caa att gcc gtt aaa aaa cca act tgg gtt gat gtc att gat ggt 624
 Glu Gln Ile Ala Val Lys Lys Pro Thr Trp Val Asp Val Ile Asp Gly
 195 200 205

gat gac aaa aag gag tgg aat gat ctc ttc caa aat gtt gat ttc act 672
 Asp Asp Lys Lys Glu Trp Asn Asp Leu Phe Gln Asn Val Asp Phe Thr
 210 215 220

aaa gac caa gat aaa gat aat atc tgg acc ggt aca gta act tta aat	720
Lys Asp Gln Asp Lys Asp Asn Ile Trp Thr Gly Thr Val Thr Leu Asn	
225 230 235 240	
aaa gat atc att caa acc att aat gga tta gat caa gaa aac aag caa	768
Lys Asp Ile Ile Gln Thr Ile Asn Gly Leu Asp Gln Glu Asn Lys Gln	
245 250 255	
aca atc cac ctt aca aaa gat gtc act att act att caa cgt gat ggt	816
Thr Ile His Leu Thr Lys Asp Val Thr Ile Thr Ile Gln Arg Asp Gly	
260 265 270	
aat act aat aac ttc aaa att ttg aca gta aat caa tct aat tgg aca	864
Asn Thr Asn Asn Phe Lys Ile Leu Thr Val Asn Gln Ser Asn Trp Thr	
275 280 285	
cca aat gat tct ctt gaa tct aca gat atc tct aag cca ggc tac aat	912
Pro Asn Asp Ser Leu Glu Ser Thr Asp Ile Ser Lys Pro Gly Tyr Asn	
290 295 300	
cac aat gtg tct gct tct att act ggt acc agt agt gac aac ttt aca	960
His Asn Val Ser Ala Ser Ile Thr Gly Thr Ser Ser Asp Asn Phe Thr	
305 310 315 320	
cat aaa gtt gaa aat ggt cat ctt tca acg aat ctt gat ttt agt aaa	1008
His Lys Val Glu Asn Gly His Leu Ser Thr Asn Leu Asp Phe Ser Lys	
325 330 335	
tta gaa aat aac aat aat caa att act atc aac tac aaa gtg tct tat	1056
Leu Glu Asn Asn Asn Asn Gln Ile Thr Ile Asn Tyr Lys Val Ser Tyr	
340 345 350	
tct cct aac ttt ggc gat att gcc tta cct cca aac atg gac cta gat	1104
Ser Pro Asn Phe Gly Asp Ile Ala Leu Pro Pro Asn Met Asp Leu Asp	
355 360 365	
gac ttg aag cca gat aaa gat aat gaa aat att ttt act ggc act att	1152
Asp Leu Lys Pro Asp Lys Asp Asn Glu Asn Ile Phe Thr Gly Thr Ile	
370 375 380	
acc act gat aaa gta atc aat caa act gtt aac ggc aaa cct gct aat	1200
Thr Thr Asp Lys Val Ile Asn Gln Thr Val Asn Gly Lys Pro Ala Asn	
385 390 395 400	
gat att act ttc tca caa act gtt tca gtt aca gtt acc tgg gac aag	1248
Asp Ile Thr Phe Ser Gln Thr Val Ser Val Thr Val Thr Trp Asp Lys	
405 410 415	
gaa aat gct caa tgg gta gtc tca gaa cct aag gtt gag att aat ggt	1296
Glu Asn Ala Gln Trp Val Val Ser Glu Pro Lys Val Glu Ile Asn Gly	
420 425 430	
tat act cca atc gac att aat aag cct ggt tac tcc atc gac aag gtt	1344
Tyr Thr Pro Ile Asp Ile Asn Lys Pro Gly Tyr Ser Ile Asp Lys Val	
435 440 445	

gaa gct gat att att ggt gaa tca gac ttt aag gtt gag gat ggt aaa	1392
Glu Ala Asp Ile Ile Gly Glu Ser Asp Phe Lys Val Glu Asp Gly Lys	
450 455 460	
ctt gta gtt aat gac aag gct ttg gct aac ctt caa aac ggc caa acc	1440
Leu Val Val Asn Asp Lys Ala Leu Ala Asn Leu Gln Asn Gly Gln Thr	
465 470 475 480	
atc aac tac acc gtg act tac tct cct gta ttt ggc gat atc atc tta	1488
Ile Asn Tyr Thr Val Thr Tyr Ser Pro Val Phe Gly Asp Ile Ile Leu	
485 490 495	
cct cca ggc atc gac aaa gat gac ttg gtt gaa aat cct gat ggt tct	1536
Pro Pro Gly Ile Asp Lys Asp Asp Leu Val Glu Asn Pro Asp Gly Ser	
500 505 510	
tgg act gct aac acc act att aat aaa gtc att act cag aat atc gct	1584
Trp Thr Ala Asn Thr Thr Ile Asn Lys Val Ile Thr Gln Asn Ile Ala	
515 520 525	
aac gct aat ggc aac att aac cag att acc cta tca caa gca gct aca	1632
Asn Ala Asn Gly Asn Ile Asn Gln Ile Thr Leu Ser Gln Ala Ala Thr	
530 535 540	
gtt aca ctt acc tta aaa gac ggg aaa tgg act gta gac att aag ggc	1680
Val Thr Leu Thr Leu Lys Asp Gly Lys Trp Thr Val Asp Ile Lys Gly	
545 550 555 560	
ttc ggt gat gtt act gtt aag gat gac aat cct att aac gtt aat aga	1728
Phe Gly Asp Val Thr Val Lys Asp Asp Asn Pro Ile Asn Val Asn Arg	
565 570 575	
cct gga tac aag cat gac gta tct gct tct atc gat ggc act aag ttt	1776
Pro Gly Tyr Lys His Asp Val Ser Ala Ser Ile Asp Gly Thr Lys Phe	
580 585 590	
gat gga ttc aag atc gat gac gat ggt aat atc gta att aat gcc agt	1824
Asp Gly Phe Lys Ile Asp Asp Asp Gly Asn Ile Val Ile Asn Ala Ser	
595 600 605	
gct tgg gac att ctt aaa gat ggc gac act atc agt tac atc gtt aac	1872
Ala Trp Asp Ile Leu Lys Asp Gly Asp Thr Ile Ser Tyr Ile Val Asn	
610 615 620	
tac act cct att aag cct caa cca gat aca gta act cct cct aac aag	1920
Tyr Thr Pro Ile Lys Pro Gln Pro Asp Thr Val Thr Pro Pro Asn Lys	
625 630 635 640	
gat gac gac aac att tgg tca gat gat gtt aca gat aag gaa aaa gac	1968
Asp Asp Asp Asn Ile Trp Ser Asp Asp Val Thr Asp Lys Glu Lys Asp	
645 650 655	
gac atc atc gat aag atc gaa gac ggg gcc ctt act tgg aca gat aat	2016
Asp Ile Ile Asp Lys Ile Glu Asp Gly Ala Leu Thr Trp Thr Asp Asn	
660 665 670	
gga gat ggc act tgg tct gca act gtt gac ttt aac aag caa ctc tca	2064

Gly Asp Gly Thr Trp Ser Ala Thr Val Asp Phe Asn Lys Gln Leu Ser	
675 680 685	
caa tcc att tct ggt aat atg atc aat ggt tta cca aac atc aca gta	2112
Gln Ser Ile Ser Gly Asn Met Ile Asn Gly Leu Pro Asn Ile Thr Val	
690 695 700	
gac gtt act aag aaa gtt aca tta act gct gaa ctt aaa ggt gat aaa	2160
Asp Val Thr Lys Lys Val Thr Leu Thr Ala Glu Leu Lys Gly Asp Lys	
705 710 715 720	
ttc cat att act agc gtt aca tca ggt aaa tgg act agc gac agt aac	2208
Phe His Ile Thr Ser Val Thr Ser Gly Lys Trp Thr Ser Asp Ser Asn	
725 730 735	
tta gga cag aaa tta cct gaa tct gac aac aaa tat gac att tct gcc	2256
Leu Gly Gln Lys Leu Pro Glu Ser Asp Asn Lys Tyr Asp Ile Ser Ala	
740 745 750	
act gtt aat ggt aat gat cat gct gga tta aaa gca gaa gtt gaa aat	2304
Thr Val Asn Gly Asn Asp His Ala Gly Leu Lys Ala Glu Val Glu Asn	
755 760 765	
aca aac aca att cca ggt ctt gat tct gac ttg att caa agt att att	2352
Thr Asn Thr Ile Pro Gly Leu Asp Ser Asp Leu Ile Gln Ser Ile Ile	
770 775 780	
aac aac cat gaa tat ggc tca ctt ctc caa tta agc tat gtc att aac	2400
Asn Asn His Glu Tyr Gly Ser Leu Leu Gln Leu Ser Tyr Val Ile Asn	
785 790 795 800	
gct aac ccc ggt tct gct gat ccc gac aag cca gct gaa cct gac act	2448
Ala Asn Pro Gly Ser Ala Asp Pro Asp Lys Pro Ala Glu Pro Asp Thr	
805 810 815	
cct aat gtc gat cct gac atg ggt gta gat cca gaa aat cca tct aat	2496
Pro Asn Val Asp Pro Asp Met Gly Val Asp Pro Glu Asn Pro Ser Asn	
820 825 830	
cct gat gat aac aat ggc tca ggt gac tca aat aac tca ggc aat aat	2544
Pro Asp Asp Asn Asn Gly Ser Gly Asp Ser Asn Asn Ser Gly Asn Asn	
835 840 845	
cct ggc tca agt gat tca acc gaa aat act aca cct aag cct gaa gaa	2592
Pro Gly Ser Ser Asp Ser Thr Glu Asn Thr Thr Pro Lys Pro Glu Glu	
850 855 860	
gga cca gaa gtt aaa cca gtt aca act cca act gaa ttc acc cct ccg	2640
Gly Pro Glu Val Lys Pro Val Thr Thr Pro Thr Glu Phe Thr Pro Pro	
865 870 875 880	
ctt tct gaa gat ata gaa gat gat gat aaa aaa gca aat cca gat tca	2688
Leu Ser Glu Asp Ile Glu Asp Asp Asp Lys Lys Ala Asn Pro Asp Ser	
885 890 895	
gat tct gct caa tct gaa agt aac aag gat aat aaa ggc aaa act gtc	2736
Asp Ser Ala Gln Ser Glu Ser Asn Lys Asp Asn Lys Gly Lys Thr Val	

900	905	910	
act ggt agc aaa gct aca ggc aag aag gca act att att tca ctt tca			2784
Thr Gly Ser Lys Ala Thr Gly Lys Lys Ala Thr Ile Ile Ser Leu Ser			
915	920	925	
gaa tca ata act gct tct caa aac agt agt gct aac tca caa aat agc			2832
Glu Ser Ile Thr Ala Ser Gln Asn Ser Ser Ala Asn Ser Gln Asn Ser			
930	935	940	
tta gct aca act gat aac gag ata gca tta cca caa act ggt gaa aat			2880
Leu Ala Thr Thr Asp Asn Glu Ile Ala Leu Pro Gln Thr Gly Glu Asn			
945	950	955	960
aag gat aac ctt tct atg atg ggt att att atg gct gga ctt gct ggt			2928
Lys Asp Asn Leu Ser Met Met Gly Ile Ile Met Ala Gly Leu Ala Gly			
965	970	975	
gca ctc act act tta ggc aca gct atc aag aaa aag aag aag aac			2973
Ala Leu Thr Thr Leu Gly Thr Ala Ile Lys Lys Lys Lys Lys Asn			
980	985	990	

<210> 54

<211> 991

<212> PRT

<213> Lactobacillus acidophilus

<400> 54

Met Gln Gly Ile Ile Lys Trp Ile Glu Asp Asn Arg Leu Ser Trp Asp			
1	5	10	15
His Ile Ser Asp Gln Glu Lys Tyr Pro Gly Trp Glu Asp Val Phe Asp			
20	25	30	
Glu Ser Leu Lys Ile Asp Arg Val Asp Pro Phe Asp His Lys Asn Pro			
35	40	45	
Gln Trp Gln Ala Thr Ala Asn Lys Glu Ile Thr Ile Thr Gln Thr Val			
50	55	60	
Asn Asn Gly Ser Gln Gln Ser Thr Gln Gln Ile Lys Val Asn Tyr Asp			
65	70	75	80
Val Val Ile Tyr Ile Ala Ile Asp Pro Asn Met Ser Gly Trp Asp Ala			
85	90	95	
Leu Phe Gly Asn Tyr Lys Phe Ile Ile Ser Asp Val Lys Val Ser Asn			
100	105	110	
Ile Asn Lys Val Asp Pro Asp Thr Asn Thr Pro Lys Asp Asp Phe Asp			
115	120	125	
Ala Val Asn Ile Pro Thr Ala Pro Glu Gly Phe Glu Asn Arg Val Thr			
130	135	140	
Gly Thr Ile Glu Gly Pro Lys Phe Asp Asp Tyr Asn Ile Asn Asn Asn			
145	150	155	160
Ile Ser Leu Glu Asp Lys Val Ile Lys Thr Asn Leu Asp Ser Ile Phe			
165	170	175	
Asn Thr Ile Leu Gln Lys Gly Thr Asp Val Thr Phe Lys Tyr Asp Ile			
180	185	190	
Glu Gln Ile Ala Val Lys Lys Pro Thr Trp Val Asp Val Ile Asp Gly			
195	200	205	
Asp Asp Lys Lys Glu Trp Asn Asp Leu Phe Gln Asn Val Asp Phe Thr			

210	215	220
Lys Asp Gln Asp Lys Asp Asn Ile Trp Thr Gly Thr Val Thr Leu Asn		
225	230	235
Lys Asp Ile Ile Gln Thr Ile Asn Gly Leu Asp Gln Glu Asn Lys Gln		240
	245	250
Thr Ile His Leu Thr Lys Asp Val Thr Ile Thr Ile Gln Arg Asp Gly		255
	260	265
Asn Thr Asn Asn Phe Lys Ile Leu Thr Val Asn Gln Ser Asn Trp Thr		270
	275	280
Pro Asn Asp Ser Leu Glu Ser Thr Asp Ile Ser Lys Pro Gly Tyr Asn		285
	290	295
His Asn Val Ser Ala Ser Ile Thr Gly Thr Ser Ser Asp Asn Phe Thr		300
305	310	315
His Lys Val Glu Asn Gly His Leu Ser Thr Asn Leu Asp Phe Ser Lys		320
	325	330
Leu Glu Asn Asn Asn Asn Gln Ile Thr Ile Asn Tyr Lys Val Ser Tyr		335
	340	345
Ser Pro Asn Phe Gly Asp Ile Ala Leu Pro Pro Asn Met Asp Leu Asp		350
	355	360
Asp Leu Lys Pro Asp Lys Asp Asn Glu Asn Ile Phe Thr Gly Thr Ile		365
	370	375
Thr Thr Asp Lys Val Ile Asn Gln Thr Val Asn Gly Lys Pro Ala Asn		380
385	390	395
Asp Ile Thr Phe Ser Gln Thr Val Ser Val Thr Val Thr Trp Asp Lys		400
	405	410
Glu Asn Ala Gln Trp Val Val Ser Glu Pro Lys Val Glu Ile Asn Gly		415
	420	425
Tyr Thr Pro Ile Asp Ile Asn Lys Pro Gly Tyr Ser Ile Asp Lys Val		430
	435	440
Glu Ala Asp Ile Ile Gly Glu Ser Asp Phe Lys Val Glu Asp Gly Lys		445
	450	455
Leu Val Val Asn Asp Lys Ala Leu Ala Asn Leu Gln Asn Gly Gln Thr		460
465	470	475
Ile Asn Tyr Thr Val Thr Tyr Ser Pro Val Phe Gly Asp Ile Ile Leu		480
	485	490
Pro Pro Gly Ile Asp Lys Asp Asp Leu Val Glu Asn Pro Asp Gly Ser		495
	500	505
Trp Thr Ala Asn Thr Thr Ile Asn Lys Val Ile Thr Gln Asn Ile Ala		510
	515	520
Asn Ala Asn Gly Asn Ile Asn Gln Ile Thr Leu Ser Gln Ala Ala Thr		525
	530	535
Val Thr Leu Thr Leu Lys Asp Gly Lys Trp Thr Val Asp Ile Lys Gly		540
545	550	555
Phe Gly Asp Val Thr Val Lys Asp Asp Asn Pro Ile Asn Val Asn Arg		560
	565	570
Pro Gly Tyr Lys His Asp Val Ser Ala Ser Ile Asp Gly Thr Lys Phe		575
	580	585
Asp Gly Phe Lys Ile Asp Asp Asp Gly Asn Ile Val Ile Asn Ala Ser		590
	595	600
Ala Trp Asp Ile Leu Lys Asp Gly Asp Thr Ile Ser Tyr Ile Val Asn		605
	610	615
Tyr Thr Pro Ile Lys Pro Gln Pro Asp Thr Val Thr Pro Pro Asn Lys		620
625	630	635
Asp Asp Asp Asn Ile Trp Ser Asp Asp Val Thr Asp Lys Glu Lys Asp		640
	645	650
Asp Ile Ile Asp Lys Ile Glu Asp Gly Ala Leu Thr Trp Thr Asp Asn		655
	660	665
		670

Gly Asp Gly Thr Trp Ser Ala Thr Val Asp Phe Asn Lys Gln Leu Ser
 675 680 685
 Gln Ser Ile Ser Gly Asn Met Ile Asn Gly Leu Pro Asn Ile Thr Val
 690 695 700
 Asp Val Thr Lys Lys Val Thr Leu Thr Ala Glu Leu Lys Gly Asp Lys
 705 710 715 720
 Phe His Ile Thr Ser Val Thr Ser Gly Lys Trp Thr Ser Asp Ser Asn
 725 730 735
 Leu Gly Gln Lys Leu Pro Glu Ser Asp Asn Lys Tyr Asp Ile Ser Ala
 740 745 750
 Thr Val Asn Gly Asn Asp His Ala Gly Leu Lys Ala Glu Val Glu Asn
 755 760 765
 Thr Asn Thr Ile Pro Gly Leu Asp Ser Asp Leu Ile Gln Ser Ile Ile
 770 775 780
 Asn Asn His Glu Tyr Gly Ser Leu Leu Gln Leu Ser Tyr Val Ile Asn
 785 790 795 800
 Ala Asn Pro Gly Ser Ala Asp Pro Asp Lys Pro Ala Glu Pro Asp Thr
 805 810 815
 Pro Asn Val Asp Pro Asp Met Gly Val Asp Pro Glu Asn Pro Ser Asn
 820 825 830
 Pro Asp Asp Asn Asn Gly Ser Gly Asp Ser Asn Asn Ser Gly Asn Asn
 835 840 845
 Pro Gly Ser Ser Asp Ser Thr Glu Asn Thr Thr Pro Lys Pro Glu Glu
 850 855 860
 Gly Pro Glu Val Lys Pro Val Thr Thr Pro Thr Glu Phe Thr Pro Pro
 865 870 875 880
 Leu Ser Glu Asp Ile Glu Asp Asp Asp Lys Lys Ala Asn Pro Asp Ser
 885 890 895
 Asp Ser Ala Gln Ser Glu Ser Asn Lys Asp Asn Lys Gly Lys Thr Val
 900 905 910
 Thr Gly Ser Lys Ala Thr Gly Lys Lys Ala Thr Ile Ile Ser Leu Ser
 915 920 925
 Glu Ser Ile Thr Ala Ser Gln Asn Ser Ser Ala Asn Ser Gln Asn Ser
 930 935 940
 Leu Ala Thr Thr Asp Asn Glu Ile Ala Leu Pro Gln Thr Gly Glu Asn
 945 950 955 960
 Lys Asp Asn Leu Ser Met Met Gly Ile Ile Met Ala Gly Leu Ala Gly
 965 970 975
 Ala Leu Thr Thr Leu Gly Thr Ala Ile Lys Lys Lys Lys Lys Asn
 980 985 990

<210> 55

<211> 2718

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1612 - fibrinogen-binding protein

<220>

<221> CDS

<222> (1)...(2718)

<400> 55

atg gtt tct	aaa aag aat atc aag atg att gaa gag aaa agt aga gat	48
Met Val Ser	Lys Lys Asn Ile Lys Met Ile Glu Glu Lys Ser Arg Asp	
1	5 10 15	
gaa aag caa cgc ttt tca att cgt aag tta agt gtg ggt gcg gct tcc	96	
Glu Lys Gln Arg Phe Ser Ile Arg Lys Leu Ser Val Gly Ala Ala Ser		
20 25 30		
gtt tta att gga ttg gct ttt aca gta tat gga ggt caa act gta caa	144	
Val Leu Ile Gly Leu Ala Phe Thr Val Tyr Gly Gly Gln Thr Val Gln		
35 40 45		
gct gac acc act gaa gct agt caa gta acc act gct caa gaa aac aat	192	
Ala Asp Thr Thr Glu Ala Ser Gln Val Thr Thr Ala Gln Glu Asn Asn		
50 55 60		
gaa gag act ggt aat gaa aag tcc gaa aat aca gtt ttg gat aat tca	240	
Glu Glu Thr Gly Asn Glu Lys Ser Glu Asn Thr Val Leu Asp Asn Ser		
65 70 75 80		
aac gat ata gaa aat agt gca act aca gcc agt aaa acc cca agt tca	288	
Asn Asp Ile Glu Asn Ser Ala Thr Thr Ala Ser Lys Thr Pro Ser Ser		
85 90 95		
agt gtt gaa gaa aaa gct cct tca ata act att gat gca agt agt tct	336	
Ser Val Glu Glu Lys Ala Pro Ser Ile Thr Ile Asp Ala Ser Ser Ser		
100 105 110		
tta aaa aat aaa aac gat aat att gaa gtt aaa gat gat aat gct aag	384	
Leu Lys Asn Lys Asn Asp Asn Ile Glu Val Lys Asp Asp Asn Ala Lys		
115 120 125		
gtt aat aaa act atg caa tca tct tca gtt gat aag gca aat aat gta	432	
Val Asn Lys Thr Met Gln Ser Ser Ser Val Asp Lys Ala Asn Asn Val		
130 135 140		
act tca aat gaa aaa aca gaa agt caa cag gct gta aat act aaa gaa	480	
Thr Ser Asn Glu Lys Thr Glu Ser Gln Gln Ala Val Asn Thr Lys Glu		
145 150 155 160		
gat aat cca act aag agt gaa gat act aaa aaa gta aat tct act gct	528	
Asp Asn Pro Thr Lys Ser Glu Asp Thr Lys Lys Val Asn Ser Thr Ala		
165 170 175		
att aat gta ggg tct aat gaa aat aca gag gtt gct tct gct caa caa	576	
Ile Asn Val Gly Ser Asn Glu Asn Thr Glu Val Ala Ser Ala Gln Gln		
180 185 190		
aca aat aat ttt gaa gta gat aag ggt act act ttt gct act aat gaa	624	
Thr Asn Asn Phe Glu Val Asp Lys Gly Thr Thr Phe Ala Thr Asn Glu		
195 200 205		
aaa aca gaa gca aat tca act aat gtt tca gaa aat gtt gat tcg att	672	
Lys Thr Glu Ala Asn Ser Thr Asn Val Ser Glu Asn Val Asp Ser Ile		
210 215 220		

gaa gta cct tca aat aag tta aca act gac act cta aat att tct aag	720
Glu Val Pro Ser Asn Lys Leu Thr Thr Asp Thr Leu Asn Ile Ser Lys	
225 230 235 240	
aaa aca gta tct gct aat gtg act aat gcc gtt tat aca atg aaa aca	768
Lys Thr Val Ser Ala Asn Val Thr Asn Ala Val Tyr Thr Met Lys Thr	
245 250 255	
gta act agt aat gcg gca aat gat gta aat aaa aac aaa ttg cgt tca	816
Val Thr Ser Asn Ala Ala Asn Asp Val Asn Lys Asn Lys Leu Arg Ser	
260 265 270	
aca act atg ata tta gct gct gaa gta gaa gat cct aat gca gta act	864
Thr Thr Met Ile Leu Ala Ala Glu Val Glu Asp Pro Asn Ala Val Thr	
275 280 285	
gtt agt gat gcg aaa gga ttt att aat gca att caa aat ggg act gct	912
Val Ser Asp Ala Lys Gly Phe Ile Asn Ala Ile Gln Asn Gly Thr Ala	
290 295 300	
act act att aat gtt gct aaa gat ctt aat tta gca gaa caa aca gat	960
Thr Thr Ile Asn Val Ala Lys Asp Leu Asn Leu Ala Glu Gln Thr Asp	
305 310 315 320	
aaa gaa tat aca gaa att acc atc aag aat aaa cgt aat att gta att	1008
Lys Glu Tyr Thr Glu Ile Thr Ile Lys Asn Lys Arg Asn Ile Val Ile	
325 330 335	
caa tca gat aat cca gaa gaa aaa cgt aca att gac ttc tcg gga tat	1056
Gln Ser Asp Asn Pro Glu Glu Lys Arg Thr Ile Asp Phe Ser Gly Tyr	
340 345 350	
tca ttt gat atg gat aca cag aat tct gta acc ttt aaa gac ttg aat	1104
Ser Phe Asp Met Asp Thr Gln Asn Ser Val Thr Phe Lys Asp Leu Asn	
355 360 365	
att tat gct cgt agt tac tgg ggt ctt gtt tat aat gct ggt gga tac	1152
Ile Tyr Ala Arg Ser Tyr Trp Gly Leu Val Tyr Asn Ala Gly Gly Tyr	
370 375 380	
aca ttt gat aat gtt aac ttt acg ggt tca caa ctt atc tat acc aaa	1200
Thr Phe Asp Asn Val Asn Phe Thr Gly Ser Gln Leu Ile Tyr Thr Lys	
385 390 395 400	
cca tgg att aat tca acc tta aca ttt aag aat aat att act gca aat	1248
Pro Trp Ile Asn Ser Thr Leu Thr Phe Lys Asn Asn Ile Thr Ala Asn	
405 410 415	
tct gtc tca tca tat gta gga cca ctt gat ggt aag aca cgc gat act	1296
Ser Val Ser Ser Tyr Val Gly Pro Leu Asp Gly Lys Thr Arg Asp Thr	
420 425 430	
caa caa aat ggt ggg cag caa att ctt caa ttt gaa ggt gga aca aat	1344
Gln Gln Asn Gly Gly Gln Gln Ile Leu Gln Phe Glu Gly Gly Thr Asn	
435 440 445	
caa att att ttt gat gaa aac agt aat gta acc tta aca aca gaa gat	1392

Gln Ile Ile Phe Asp Glu Asn Ser Asn Val Thr Leu Thr Thr Glu Asp	
450 455 460	
gct aat gct ctt gaa att gac ggc ggc acc gca aca att gat gta aaa	1440
Ala Asn Ala Leu Glu Ile Asp Gly Gly Thr Ala Thr Ile Asp Val Lys	
465 470 475 480	
gac ggt gca aat gta gca att aat cca cat tct aaa ggt aat cct gaa	1488
Asp Gly Ala Asn Val Ala Ile Asn Pro His Ser Lys Gly Asn Pro Glu	
485 490 495	
cat cgt aat gga att gga act ggg gac gtt gca cgt gct att gct gcc	1536
His Arg Asn Gly Ile Gly Thr Gly Asp Val Ala Arg Ala Ile Ala Ala	
500 505 510	
aat gca aag atg aca att aat att gat cca aat tca act tta act att	1584
Asn Ala Lys Met Thr Ile Asn Ile Asp Pro Asn Ser Thr Leu Thr Ile	
515 520 525	
aat act gaa aag gta gat ggc gat aaa gat gtt gca gga gca tta tat	1632
Asn Thr Glu Lys Val Asp Gly Asp Lys Asp Val Ala Gly Ala Leu Tyr	
530 535 540	
tta aat tct gag gct gcc ctt aat gta aat ggt aaa tta gtt atc aac	1680
Leu Asn Ser Glu Ala Ala Leu Asn Val Asn Gly Lys Leu Val Ile Asn	
545 550 555 560	
tca aat gga aca cca agt gca aat aaa agt aac ggg gtt cca gta tat	1728
Ser Asn Gly Thr Ser Ser Ala Asn Lys Ser Asn Gly Val Pro Val Tyr	
565 570 575	
att aat gga agt gca aag att aat gtt gga aat ggt ggt agc ttc tca	1776
Ile Asn Gly Ser Ala Lys Ile Asn Val Gly Asn Gly Gly Ser Phe Ser	
580 585 590	
tta gat gct aca aat ctt gga aat tac agc tct agc cta att tct att	1824
Leu Asp Ala Thr Asn Leu Gly Asn Tyr Ser Ser Ser Leu Ile Ser Ile	
595 600 605	
aat ggt aag ggg act gtt aag tta gat cct cac tct agt ttc aag att	1872
Asn Gly Lys Gly Thr Val Lys Leu Asp Pro His Ser Ser Ser Phe Lys Ile	
610 615 620	
agc ggt gac ggt act gga aat gta act gca att aat ctt tca agc ggt	1920
Ser Gly Asp Gly Thr Gly Asn Val Thr Ala Ile Asn Leu Ser Ser Gly	
625 630 635 640	
agt act ttc act tcc gat caa cca gat tca ttt act att gat ctt tct	1968
Ser Thr Phe Thr Ser Asp Gln Pro Asp Ser Phe Thr Ile Asp Leu Ser	
645 650 655	
gca aat acc agt act ggc aaa tca tta att aaa aac gga gcc atc aat	2016
Ala Asn Thr Ser Thr Gly Lys Ser Leu Ile Lys Asn Gly Ala Ile Asn	
660 665 670	
ttc acc cgt gtt aag aca gtt act gat gga agc gaa tca cag cct tta	2064
Phe Thr Arg Val Lys Thr Val Thr Asp Gly Ser Glu Ser Gln Pro Leu	

675	680	685	
ggc aaa att gat gta act tat gat aga aat ggt aat gct act tct tac Gly Lys Ile Asp Val Thr Tyr Asp Arg Asn Gly Asn Ala Thr Ser Tyr 690 695 700			2112
att att acg gca caa gat gaa aat act gtt aaa caa gtt gga gaa ggt Ile Ile Thr Ala Gln Asp Glu Asn Thr Val Lys Gln Val Gly Glu Gly 705 710 715 720			2160
ctt gct aat aag aac ttg att gat ctt gtt aag gct ggt gaa gat gtt Leu Ala Asn Lys Asn Leu Ile Asp Leu Val Lys Ala Gly Glu Asp Val 725 730 735			2208
act cta tct aat ctt cat tta agt aag aat aat gta ttg act ggt act Thr Leu Ser Asn Leu His Leu Ser Lys Asn Asn Val Leu Thr Gly Thr 740 745 750			2256
gtg gct tca agc ggt agc aac aat cca att tat gta act gtt acc gtt Val Ala Ser Ser Gly Ser Asn Asn Pro Ile Tyr Val Thr Val Thr Val 755 760 765			2304
ggg ggt gta agc act aat gtg cca gta gcc gga aat tat act gtg tac Gly Gly Val Ser Thr Asn Val Pro Val Ala Gly Asn Tyr Thr Val Tyr 770 775 780			2352
acc aac act aaa ggc aca gta act tca aac aat att gct tac gct gca Thr Asn Thr Lys Gly Thr Val Thr Ser Asn Asn Ile Ala Tyr Ala Ala 785 790 795 800			2400
caa act gct tca act ggt ggt aat ttc tct att gat tta tcc aag ctt Gln Thr Ala Ser Thr Gly Gly Asn Phe Ser Ile Asp Leu Ser Lys Leu 805 810 815			2448
gca agc aag ttg act gat gat acg caa gtt aaa gtg act gct aca aaa Ala Ser Lys Leu Thr Asp Asp Thr Gln Val Lys Val Thr Ala Thr Lys 820 825 830			2496
gat ttc gtt gaa gca act caa att gaa agt gtg gca gca tta cgt gcg Asp Phe Val Glu Ala Thr Gln Ile Glu Ser Val Ala Ala Leu Arg Ala 835 840 845			2544
ctt aat act act act ctt caa gaa tta gta gat gct gct cca gca gaa Leu Asn Thr Thr Thr Leu Gln Glu Leu Val Asp Ala Ala Pro Ala Glu 850 855 860			2592
gaa gca aag cca agc tac tac aat gca act gca gaa gcc caa aag gca Glu Ala Lys Pro Ser Tyr Tyr Asn Ala Thr Ala Glu Ala Gln Lys Ala 865 870 875 880			2640
tat acg gat gca att tca act ggt aaa cta ttc ttg cta atc caa ata Tyr Thr Asp Ala Ile Ser Thr Gly Lys Leu Phe Leu Leu Ile Gln Ile 885 890 895			2688
att acg atc aag ttg acg ttg atg atg ccg Ile Thr Ile Lys Leu Thr Leu Met Met Pro 900 905			2718

<210> 56
 <211> 906
 <212> PRT
 <213> *Lactobacillus acidophilus*

<400> 56
 Met Val Ser Lys Lys Asn Ile Lys Met Ile Glu Glu Lys Ser Arg Asp
 1 5 10 15
 Glu Lys Gln Arg Phe Ser Ile Arg Lys Leu Ser Val Gly Ala Ala Ser
 20 25 30
 Val Leu Ile Gly Leu Ala Phe Thr Val Tyr Gly Gly Gln Thr Val Gln
 35 40 45
 Ala Asp Thr Thr Glu Ala Ser Gln Val Thr Thr Ala Gln Glu Asn Asn
 50 55 60
 Glu Glu Thr Gly Asn Glu Lys Ser Glu Asn Thr Val Leu Asp Asn Ser
 65 70 75 80
 Asn Asp Ile Glu Asn Ser Ala Thr Thr Ala Ser Lys Thr Pro Ser Ser
 85 90 95
 Ser Val Glu Glu Lys Ala Pro Ser Ile Thr Ile Asp Ala Ser Ser Ser
 100 105 110
 Leu Lys Asn Lys Asn Asp Asn Ile Glu Val Lys Asp Asp Asn Ala Lys
 115 120 125
 Val Asn Lys Thr Met Gln Ser Ser Ser Val Asp Lys Ala Asn Asn Val
 130 135 140
 Thr Ser Asn Glu Lys Thr Glu Ser Gln Gln Ala Val Asn Thr Lys Glu
 145 150 155 160
 Asp Asn Pro Thr Lys Ser Glu Asp Thr Lys Lys Val Asn Ser Thr Ala
 165 170 175
 Ile Asn Val Gly Ser Asn Glu Asn Thr Glu Val Ala Ser Ala Gln Gln
 180 185 190
 Thr Asn Asn Phe Glu Val Asp Lys Gly Thr Thr Phe Ala Thr Asn Glu
 195 200 205
 Lys Thr Glu Ala Asn Ser Thr Asn Val Ser Glu Asn Val Asp Ser Ile
 210 215 220
 Glu Val Pro Ser Asn Lys Leu Thr Thr Asp Thr Leu Asn Ile Ser Lys
 225 230 235 240
 Lys Thr Val Ser Ala Asn Val Thr Asn Ala Val Tyr Thr Met Lys Thr
 245 250 255
 Val Thr Ser Asn Ala Ala Asn Asp Val Asn Lys Asn Lys Leu Arg Ser
 260 265 270
 Thr Thr Met Ile Leu Ala Ala Glu Val Glu Asp Pro Asn Ala Val Thr
 275 280 285
 Val Ser Asp Ala Lys Gly Phe Ile Asn Ala Ile Gln Asn Gly Thr Ala
 290 295 300
 Thr Thr Ile Asn Val Ala Lys Asp Leu Asn Leu Ala Glu Gln Thr Asp
 305 310 315 320
 Lys Glu Tyr Thr Glu Ile Thr Ile Lys Asn Lys Arg Asn Ile Val Ile
 325 330 335
 Gln Ser Asp Asn Pro Glu Glu Lys Arg Thr Ile Asp Phe Ser Gly Tyr
 340 345 350
 Ser Phe Asp Met Asp Thr Gln Asn Ser Val Thr Phe Lys Asp Leu Asn
 355 360 365
 Ile Tyr Ala Arg Ser Tyr Trp Gly Leu Val Tyr Asn Ala Gly Gly Tyr
 370 375 380
 Thr Phe Asp Asn Val Asn Phe Thr Gly Ser Gln Leu Ile Tyr Thr Lys

385					390					395				400	
Pro	Trp	Ile	Asn	Ser	Thr	Leu	Thr	Phe	Lys	Asn	Asn	Ile	Thr	Ala	Asn
				405					410					415	
Ser	Val	Ser	Ser	Tyr	Val	Gly	Pro	Leu	Asp	Gly	Lys	Thr	Arg	Asp	Thr
				420				425					430		
Gln	Gln	Asn	Gly	Gly	Gln	Gln	Ile	Leu	Gln	Phe	Glu	Gly	Gly	Thr	Asn
		435					440					445			
Gln	Ile	Ile	Phe	Asp	Glu	Asn	Ser	Asn	Val	Thr	Leu	Thr	Thr	Glu	Asp
	450					455					460				
Ala	Asn	Ala	Leu	Glu	Ile	Asp	Gly	Gly	Thr	Ala	Thr	Ile	Asp	Val	Lys
465					470					475					480
Asp	Gly	Ala	Asn	Val	Ala	Ile	Asn	Pro	His	Ser	Lys	Gly	Asn	Pro	Glu
			485					490						495	
His	Arg	Asn	Gly	Ile	Gly	Thr	Gly	Asp	Val	Ala	Arg	Ala	Ile	Ala	Ala
		500					505						510		
Asn	Ala	Lys	Met	Thr	Ile	Asn	Ile	Asp	Pro	Asn	Ser	Thr	Leu	Thr	Ile
		515					520					525			
Asn	Thr	Glu	Lys	Val	Asp	Gly	Asp	Lys	Asp	Val	Ala	Gly	Ala	Leu	Tyr
	530					535					540				
Leu	Asn	Ser	Glu	Ala	Ala	Leu	Asn	Val	Asn	Gly	Lys	Leu	Val	Ile	Asn
545					550					555					560
Ser	Asn	Gly	Thr	Pro	Ser	Ala	Asn	Lys	Ser	Asn	Gly	Val	Pro	Val	Tyr
				565					570						575
Ile	Asn	Gly	Ser	Ala	Lys	Ile	Asn	Val	Gly	Asn	Gly	Gly	Ser	Phe	Ser
			580				585						590		
Leu	Asp	Ala	Thr	Asn	Leu	Gly	Asn	Tyr	Ser	Ser	Ser	Leu	Ile	Ser	Ile
	595					600						605			
Asn	Gly	Lys	Gly	Thr	Val	Lys	Leu	Asp	Pro	His	Ser	Ser	Phe	Lys	Ile
	610					615					620				
Ser	Gly	Asp	Gly	Thr	Gly	Asn	Val	Thr	Ala	Ile	Asn	Leu	Ser	Ser	Gly
625					630					635					640
Ser	Thr	Phe	Thr	Ser	Asp	Gln	Pro	Asp	Ser	Phe	Thr	Ile	Asp	Leu	Ser
				645					650					655	
Ala	Asn	Thr	Ser	Thr	Gly	Lys	Ser	Leu	Ile	Lys	Asn	Gly	Ala	Ile	Asn
			660					665					670		
Phe	Thr	Arg	Val	Lys	Thr	Val	Thr	Asp	Gly	Ser	Glu	Ser	Gln	Pro	Leu
		675					680				685				
Gly	Lys	Ile	Asp	Val	Thr	Tyr	Asp	Arg	Asn	Gly	Asn	Ala	Thr	Ser	Tyr
	690					695					700				
Ile	Ile	Thr	Ala	Gln	Asp	Glu	Asn	Thr	Val	Lys	Gln	Val	Gly	Glu	Gly
705					710					715					720
Leu	Ala	Asn	Lys	Asn	Leu	Ile	Asp	Leu	Val	Lys	Ala	Gly	Glu	Asp	Val
				725					730					735	
Thr	Leu	Ser	Asn	Leu	His	Leu	Ser	Lys	Asn	Asn	Val	Leu	Thr	Gly	Thr
			740					745					750		
Val	Ala	Ser	Ser	Gly	Ser	Asn	Asn	Pro	Ile	Tyr	Val	Thr	Val	Thr	Val
		755					760					765			
Gly	Gly	Val	Ser	Thr	Asn	Val	Pro	Val	Ala	Gly	Asn	Tyr	Thr	Val	Tyr
	770					775					780				
Thr	Asn	Thr	Lys	Gly	Thr	Val	Thr	Ser	Asn	Asn	Ile	Ala	Tyr	Ala	Ala
785					790					795					800
Gln	Thr	Ala	Ser	Thr	Gly	Gly	Asn	Phe	Ser	Ile	Asp	Leu	Ser	Lys	Leu
				805					810					815	
Ala	Ser	Lys	Leu	Thr	Asp	Asp	Thr	Gln	Val	Lys	Val	Thr	Ala	Thr	Lys
			820					825					830		
Asp	Phe	Val	Glu	Ala	Thr	Gln	Ile	Glu	Ser	Val	Ala	Ala	Leu	Arg	Ala
	835						840					845			

```

Leu Asn Thr Thr Thr Leu Gln Glu Leu Val Asp Ala Ala Pro Ala Glu
   850               855               860
Glu Ala Lys Pro Ser Tyr Tyr Asn Ala Thr Ala Glu Ala Gln Lys Ala
   865               870               875               880
Tyr Thr Asp Ala Ile Ser Thr Gly Lys Leu Phe Leu Leu Ile Gln Ile
               885               890               895
Ile Thr Ile Lys Leu Thr Leu Met Met Pro
   900               905

```

<210> 57

<211> 1698

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1148 - fibronectin-binding protein

<220>

<221> CDS

<222> (1)...(1698)

<400> 57

```

gtg ata tac atg gca ttt gac gga tta ttt atc cat agt tta cta caa   48
Met Ile Tyr Met Ala Phe Asp Gly Leu Phe Ile His Ser Leu Leu Gln
  1             5             10             15

gat ttg acc cct aca tta gta gat ggt cga tta tca aaa att tac caa   96
Asp Leu Thr Pro Thr Leu Val Asp Gly Arg Leu Ser Lys Ile Tyr Gln
             20             25             30

cca ttt gaa caa gat cta ata tta act ttt aga aaa aat aga aag aat   144
Pro Phe Glu Gln Asp Leu Ile Leu Thr Phe Arg Lys Asn Arg Lys Asn
             35             40             45

tat caa tta tta att tca gcc aac gct caa tat cct aga atg tat tta   192
Tyr Gln Leu Leu Ile Ser Ala Asn Ala Gln Tyr Pro Arg Met Tyr Leu
             50             55             60

act gag cag act att gct aat cca gac aaa gca cct att ttt gtt atg   240
Thr Glu Gln Thr Ile Ala Asn Pro Asp Lys Ala Pro Ile Phe Val Met
             65             70             75             80

gtt tta aga aag tat ttg gaa ggt tca gtc tta caa tct att gaa caa   288
Val Leu Arg Lys Tyr Leu Glu Gly Ser Val Leu Gln Ser Ile Glu Gln
             85             90             95

att ggt gtg aac cga att ata aac ctt cat ttc agt aat cga aac gaa   336
Ile Gly Val Asn Arg Ile Ile Asn Leu His Phe Ser Asn Arg Asn Glu
             100            105            110

tta ggt gat caa gta aaa tta gta tta tcc gtt gaa tta atg gga cga   384
Leu Gly Asp Gln Val Lys Leu Val Leu Ser Val Glu Leu Met Gly Arg
             115            120            125

```

cat agt aat gta att ctc tat gat caa cag aat ggt cat att att gat	432
His Ser Asn Val Ile Leu Tyr Asp Gln Gln Asn Gly His Ile Ile Asp	
130 135 140	
cta ttg aag cga ata aat cct gat gaa aat aga gct cgt att tta tta	480
Leu Leu Lys Arg Ile Asn Pro Asp Glu Asn Arg Ala Arg Ile Leu Leu	
145 150 155 160	
cct aag gca aaa tat gag ctt ccc cct ctt aaa cct ggt ata aat ggt	528
Pro Lys Ala Lys Tyr Glu Leu Pro Pro Leu Lys Pro Gly Ile Asn Gly	
165 170 175	
tta gta gta act gaa aat caa ttt aaa aag tta agc aat gaa aaa agc	576
Leu Val Val Thr Glu Asn Gln Phe Lys Lys Leu Ser Asn Glu Lys Ser	
180 185 190	
att cca gat tta gtg aaa tca atg gat ggt tta gac aga gac gat cgt	624
Ile Pro Asp Leu Val Lys Ser Met Asp Gly Leu Asp Arg Asp Asp Arg	
195 200 205	
gaa gaa tta act ggt tat ctt gaa gat gat ttt agc tat tct tca ttt	672
Glu Glu Leu Thr Gly Tyr Leu Glu Asp Asp Phe Ser Tyr Ser Ser Phe	
210 215 220	
aag act ttc ttt gat cag ttt aat aat cca aga gct ttc gtt tta aaa	720
Lys Thr Phe Phe Asp Gln Phe Asn Asn Pro Arg Ala Phe Val Leu Lys	
225 230 235 240	
act cca aga aat aaa cgt aag att ttc tgt tat ctt ccc tat cat tta	768
Thr Pro Arg Asn Lys Arg Lys Ile Phe Cys Tyr Leu Pro Tyr His Leu	
245 250 255	
gat tta gag aaa gaa aat tct aat cct gat tta aat aaa ggt tta gat	816
Asp Leu Glu Lys Glu Asn Ser Asn Pro Asp Leu Asn Lys Gly Leu Asp	
260 265 270	
gaa ttt tat gaa tac caa gca aca cgt gat tgg gtt aaa caa cgt gct	864
Glu Phe Tyr Glu Tyr Gln Ala Thr Arg Asp Trp Val Lys Gln Arg Ala	
275 280 285	
agt cag gtt gaa cgt gtc gtc aaa aac gaa cag aac aaa cta agt aag	912
Ser Gln Val Glu Arg Val Val Lys Asn Glu Gln Asn Lys Leu Ser Lys	
290 295 300	
aag att aag aaa tta gaa aag caa tta aac tta gca gaa aat tct gag	960
Lys Ile Lys Lys Leu Glu Lys Gln Leu Asn Leu Ala Glu Asn Ser Glu	
305 310 315 320	
ggc tat cgt atc aag ggt gaa ata tta aat gct aat tta gga caa gta	1008
Gly Tyr Arg Ile Lys Gly Glu Ile Leu Asn Ala Asn Leu Gly Gln Val	
325 330 335	
aaa cca gga atg act gag gtt tcc tta cct aac tat tat gaa aat aat	1056
Lys Pro Gly Met Thr Glu Val Ser Leu Pro Asn Tyr Tyr Glu Asn Asn	
340 345 350	

aaa cct ata agc att aaa ctt gat cca gct tta tct ccg gct cga aat	1104
Lys Pro Ile Ser Ile Lys Leu Asp Pro Ala Leu Ser Pro Ala Arg Asn	
355 360 365	
gca caa aaa tat ttc act cgc tat aaa aaa tta cgt gat tct atc aaa	1152
Ala Gln Lys Tyr Phe Thr Arg Tyr Lys Lys Leu Arg Asp Ser Ile Lys	
370 375 380	
cac gtt aac gaa caa att aaa atc gct aaa gaa aat ctt cgc tat ttt	1200
His Val Asn Glu Gln Ile Lys Ile Ala Lys Glu Asn Leu Arg Tyr Phe	
385 390 395 400	
gat tct atc caa aca gct att gat aat gct gat cca caa gat att gat	1248
Asp Ser Ile Gln Thr Ala Ile Asp Asn Ala Asp Pro Gln Asp Ile Asp	
405 410 415	
caa ata act gac gaa ttg att aat caa ggt tat att aga aag caa caa	1296
Gln Ile Thr Asp Glu Leu Ile Asn Gln Gly Tyr Ile Arg Lys Gln Gln	
420 425 430	
aaa aat aga cgt aag aag aaa att act gaa cgc aat cta aat gaa ttc	1344
Lys Asn Arg Arg Lys Lys Lys Ile Thr Glu Arg Asn Leu Asn Glu Phe	
435 440 445	
cag ctt tct tct gga aaa cat gtc tta gtg ggt aaa aat aat tac caa	1392
Gln Leu Ser Ser Gly Lys His Val Leu Val Gly Lys Asn Asn Tyr Gln	
450 455 460	
aat gac tgg ctt act cta aaa aaa gct aat aaa tta gat tat tgg ttc	1440
Asn Asp Trp Leu Thr Leu Lys Lys Ala Asn Lys Leu Asp Tyr Trp Phe	
465 470 475 480	
cac gtt aaa aat atg cct ggt tca cat gtt att ttg cga gat gat caa	1488
His Val Lys Asn Met Pro Gly Ser His Val Ile Leu Arg Asp Asp Gln	
485 490 495	
cct acc gat caa gat att aaa gaa gct gca gag att gct gca ttt ttc	1536
Pro Thr Asp Gln Asp Ile Lys Glu Ala Ala Glu Ile Ala Ala Phe Phe	
500 505 510	
tct aaa gcc aaa aat tct gcc cac gtt caa gtt gac tac gtt caa gat	1584
Ser Lys Ala Lys Asn Ser Ala His Val Gln Val Asp Tyr Val Gln Asp	
515 520 525	
aag cgt gta aag aag cct aat ggg gct aag cca gga ttc gta att tac	1632
Lys Arg Val Lys Lys Pro Asn Gly Ala Lys Pro Gly Phe Val Ile Tyr	
530 535 540	
aca gga cag aat tca atc gaa gtt aca cct aaa gaa gac gaa att atg	1680
Thr Gly Gln Asn Ser Ile Glu Val Thr Pro Lys Glu Asp Glu Ile Met	
545 550 555 560	
gct aaa aaa atc aat aaa	1698
Ala Lys Lys Ile Asn Lys	
565	

<210> 58
 <211> 566
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 58

```

Met Ile Tyr Met Ala Phe Asp Gly Leu Phe Ile His Ser Leu Leu Gln
 1           5           10           15
Asp Leu Thr Pro Thr Leu Val Asp Gly Arg Leu Ser Lys Ile Tyr Gln
           20           25           30
Pro Phe Glu Gln Asp Leu Ile Leu Thr Phe Arg Lys Asn Arg Lys Asn
           35           40           45
Tyr Gln Leu Leu Ile Ser Ala Asn Ala Gln Tyr Pro Arg Met Tyr Leu
 50           55           60
Thr Glu Gln Thr Ile Ala Asn Pro Asp Lys Ala Pro Ile Phe Val Met
 65           70           75           80
Val Leu Arg Lys Tyr Leu Glu Gly Ser Val Leu Gln Ser Ile Glu Gln
           85           90           95
Ile Gly Val Asn Arg Ile Ile Asn Leu His Phe Ser Asn Arg Asn Glu
           100          105          110
Leu Gly Asp Gln Val Lys Leu Val Leu Ser Val Glu Leu Met Gly Arg
           115          120          125
His Ser Asn Val Ile Leu Tyr Asp Gln Gln Asn Gly His Ile Ile Asp
           130          135          140
Leu Leu Lys Arg Ile Asn Pro Asp Glu Asn Arg Ala Arg Ile Leu Leu
 145          150          155          160
Pro Lys Ala Lys Tyr Glu Leu Pro Pro Leu Lys Pro Gly Ile Asn Gly
           165          170          175
Leu Val Val Thr Glu Asn Gln Phe Lys Lys Leu Ser Asn Glu Lys Ser
           180          185          190
Ile Pro Asp Leu Val Lys Ser Met Asp Gly Leu Asp Arg Asp Asp Arg
           195          200          205
Glu Glu Leu Thr Gly Tyr Leu Glu Asp Asp Phe Ser Tyr Ser Ser Phe
           210          215          220
Lys Thr Phe Phe Asp Gln Phe Asn Asn Pro Arg Ala Phe Val Leu Lys
 225          230          235          240
Thr Pro Arg Asn Lys Arg Lys Ile Phe Cys Tyr Leu Pro Tyr His Leu
           245          250          255
Asp Leu Glu Lys Glu Asn Ser Asn Pro Asp Leu Asn Lys Gly Leu Asp
           260          265          270
Glu Phe Tyr Glu Tyr Gln Ala Thr Arg Asp Trp Val Lys Gln Arg Ala
           275          280          285
Ser Gln Val Glu Arg Val Val Lys Asn Glu Gln Asn Lys Leu Ser Lys
           290          295          300
Lys Ile Lys Lys Leu Glu Lys Gln Leu Asn Leu Ala Glu Asn Ser Glu
 305          310          315          320
Gly Tyr Arg Ile Lys Gly Glu Ile Leu Asn Ala Asn Leu Gly Gln Val
           325          330          335
Lys Pro Gly Met Thr Glu Val Ser Leu Pro Asn Tyr Tyr Glu Asn Asn
           340          345          350
Lys Pro Ile Ser Ile Lys Leu Asp Pro Ala Leu Ser Pro Ala Arg Asn
           355          360          365
Ala Gln Lys Tyr Phe Thr Arg Tyr Lys Lys Leu Arg Asp Ser Ile Lys
           370          375          380
His Val Asn Glu Gln Ile Lys Ile Ala Lys Glu Asn Leu Arg Tyr Phe
 385          390          395          400
Asp Ser Ile Gln Thr Ala Ile Asp Asn Ala Asp Pro Gln Asp Ile Asp

```

```

          405          410          415
Gln Ile Thr Asp Glu Leu Ile Asn Gln Gly Tyr Ile Arg Lys Gln Gln
          420          425          430
Lys Asn Arg Arg Lys Lys Lys Ile Thr Glu Arg Asn Leu Asn Glu Phe
          435          440          445
Gln Leu Ser Ser Gly Lys His Val Leu Val Gly Lys Asn Asn Tyr Gln
          450          455          460
Asn Asp Trp Leu Thr Leu Lys Lys Ala Asn Lys Leu Asp Tyr Trp Phe
          465          470          475          480
His Val Lys Asn Met Pro Gly Ser His Val Ile Leu Arg Asp Asp Gln
          485          490          495
Pro Thr Asp Gln Asp Ile Lys Glu Ala Ala Glu Ile Ala Ala Phe Phe
          500          505          510
Ser Lys Ala Lys Asn Ser Ala His Val Gln Val Asp Tyr Val Gln Asp
          515          520          525
Lys Arg Val Lys Lys Pro Asn Gly Ala Lys Pro Gly Phe Val Ile Tyr
          530          535          540
Thr Gly Gln Asn Ser Ile Glu Val Thr Pro Lys Glu Asp Glu Ile Met
          545          550          555          560
Ala Lys Lys Ile Asn Lys
          565

```

<210> 59
 <211> 1332
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 169 - s-layer slpA

<220>
 <221> CDS
 <222> (1)...(1332)

```

<400> 59
atg aag aaa aat tta aga atc gtt agc gct gct gct gct gct tta ctt 48
Met Lys Lys Asn Leu Arg Ile Val Ser Ala Ala Ala Ala Leu Leu
  1          5          10          15

gct gtt gct cca gtt gct gct tct gct gta tct act gtt agc gct gct 96
Ala Val Ala Pro Val Ala Ala Ser Ala Val Ser Thr Val Ser Ala Ala
          20          25          30

act act att aac gca agt tca tca gca atc aat acc aac act aat gct 144
Thr Thr Ile Asn Ala Ser Ser Ser Ala Ile Asn Thr Asn Thr Asn Ala
          35          40          45

aag tac gat gtt gat gta act cct agt gtt tct gca gtt gct gca aat 192
Lys Tyr Asp Val Asp Val Thr Pro Ser Val Ser Ala Val Ala Ala Asn
          50          55          60

act gct aac aac act cca gct att gcc ggt aac ctt act ggt act att 240
Thr Ala Asn Asn Thr Pro Ala Ile Ala Gly Asn Leu Thr Gly Thr Ile

```

65	70	75	80	
tca gca agt tac aat ggt aag act tat act gct aac tta aag gca gat	288			
Ser Ala Ser Tyr Asn Gly Lys Thr Tyr Thr Ala Asn Leu Lys Ala Asp				
85 90 95				
act gaa aat gcc act att act gct gct ggt agc act act gcc gtt aaa	336			
Thr Glu Asn Ala Thr Ile Thr Ala Ala Gly Ser Thr Thr Ala Val Lys				
100 105 110				
cct gct gaa tta gct gca ggt gtg gct tac act gta act gtt aac gat	384			
Pro Ala Glu Leu Ala Ala Gly Val Ala Tyr Thr Val Thr Val Asn Asp				
115 120 125				
gtt tca ttt aac ttc ggt tca gaa aat gca ggt aag act gtt acc ctt	432			
Val Ser Phe Asn Phe Gly Ser Glu Asn Ala Gly Lys Thr Val Thr Leu				
130 135 140				
ggt tca gct aac tca aat gta aaa ttc acc ggt aca aac agt gat aat	480			
Gly Ser Ala Asn Ser Asn Val Lys Phe Thr Gly Thr Asn Ser Asp Asn				
145 150 155 160				
caa act gaa act aat gtt tct act ttg aaa gtt aag tta gac caa aac	528			
Gln Thr Glu Thr Asn Val Ser Thr Leu Lys Val Lys Leu Asp Gln Asn				
165 170 175				
ggt gtt gct tca ctt act aat gtt tca att gca aac gta tac gca att	576			
Gly Val Ala Ser Leu Thr Asn Val Ser Ile Ala Asn Val Tyr Ala Ile				
180 185 190				
aac act act gat aac agt aac gta aac ttc tac gac gta act agt ggt	624			
Asn Thr Thr Asp Asn Ser Asn Val Asn Phe Tyr Asp Val Thr Ser Gly				
195 200 205				
gct act gta act aac ggt gcc gtt tca gtt aat gct gat aac caa ggt	672			
Ala Thr Val Thr Asn Gly Ala Val Ser Val Asn Ala Asp Asn Gln Gly				
210 215 220				
caa gtt aat gtt gca aac gta gtt gca gca att aat tca aaa tac ttt	720			
Gln Val Asn Val Ala Asn Val Val Ala Ala Ile Asn Ser Lys Tyr Phe				
225 230 235 240				
gca gca caa tac gca gat aag aag tta aat act cgt act gct aat act	768			
Ala Ala Gln Tyr Ala Asp Lys Lys Leu Asn Thr Arg Thr Ala Asn Thr				
245 250 255				
gaa gat gct att aag gca gcc tta aag gac caa aag att gat gta aac	816			
Glu Asp Ala Ile Lys Ala Ala Leu Lys Asp Gln Lys Ile Asp Val Asn				
260 265 270				
tca gta ggt tac ttc aaa gca cct cat act ttc act gtt aac gtt aaa	864			
Ser Val Gly Tyr Phe Lys Ala Pro His Thr Phe Thr Val Asn Val Lys				
275 280 285				
gca act tca aat act aat ggt aag tca gct act ttg cca gta gtt gtt	912			
Ala Thr Ser Asn Thr Asn Gly Lys Ser Ala Thr Leu Pro Val Val Val				
290 295 300				

act gtt cct aat gtt gct gag cca act gta gcc agc gta agc aag aga 960
 Thr Val Pro Asn Val Ala Glu Pro Thr Val Ala Ser Val Ser Lys Arg
 305 310 315 320

att atg cac aac gca tac tac tac gac aag gac gct aag cgt gtt ggt 1008
 Ile Met His Asn Ala Tyr Tyr Tyr Asp Lys Asp Ala Lys Arg Val Gly
 325 330 335

act gac agc gtt aag cgt tac aac tca gta agc gta ttg cca aac act 1056
 Thr Asp Ser Val Lys Arg Tyr Asn Ser Val Ser Val Leu Pro Asn Thr
 340 345 350

act act atc aac ggt aag act tac tac caa gta gtt gaa aac ggt aag 1104
 Thr Thr Ile Asn Gly Lys Thr Tyr Tyr Gln Val Val Glu Asn Gly Lys
 355 360 365

gct gtt gac aag tac atc aac gct gca aac atc gat ggt act aag cgt 1152
 Ala Val Asp Lys Tyr Ile Asn Ala Ala Asn Ile Asp Gly Thr Lys Arg
 370 375 380

act ttg aag cac aac gct tac gtt tac gca tca tca aag aag cgt gct 1200
 Thr Leu Lys His Asn Ala Tyr Val Tyr Ala Ser Ser Lys Lys Arg Ala
 385 390 395 400

aac aag gtt gta ttg aag aag ggt gaa gtt gta act act tac ggt gct 1248
 Asn Lys Val Val Leu Lys Lys Gly Glu Val Val Thr Thr Tyr Gly Ala
 405 410 415

tca tac aca ttc aag aac ggc caa aag tac tac aag atc ggt gac aac 1296
 Ser Tyr Thr Phe Lys Asn Gly Gln Lys Tyr Tyr Lys Ile Gly Asp Asn
 420 425 430

act gac aag act tac gtt aag gtt gca aac ttt aga 1332
 Thr Asp Lys Thr Tyr Val Lys Val Ala Asn Phe Arg
 435 440

<210> 60

<211> 444

<212> PRT

<213> Lactobacillus acidophilus

<400> 60

Met Lys Lys Asn Leu Arg Ile Val Ser Ala Ala Ala Ala Leu Leu
 1 5 10 15
 Ala Val Ala Pro Val Ala Ala Ser Ala Val Ser Thr Val Ser Ala Ala
 20 25 30
 Thr Thr Ile Asn Ala Ser Ser Ser Ala Ile Asn Thr Asn Thr Asn Ala
 35 40 45
 Lys Tyr Asp Val Asp Val Thr Pro Ser Val Ser Ala Val Ala Ala Asn
 50 55 60
 Thr Ala Asn Asn Thr Pro Ala Ile Ala Gly Asn Leu Thr Gly Thr Ile
 65 70 75 80
 Ser Ala Ser Tyr Asn Gly Lys Thr Tyr Thr Ala Asn Leu Lys Ala Asp
 85 90 95
 Thr Glu Asn Ala Thr Ile Thr Ala Ala Gly Ser Thr Thr Ala Val Lys

```

      100      105      110
Pro Ala Glu Leu Ala Ala Gly Val Ala Tyr Thr Val Thr Val Asn Asp
      115      120      125
Val Ser Phe Asn Phe Gly Ser Glu Asn Ala Gly Lys Thr Val Thr Leu
      130      135      140
Gly Ser Ala Asn Ser Asn Val Lys Phe Thr Gly Thr Asn Ser Asp Asn
145      150      155      160
Gln Thr Glu Thr Asn Val Ser Thr Leu Lys Val Lys Leu Asp Gln Asn
      165      170      175
Gly Val Ala Ser Leu Thr Asn Val Ser Ile Ala Asn Val Tyr Ala Ile
      180      185      190
Asn Thr Thr Asp Asn Ser Asn Val Asn Phe Tyr Asp Val Thr Ser Gly
      195      200      205
Ala Thr Val Thr Asn Gly Ala Val Ser Val Asn Ala Asp Asn Gln Gly
      210      215      220
Gln Val Asn Val Ala Asn Val Val Ala Ala Ile Asn Ser Lys Tyr Phe
225      230      235      240
Ala Ala Gln Tyr Ala Asp Lys Lys Leu Asn Thr Arg Thr Ala Asn Thr
      245      250      255
Glu Asp Ala Ile Lys Ala Ala Leu Lys Asp Gln Lys Ile Asp Val Asn
      260      265      270
Ser Val Gly Tyr Phe Lys Ala Pro His Thr Phe Thr Val Asn Val Lys
      275      280      285
Ala Thr Ser Asn Thr Asn Gly Lys Ser Ala Thr Leu Pro Val Val Val
      290      295      300
Thr Val Pro Asn Val Ala Glu Pro Thr Val Ala Ser Val Ser Lys Arg
305      310      315      320
Ile Met His Asn Ala Tyr Tyr Tyr Asp Lys Asp Ala Lys Arg Val Gly
      325      330      335
Thr Asp Ser Val Lys Arg Tyr Asn Ser Val Ser Val Leu Pro Asn Thr
      340      345      350
Thr Thr Ile Asn Gly Lys Thr Tyr Tyr Gln Val Val Glu Asn Gly Lys
      355      360      365
Ala Val Asp Lys Tyr Ile Asn Ala Ala Asn Ile Asp Gly Thr Lys Arg
      370      375      380
Thr Leu Lys His Asn Ala Tyr Val Tyr Ala Ser Ser Lys Lys Arg Ala
385      390      395      400
Asn Lys Val Val Leu Lys Lys Gly Glu Val Val Thr Thr Tyr Gly Ala
      405      410      415
Ser Tyr Thr Phe Lys Asn Gly Gln Lys Tyr Tyr Lys Ile Gly Asp Asn
      420      425      430
Thr Asp Lys Thr Tyr Val Lys Val Ala Asn Phe Arg
      435      440

```

<210> 61

<211> 1371

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 175 - s-layer slpB

<220>

<221> CDS

<222> (1)...(1371)

<400> 61

atg aag aaa aat tta aga atc gtt agc gct gct gct gct gct tta ctt	48
Met Lys Lys Asn Leu Arg Ile Val Ser Ala Ala Ala Ala Leu Leu	
1 5 10 15	
gct gtt gct cca gtt gct gct tct gct gta tct act gtt aac gct gcc	96
Ala Val Ala Pro Val Ala Ala Ser Ala Val Ser Thr Val Asn Ala Ala	
20 25 30	
gct gtt aat gct att gct gtt ggc ggt tca gct acc cca tta cca aac	144
Ala Val Asn Ala Ile Ala Val Gly Gly Ser Ala Thr Pro Leu Pro Asn	
35 40 45	
aac tca gat gta caa att agt tca tca gtt gct ggt gta act act aag	192
Asn Ser Asp Val Gln Ile Ser Ser Val Ala Gly Val Thr Thr Lys	
50 55 60	
aat ggc tca agc tac act aac ggt aga att tct ggt tct atc aac gct	240
Asn Gly Ser Ser Tyr Thr Asn Gly Arg Ile Ser Gly Ser Ile Asn Ala	
65 70 75 80	
tct tac aac ggt aca agc tat tca gca aac ttt agt tca tca aat gca	288
Ser Tyr Asn Gly Thr Ser Tyr Ser Ala Asn Phe Ser Ser Ser Asn Ala	
85 90 95	
ggt gtt gtt gtt tca act cca ggc cat act gaa ctt agt ggt gaa caa	336
Gly Val Val Val Ser Thr Pro Gly His Thr Glu Leu Ser Gly Glu Gln	
100 105 110	
att aac ggt ctt gaa cca ggt agt gct gta act gtt act tta aga gat	384
Ile Asn Gly Leu Glu Pro Gly Ser Ala Val Thr Val Thr Leu Arg Asp	
115 120 125	
ggt gtt tca ttt aac ttt ggt tca act aat gct aac aag act att act	432
Gly Val Ser Phe Asn Phe Gly Ser Thr Asn Ala Asn Lys Thr Ile Thr	
130 135 140	
tta gca ttt cca aag aac gta tca gct gct ggt tta gct gat gct aac	480
Leu Ala Phe Pro Lys Asn Val Ser Ala Ala Gly Leu Ala Asp Ala Asn	
145 150 155 160	
aag gtt tca gct act tca gaa act tca gtt gat gca ggc aag act atc	528
Lys Val Ser Ala Thr Ser Glu Thr Ser Val Asp Ala Gly Lys Thr Ile	
165 170 175	
caa gtt aag act gac aag aac ggt gtt gta agc ttc ggt tca gca caa	576
Gln Val Lys Thr Asp Lys Asn Gly Val Val Ser Phe Gly Ser Ala Gln	
180 185 190	
gtt ctt aac gtt aag gtt gtt gaa act agc gac gtt aga gct gtt tca	624
Val Leu Asn Val Lys Val Val Glu Thr Ser Asp Val Arg Ala Val Ser	
195 200 205	
ttc tac gac atc caa act ggt aag act gta gaa aac ggt act ctt tca	672

Phe	Tyr	Asp	Ile	Gln	Thr	Gly	Lys	Thr	Val	Glu	Asn	Gly	Thr	Leu	Ser		
210						215					220						
atc	ggt	gct	ggt	tct	aac	gca	cgt	gct	aac	gta	caa	gaa	atc	ggt	aac	720	
Ile	Val	Ala	Gly	Ser	Asn	Ala	Arg	Ala	Asn	Val	Gln	Glu	Ile	Val	Asn		
225					230					235					240		
gca	ttt	aac	gct	aag	tac	caa	gct	tct	caa	ttg	aac	aac	gct	aac	agc	768	
Ala	Phe	Asn	Ala	Lys	Tyr	Gln	Ala	Ser	Gln	Leu	Asn	Asn	Ala	Asn	Ser		
				245					250						255		
aat	gct	aac	ggt	cgt	ttg	act	gac	aac	aac	gct	caa	gct	ggt	gct	act	816	
Asn	Ala	Asn	Val	Arg	Leu	Thr	Asp	Asn	Asn	Ala	Gln	Ala	Val	Ala	Thr		
			260					265						270			
atg	tta	aga	gct	caa	aac	att	gat	ggt	gat	gca	caa	ggt	tac	ttc	act	864	
Met	Leu	Arg	Ala	Gln	Asn	Ile	Asp	Val	Asp	Ala	Gln	Gly	Tyr	Phe	Thr		
		275					280						285				
gca	cca	gct	tca	ttg	agc	tta	act	ttc	cac	gca	gaa	tca	act	caa	aac	912	
Ala	Pro	Ala	Ser	Leu	Ser	Leu	Thr	Phe	His	Ala	Glu	Ser	Thr	Gln	Asn		
		290					295					300					
aat	gaa	act	gca	caa	tta	cca	gta	act	ggt	tca	gta	act	aac	ggt	aag	960	
Asn	Glu	Thr	Ala	Gln	Leu	Pro	Val	Thr	Val	Ser	Val	Thr	Asn	Gly	Lys		
305					310					315					320		
gaa	ggt	act	cct	tca	act	gta	gac	agc	gta	agc	aag	aga	att	atg	cac	1008	
Glu	Val	Thr	Pro	Ser	Thr	Val	Asp	Ser	Val	Ser	Lys	Arg	Ile	Met	His		
				325					330						335		
aat	gca	tac	tac	tac	gac	aag	gac	gct	aag	cgt	ggt	ggt	act	gac	agc	1056	
Asn	Ala	Tyr	Tyr	Tyr	Asp	Lys	Asp	Ala	Lys	Arg	Val	Gly	Thr	Asp	Ser		
			340					345						350			
ggt	aag	cgt	tac	aac	tca	gta	agc	gta	ttg	cca	aac	act	act	act	atc	1104	
Val	Lys	Arg	Tyr	Asn	Ser	Val	Ser	Val	Leu	Pro	Asn	Thr	Thr	Thr	Ile		
		355					360						365				
aac	ggt	aag	gct	tac	tac	caa	gta	ggt	gaa	aac	ggc	aag	gca	ggt	gac	1152	
Asn	Gly	Lys	Ala	Tyr	Tyr	Gln	Val	Val	Glu	Asn	Gly	Lys	Ala	Val	Asp		
		370				375					380						
aag	tac	atc	aac	gct	gca	aac	atc	gat	ggt	act	aag	cgt	act	ttg	aag	1200	
Lys	Tyr	Ile	Asn	Ala	Ala	Asn	Ile	Asp	Gly	Thr	Lys	Arg	Thr	Leu	Lys		
385					390					395					400		
cac	aac	gct	tac	ggt	tac	gca	tca	tca	aag	aaa	cgt	gct	aac	aag	ggt	1248	
His	Asn	Ala	Tyr	Val	Tyr	Ala	Ser	Ser	Lys	Lys	Arg	Ala	Asn	Lys	Val		
				405					410						415		
gta	ttg	aag	aag	ggt	gaa	ggt	gta	act	act	tac	ggt	gct	tca	tac	aca	1296	
Val	Leu	Lys	Lys	Gly	Glu	Val	Val	Thr	Thr	Tyr	Gly	Ala	Ser	Tyr	Thr		
			420					425						430			
ttc	aag	aac	ggc	caa	aag	tac	tac	aag	atc	ggt	gac	aac	act	gac	aag	1344	
Phe	Lys	Asn	Gly	Gln	Lys	Tyr	Tyr	Lys	Ile	Gly	Asp	Asn	Thr	Asp	Lys		

435	440	445	
act tac gtt aag gtt gca aac ttt aga			1371
Thr Tyr Val Lys Val Ala Asn Phe Arg			
450	455		

<210> 62
 <211> 457
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 62
 Met Lys Lys Asn Leu Arg Ile Val Ser Ala Ala Ala Ala Ala Leu Leu
 1 5 10 15
 Ala Val Ala Pro Val Ala Ala Ser Ala Val Ser Thr Val Asn Ala Ala
 20 25 30
 Ala Val Asn Ala Ile Ala Val Gly Gly Ser Ala Thr Pro Leu Pro Asn
 35 40 45
 Asn Ser Asp Val Gln Ile Ser Ser Ser Val Ala Gly Val Thr Thr Lys
 50 55 60
 Asn Gly Ser Ser Tyr Thr Asn Gly Arg Ile Ser Gly Ser Ile Asn Ala
 65 70 75 80
 Ser Tyr Asn Gly Thr Ser Tyr Ser Ala Asn Phe Ser Ser Ser Asn Ala
 85 90 95
 Gly Val Val Val Ser Thr Pro Gly His Thr Glu Leu Ser Gly Glu Gln
 100 105 110
 Ile Asn Gly Leu Glu Pro Gly Ser Ala Val Thr Val Thr Leu Arg Asp
 115 120 125
 Gly Val Ser Phe Asn Phe Gly Ser Thr Asn Ala Asn Lys Thr Ile Thr
 130 135 140
 Leu Ala Phe Pro Lys Asn Val Ser Ala Ala Gly Leu Ala Asp Ala Asn
 145 150 155 160
 Lys Val Ser Ala Thr Ser Glu Thr Ser Val Asp Ala Gly Lys Thr Ile
 165 170 175
 Gln Val Lys Thr Asp Lys Asn Gly Val Val Ser Phe Gly Ser Ala Gln
 180 185 190
 Val Leu Asn Val Lys Val Val Glu Thr Ser Asp Val Arg Ala Val Ser
 195 200 205
 Phe Tyr Asp Ile Gln Thr Gly Lys Thr Val Glu Asn Gly Thr Leu Ser
 210 215 220
 Ile Val Ala Gly Ser Asn Ala Arg Ala Asn Val Gln Glu Ile Val Asn
 225 230 235 240
 Ala Phe Asn Ala Lys Tyr Gln Ala Ser Gln Leu Asn Asn Ala Asn Ser
 245 250 255
 Asn Ala Asn Val Arg Leu Thr Asp Asn Asn Ala Gln Ala Val Ala Thr
 260 265 270
 Met Leu Arg Ala Gln Asn Ile Asp Val Asp Ala Gln Gly Tyr Phe Thr
 275 280 285
 Ala Pro Ala Ser Leu Ser Leu Thr Phe His Ala Glu Ser Thr Gln Asn
 290 295 300
 Asn Glu Thr Ala Gln Leu Pro Val Thr Val Ser Val Thr Asn Gly Lys
 305 310 315 320
 Glu Val Thr Pro Ser Thr Val Asp Ser Val Ser Lys Arg Ile Met His
 325 330 335
 Asn Ala Tyr Tyr Asp Lys Asp Ala Lys Arg Val Gly Thr Asp Ser
 340 345 350

```

Val Lys Arg Tyr Asn Ser Val Ser Val Leu Pro Asn Thr Thr Thr Ile
      355      360      365
Asn Gly Lys Ala Tyr Tyr Gln Val Val Glu Asn Gly Lys Ala Val Asp
      370      375      380
Lys Tyr Ile Asn Ala Ala Asn Ile Asp Gly Thr Lys Arg Thr Leu Lys
385      390      395      400
His Asn Ala Tyr Val Tyr Ala Ser Ser Lys Lys Arg Ala Asn Lys Val
      405      410      415
Val Leu Lys Lys Gly Glu Val Val Thr Thr Tyr Gly Ala Ser Tyr Thr
      420      425      430
Phe Lys Asn Gly Gln Lys Tyr Tyr Lys Ile Gly Asp Asn Thr Asp Lys
      435      440      445
Thr Tyr Val Lys Val Ala Asn Phe Arg
      450      455

```

<210> 63

<211> 1701

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 223 - s-layer protein slpB

<220>

<221> CDS

<222> (1)...(1701)

<400> 63

```

atg cga ggt ata tta tcg atg aaa tta aat cat aag ttg att atg gta 48
Met Arg Gly Ile Leu Ser Met Lys Leu Asn His Lys Leu Ile Met Val
1      5      10      15

tca gca gct gca tta atg agc gta agt cca ttt gta ggt act gtg caa 96
Ser Ala Ala Ala Leu Met Ser Val Ser Pro Phe Val Gly Thr Val Gln
      20      25      30

aat gtt caa gct gct act act aaa tca tca agc aaa act act gct aag 144
Asn Val Gln Ala Ala Thr Thr Lys Ser Ser Ser Lys Thr Thr Ala Lys
      35      40      45

aag act act tca gct tca aag act aag act aag tct tca tca aag aag 192
Lys Thr Thr Ser Ala Ser Lys Thr Lys Thr Lys Ser Ser Ser Lys Lys
      50      55      60

gct act agt caa tct act tca act aag aag aca agt tca aca aaa tca 240
Ala Thr Ser Gln Ser Thr Ser Thr Lys Lys Thr Ser Ser Thr Lys Ser
      65      70      75      80

agc tct aag act act tct tca act agt gca aag agt act tca act aag 288
Ser Ser Lys Thr Thr Ser Ser Thr Ser Ala Lys Ser Thr Ser Thr Lys
      85      90      95

aag gca gct tca aac act att aag tta gtt cac aat gct tat gtt tat 336

```

Lys	Ala	Ala	Ser	Asn	Thr	Ile	Lys	Leu	Val	His	Asn	Ala	Tyr	Val	Tyr		
			100					105					110				
gac	aag	aat	ggt	aag	cgt	ctt	act	aag	tac	atg	ggc	agt	gca	aag	tac	384	
Asp	Lys	Asn	Gly	Lys	Arg	Leu	Thr	Lys	Tyr	Met	Gly	Ser	Ala	Lys	Tyr		
		115					120					125					
act	act	att	gct	aaa	ggt	gta	act	ctt	aag	tct	aat	ggt	aca	gtg	aag	432	
Thr	Thr	Ile	Ala	Lys	Gly	Val	Thr	Leu	Lys	Ser	Asn	Gly	Thr	Val	Lys		
		130					135					140					
atc	gat	ggt	gtt	ctt	tac	tac	agc	ctc	ggt	aat	aat	gcc	tat	att	aag	480	
Ile	Asp	Gly	Val	Leu	Tyr	Tyr	Ser	Leu	Gly	Asn	Asn	Ala	Tyr	Ile	Lys		
		145			150					155					160		
gct	gtt	aac	gta	gat	ggc	cca	tct	gct	tca	gct	tca	tca	act	act	aag	528	
Ala	Val	Asn	Val	Asp	Gly	Pro	Ser	Ala	Ser	Ala	Ser	Ser	Thr	Thr	Lys		
			165					170							175		
aag	cca	tct	tca	agt	act	tct	tca	aca	gta	act	gct	gta	agc	att	aag	576	
Lys	Pro	Ser	Ser	Ser	Thr	Ser	Ser	Thr	Val	Thr	Ala	Val	Ser	Ile	Lys		
			180					185					190				
att	gct	cgt	aat	tca	tac	gtt	tat	gat	gaa	aat	ggt	aag	cgt	att	aaa	624	
Ile	Ala	Arg	Asn	Ser	Tyr	Val	Tyr	Asp	Glu	Asn	Gly	Lys	Arg	Ile	Lys		
		195					200					205					
aag	tat	gaa	ggt	aaa	gat	aaa	ctt	act	aag	ggt	act	act	gtt	gat	tca	672	
Lys	Tyr	Glu	Gly	Lys	Asp	Lys	Leu	Thr	Lys	Gly	Thr	Thr	Val	Asp	Ser		
		210				215					220						
tac	ggt	aca	gaa	act	att	gat	ggt	aag	tta	tac	tac	caa	ctt	aat	aaa	720	
Tyr	Gly	Thr	Glu	Thr	Ile	Asp	Gly	Lys	Leu	Tyr	Tyr	Gln	Leu	Asn	Lys		
					230					235					240		
aag	ggt	aca	gct	ttt	gta	aag	gca	agt	aat	gta	gat	aca	aat	gaa	aca	768	
Lys	Gly	Thr	Ala	Phe	Val	Lys	Ala	Ser	Asn	Val	Asp	Thr	Asn	Glu	Thr		
				245					250					255			
gct	act	att	act	tta	aag	aag	aat	gcc	tac	att	tat	gat	ggc	aat	ggc	816	
Ala	Thr	Ile	Thr	Leu	Lys	Lys	Asn	Ala	Tyr	Ile	Tyr	Asp	Gly	Asn	Gly		
			260					265					270				
gat	act	aag	aaa	aag	aaa	att	aag	aag	ggc	aag	agt	gta	aag	gct	act	864	
Asp	Thr	Lys	Lys	Lys	Lys	Ile	Lys	Lys	Gly	Lys	Ser	Val	Lys	Ala	Thr		
		275					280					285					
gaa	gca	aga	tac	att	ggt	act	aag	ctt	tac	tac	aag	att	ggt	gat	gat	912	
Glu	Ala	Arg	Tyr	Ile	Gly	Thr	Lys	Leu	Tyr	Tyr	Lys	Ile	Gly	Asp	Asp		
		290				295					300						
caa	ttt	gta	aag	gct	gct	aat	gtg	ggt	aaa	gtt	tca	ggt	gct	aag	ctt	960	
Gln	Phe	Val	Lys	Ala	Ala	Asn	Val	Gly	Lys	Val	Ser	Gly	Ala	Lys	Leu		
		305				310				315					320		
gat	cct	atc	aat	gaa	cca	gat	gga	gaa	gca	act	gtt	gat	gat	cca	tcg	1008	
Asp	Pro	Ile	Asn	Glu	Pro	Asp	Gly	Glu	Ala	Thr	Val	Asp	Asp	Pro	Ser		

325										330					335					
act	gat	aat	gtt	aac	cca	gat	gta	act	aag	gta	act	acc	att	ggg	gta	1056				
Thr	Asp	Asn	Val	Asn	Pro	Asp	Val	Thr	Lys	Val	Thr	Thr	Ile	Gly	Val					
340					345					350										
act	cca	ctt	tac	aat	att	aag	ggg	caa	aaa	gac	gac	acc	aga	tta	ttt	1104				
Thr	Pro	Leu	Tyr	Asn	Ile	Lys	Gly	Gln	Lys	Asp	Asp	Thr	Arg	Leu	Phe					
355					360					365										
ggg	gct	ggg	caa	agt	caa	caa	gtt	tca	gaa	tta	aga	tat	att	gca	act	1152				
Gly	Ala	Gly	Gln	Ser	Gln	Gln	Val	Ser	Glu	Leu	Arg	Tyr	Ile	Ala	Thr					
370					375					380										
tca	gca	aac	ggg	acc	cca	gac	ttg	ttc	tac	aaa	tta	gct	agt	ggg	aga	1200				
Ser	Ala	Asn	Gly	Thr	Pro	Asp	Leu	Phe	Tyr	Lys	Leu	Ala	Ser	Gly	Arg					
385					390					395					400					
ggg	tac	ttg	aag	gct	agt	gat	gta	att	gtt	agt	ggg	aag	act	ttg	tca	1248				
Gly	Tyr	Leu	Lys	Ala	Ser	Asp	Val	Ile	Val	Ser	Gly	Lys	Thr	Leu	Ser					
405					410					415										
cct	gtt	aat	act	cca	gaa	caa	gct	aag	gct	gat	gta	act	gtt	gca	act	1296				
Pro	Val	Asn	Thr	Pro	Glu	Gln	Ala	Lys	Ala	Asp	Val	Thr	Val	Ala	Thr					
420					425					430										
gca	gca	gat	aag	act	aag	ttg	tca	gaa	agt	att	aat	aat	tct	aag	aac	1344				
Ala	Ala	Asp	Lys	Thr	Lys	Leu	Ser	Glu	Ser	Ile	Asn	Asn	Ser	Lys	Asn					
435					440					445										
gtt	aaa	aat	tct	act	act	tac	aag	ctt	tca	tca	tca	gac	tta	aga	aat	1392				
Val	Lys	Asn	Ser	Thr	Thr	Tyr	Lys	Leu	Ser	Ser	Ser	Asp	Leu	Arg	Asn					
450					455					460										
aac	tat	gat	aag	gct	gtt	tct	gat	gca	act	gct	gtt	aat	aac	aat	gct	1440				
Asn	Tyr	Asp	Lys	Ala	Val	Ser	Asp	Ala	Thr	Ala	Val	Asn	Asn	Asn	Ala					
465					470					475					480					
tca	gca	act	att	gct	caa	gtt	aat	gaa	gca	gta	gct	aac	att	aat	gaa	1488				
Ser	Ala	Thr	Ile	Ala	Gln	Val	Asn	Glu	Ala	Val	Ala	Asn	Ile	Asn	Glu					
485					490					495										
gct	tac	gct	aag	ctt	aac	ggg	caa	aaa	ata	gtt	gta	gct	aac	tta	agt	1536				
Ala	Tyr	Ala	Lys	Leu	Asn	Gly	Gln	Lys	Ile	Val	Val	Ala	Asn	Leu	Ser					
500					505					510										
aat	ctt	act	tta	gat	gaa	gcc	aac	caa	att	gtt	aag	tta	gtt	gct	agt	1584				
Asn	Leu	Thr	Leu	Asp	Glu	Ala	Asn	Gln	Ile	Val	Lys	Leu	Val	Ala	Ser					
515					520					525										
gta	aga	aac	gtt	cca	gaa	agt	aat	gtt	caa	ttc	tca	aat	aac	aac	act	1632				
Val	Arg	Asn	Val	Pro	Glu	Ser	Asn	Val	Gln	Phe	Ser	Asn	Asn	Asn	Thr					
530					535					540										
act	tta	gca	atc	gtt	tca	tca	aat	ggc	tac	aat	gaa	cct	ttg	aat	att	1680				
Thr	Leu	Ala	Ile	Val	Ser	Ser	Asn	Gly	Tyr	Asn	Glu	Pro	Leu	Asn	Ile					
545					550					555					560					

agc gac ttt gct caa caa aga
 Ser Asp Phe Ala Gln Gln Arg
 565

1701

<210> 64
 <211> 567
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 64
 Met Arg Gly Ile Leu Ser Met Lys Leu Asn His Lys Leu Ile Met Val
 1 5 10 15
 Ser Ala Ala Ala Leu Met Ser Val Ser Pro Phe Val Gly Thr Val Gln
 20 25 30
 Asn Val Gln Ala Ala Thr Thr Lys Ser Ser Ser Lys Thr Thr Ala Lys
 35 40 45
 Lys Thr Thr Ser Ala Ser Lys Thr Lys Thr Lys Ser Ser Ser Lys Lys
 50 55 60
 Ala Thr Ser Gln Ser Thr Ser Thr Lys Lys Thr Ser Ser Thr Lys Ser
 65 70 75 80
 Ser Ser Lys Thr Thr Ser Ser Thr Ser Ala Lys Ser Thr Ser Thr Lys
 85 90 95
 Lys Ala Ala Ser Asn Thr Ile Lys Leu Val His Asn Ala Tyr Val Tyr
 100 105 110
 Asp Lys Asn Gly Lys Arg Leu Thr Lys Tyr Met Gly Ser Ala Lys Tyr
 115 120 125
 Thr Thr Ile Ala Lys Gly Val Thr Leu Lys Ser Asn Gly Thr Val Lys
 130 135 140
 Ile Asp Gly Val Leu Tyr Tyr Ser Leu Gly Asn Asn Ala Tyr Ile Lys
 145 150 155 160
 Ala Val Asn Val Asp Gly Pro Ser Ala Ser Ala Ser Ser Thr Thr Lys
 165 170 175
 Lys Pro Ser Ser Ser Thr Ser Ser Thr Val Thr Ala Val Ser Ile Lys
 180 185 190
 Ile Ala Arg Asn Ser Tyr Val Tyr Asp Glu Asn Gly Lys Arg Ile Lys
 195 200 205
 Lys Tyr Glu Gly Lys Asp Lys Leu Thr Lys Gly Thr Thr Val Asp Ser
 210 215 220
 Tyr Gly Thr Glu Thr Ile Asp Gly Lys Leu Tyr Tyr Gln Leu Asn Lys
 225 230 235 240
 Lys Gly Thr Ala Phe Val Lys Ala Ser Asn Val Asp Thr Asn Glu Thr
 245 250 255
 Ala Thr Ile Thr Leu Lys Lys Asn Ala Tyr Ile Tyr Asp Gly Asn Gly
 260 265 270
 Asp Thr Lys Lys Lys Lys Ile Lys Lys Gly Lys Ser Val Lys Ala Thr
 275 280 285
 Glu Ala Arg Tyr Ile Gly Thr Lys Leu Tyr Tyr Lys Ile Gly Asp Asp
 290 295 300
 Gln Phe Val Lys Ala Ala Asn Val Gly Lys Val Ser Gly Ala Lys Leu
 305 310 315 320
 Asp Pro Ile Asn Glu Pro Asp Gly Glu Ala Thr Val Asp Asp Pro Ser
 325 330 335
 Thr Asp Asn Val Asn Pro Asp Val Thr Lys Val Thr Thr Ile Gly Val
 340 345 350
 Thr Pro Leu Tyr Asn Ile Lys Gly Gln Lys Asp Asp Thr Arg Leu Phe

```

      355      360      365
Gly Ala Gly Gln Ser Gln Gln Val Ser Glu Leu Arg Tyr Ile Ala Thr
  370      375      380
Ser Ala Asn Gly Thr Pro Asp Leu Phe Tyr Lys Leu Ala Ser Gly Arg
  385      390      395      400
Gly Tyr Leu Lys Ala Ser Asp Val Ile Val Ser Gly Lys Thr Leu Ser
      405      410      415
Pro Val Asn Thr Pro Glu Gln Ala Lys Ala Asp Val Thr Val Ala Thr
      420      425      430
Ala Ala Asp Lys Thr Lys Leu Ser Glu Ser Ile Asn Asn Ser Lys Asn
      435      440      445
Val Lys Asn Ser Thr Thr Tyr Lys Leu Ser Ser Ser Asp Leu Arg Asn
      450      455      460
Asn Tyr Asp Lys Ala Val Ser Asp Ala Thr Ala Val Asn Asn Asn Ala
  465      470      475      480
Ser Ala Thr Ile Ala Gln Val Asn Glu Ala Val Ala Asn Ile Asn Glu
      485      490      495
Ala Tyr Ala Lys Leu Asn Gly Gln Lys Ile Val Val Ala Asn Leu Ser
      500      505      510
Asn Leu Thr Leu Asp Glu Ala Asn Gln Ile Val Lys Leu Val Ala Ser
      515      520      525
Val Arg Asn Val Pro Glu Ser Asn Val Gln Phe Ser Asn Asn Asn Thr
      530      535      540
Thr Leu Ala Ile Val Ser Ser Asn Gly Tyr Asn Glu Pro Leu Asn Ile
  545      550      555      560
Ser Asp Phe Ala Gln Gln Arg
      565

```

<210> 65
 <211> 531
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 221 - s-layer

<220>
 <221> CDS
 <222> (1)...(531)

```

<400> 65
ttg ggc aac ggt cag tat att aag gct aaa aat gtg gat gga act ggt   48
Met Gly Asn Gly Gln Tyr Ile Lys Ala Lys Asn Val Asp Gly Thr Gly
  1           5           10           15

tcg att aaa gct cat gta gaa gta act cct aga tcc tct ggc gct aca   96
Ser Ile Lys Ala His Val Glu Val Thr Pro Arg Ser Ser Gly Ala Thr
      20           25           30

ccc aca gat tat agt aag cca act tta act ttg aaa agt aat gca tat   144
Pro Thr Asp Tyr Ser Lys Pro Thr Leu Thr Leu Lys Ser Asn Ala Tyr
      35           40           45

cca tat aat tta aat ggt gaa cga att aat aat tat tta ggc ttt acc   192

```

Pro Tyr Asn Leu Asn Gly Glu Arg Ile Asn Asn Tyr Leu Gly Phe Thr
50 55 60
tat atc aaa aaa ggt gcc aca ctt aac tat cag ggc tct gag aga atc 240
Tyr Ile Lys Lys Gly Ala Thr Leu Asn Tyr Gln Gly Ser Glu Arg Ile
65 70 75 80
aat ggt cag aat tat tat tat att ggc gat ggt gct tat att aaa aac 288
Asn Gly Gln Asn Tyr Tyr Tyr Ile Gly Asp Gly Ala Tyr Ile Lys Asn
85 90 95
aca acg gtt gga tca act aat aat aca aat gca gca cac aat aat act 336
Thr Thr Val Gly Ser Thr Asn Asn Thr Asn Ala Ala His Asn Asn Thr
100 105 110
att acc tta aat aaa aag acc tat gcc tat act gca tct ggt aaa aag 384
Ile Thr Leu Asn Lys Lys Thr Tyr Ala Tyr Thr Ala Ser Gly Lys Lys
115 120 125
atg tct aaa tac ttg gga tat act tat ata aat aaa ggt acc aca tta 432
Met Ser Lys Tyr Leu Gly Tyr Thr Tyr Ile Asn Lys Gly Thr Thr Leu
130 135 140
aat tat tac ggc act aaa aag att aag gga aaa aca ttt tat tat att 480
Asn Tyr Tyr Gly Thr Lys Lys Ile Lys Gly Lys Thr Phe Tyr Tyr Ile
145 150 155 160
ggc gac cat gca tac gtg aac gcc gca aat gtt ggt aaa gtt act aat 528
Gly Asp His Ala Tyr Val Asn Ala Ala Asn Val Gly Lys Val Thr Asn
165 170 175
gaa 531
Glu

<210> 66

<211> 177

<212> PRT

<213> Lactobacillus acidophilus

<400> 66

Met Gly Asn Gly Gln Tyr Ile Lys Ala Lys Asn Val Asp Gly Thr Gly
1 5 10 15
Ser Ile Lys Ala His Val Glu Val Thr Pro Arg Ser Ser Gly Ala Thr
20 25 30
Pro Thr Asp Tyr Ser Lys Pro Thr Leu Thr Leu Lys Ser Asn Ala Tyr
35 40 45
Pro Tyr Asn Leu Asn Gly Glu Arg Ile Asn Asn Tyr Leu Gly Phe Thr
50 55 60
Tyr Ile Lys Lys Gly Ala Thr Leu Asn Tyr Gln Gly Ser Glu Arg Ile
65 70 75 80
Asn Gly Gln Asn Tyr Tyr Tyr Ile Gly Asp Gly Ala Tyr Ile Lys Asn
85 90 95
Thr Thr Val Gly Ser Thr Asn Asn Thr Asn Ala Ala His Asn Asn Thr
100 105 110
Ile Thr Leu Asn Lys Lys Thr Tyr Ala Tyr Thr Ala Ser Gly Lys Lys

```

      115      120      125
Met Ser Lys Tyr Leu Gly Tyr Thr Tyr Ile Asn Lys Gly Thr Thr Leu
      130      135      140
Asn Tyr Tyr Gly Thr Lys Lys Ile Lys Gly Lys Thr Phe Tyr Tyr Ile
145      150      155      160
Gly Asp His Ala Tyr Val Asn Ala Ala Asn Val Gly Lys Val Thr Asn
      165      170      175
Glu

```

<210> 67

<211> 519

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 220 - s-layer protein

<220>

<221> CDS

<222> (1)...(519)

<400> 67

```

ttg atg cag atg aat cgt aag att att atg gct tca gtt gcc gca ata 48
Met Met Gln Met Asn Arg Lys Ile Ile Met Ala Ser Val Ala Ala Ile
 1          5          10          15

ata ggg att ggg agc att att ggt ata aat aca gca aca tct ggt gaa 96
Ile Gly Ile Gly Ser Ile Ile Gly Ile Asn Thr Ala Thr Ser Gly Glu
      20          25          30

aat gtg gtt tat gct agt gtt tat aaa act aca ggt aac aat aaa gta 144
Asn Val Val Tyr Ala Ser Val Tyr Lys Thr Thr Gly Asn Asn Lys Val
      35          40          45

aaa gtt gtt aag agt act agt ttt gtg aat aat cga ggt gta aag cag 192
Lys Val Val Lys Ser Thr Ser Phe Val Asn Asn Arg Gly Val Lys Gln
      50          55          60

gct ata agt gcc gag aag ggt ggt agc tat act gtt tat gca gtt aac 240
Ala Ile Ser Ala Glu Lys Gly Gly Ser Tyr Thr Val Tyr Ala Val Asn
      65          70          75          80

tat att gat ggt gtt gcc tac gta agt gtt cat aaa agt aat cga tat 288
Tyr Ile Asp Gly Val Ala Tyr Val Ser Val His Lys Ser Asn Arg Tyr
      85          90          95

tgg tta ccg gtt tct gcg gta aaa ggc aag atc ttt tat caa cgt ggt 336
Trp Leu Pro Val Ser Ala Val Lys Gly Lys Ile Phe Tyr Gln Arg Gly
      100          105          110

agg gat aat gct act tat atg att agt gca gga aat aac tct gat act 384
Arg Asp Asn Ala Thr Tyr Met Ile Ser Ala Gly Asn Asn Ser Asp Thr

```

```

          115              120              125
gta tct tta caa aca aat aat aaa gga aac gta act tta aaa tct aac 432
Val Ser Leu Gln Thr Asn Asn Lys Gly Asn Val Thr Leu Lys Ser Asn
      130              135              140

gct tat gta tat aat tta aaa ggc aaa cgg gtt aat aat gat ttg ggt 480
Ala Tyr Val Tyr Asn Leu Lys Gly Lys Arg Val Asn Asn Asp Leu Gly
145              150              155              160

aaa tac ttc att act aaa gga gca tcg att cca tat tat 519
Lys Tyr Phe Ile Thr Lys Gly Ala Ser Ile Pro Tyr Tyr
      165              170

```

<210> 68
 <211> 173
 <212> PRT
 <213> Lactobacillus acidophilus

```

<400> 68
Met Met Gln Met Asn Arg Lys Ile Ile Met Ala Ser Val Ala Ala Ile
1      5      10      15
Ile Gly Ile Gly Ser Ile Ile Gly Ile Asn Thr Ala Thr Ser Gly Glu
      20      25      30
Asn Val Val Tyr Ala Ser Val Tyr Lys Thr Thr Gly Asn Asn Lys Val
      35      40      45
Lys Val Val Lys Ser Thr Ser Phe Val Asn Asn Arg Gly Val Lys Gln
      50      55      60
Ala Ile Ser Ala Glu Lys Gly Gly Ser Tyr Thr Val Tyr Ala Val Asn
      65      70      75      80
Tyr Ile Asp Gly Val Ala Tyr Val Ser Val His Lys Ser Asn Arg Tyr
      85      90      95
Trp Leu Pro Val Ser Ala Val Lys Gly Lys Ile Phe Tyr Gln Arg Gly
      100      105      110
Arg Asp Asn Ala Thr Tyr Met Ile Ser Ala Gly Asn Asn Ser Asp Thr
      115      120      125
Val Ser Leu Gln Thr Asn Asn Lys Gly Asn Val Thr Leu Lys Ser Asn
      130      135      140
Ala Tyr Val Tyr Asn Leu Lys Gly Lys Arg Val Asn Asn Asp Leu Gly
145      150      155      160
Lys Tyr Phe Ile Thr Lys Gly Ala Ser Ile Pro Tyr Tyr
      165      170

```

<210> 69
 <211> 876
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 514 - surface layer protein

<220>

<221> CDS

<222> (1)...(876)

<400> 69

ttg aat gga caa gta ttc caa gtt gct gtt ggt tca aac ttc aat cca	48
Met Asn Gly Gln Val Phe Gln Val Ala Val Gly Ser Asn Phe Asn Pro	
1 5 10 15	
ttg aac ttt act aac agt aac ggt gaa aac atc att gtt tct gct caa	96
Leu Asn Phe Thr Asn Ser Asn Gly Glu Asn Ile Ile Val Ser Ala Gln	
20 25 30	
caa agt aag aac aac act act ttt gca agc att gaa gca act tca aac	144
Gln Ser Lys Asn Asn Thr Thr Phe Ala Ser Ile Glu Ala Thr Ser Asn	
35 40 45	
cca gtt aat act tca gaa gca ggc cgt tac tac aat gta act tta act	192
Pro Val Asn Thr Ser Glu Ala Gly Arg Tyr Tyr Asn Val Thr Leu Thr	
50 55 60	
gca act ggt aac act ggc aag aag act aca gct act tat act gtt tta	240
Ala Thr Gly Asn Thr Gly Lys Lys Thr Thr Ala Thr Tyr Thr Val Leu	
65 70 75 80	
att act tca agc caa aag caa act tta tac ggt aat ggt gaa agt acg	288
Ile Thr Ser Ser Gln Lys Gln Thr Leu Tyr Gly Asn Gly Glu Ser Thr	
85 90 95	
att tct act tac agt att tac ggt aac aac gtt tta agt aac tca acc	336
Ile Ser Thr Tyr Ser Ile Tyr Gly Asn Asn Val Leu Ser Asn Ser Thr	
100 105 110	
act ttt aaa gat ggt gat caa gtt tat gtt tca gat caa act aag act	384
Thr Phe Lys Asp Gly Asp Gln Val Tyr Val Ser Asp Gln Thr Lys Thr	
115 120 125	
gtt ggt gga gtt tca tac tca caa gtt tca cct aaa tca aag aat gat	432
Val Gly Gly Val Ser Tyr Ser Gln Val Ser Pro Lys Ser Lys Asn Asp	
130 135 140	
gct aac tca agt aac att tgg gta aag acc tca gca ctt gtg aag cca	480
Ala Asn Ser Ser Asn Ile Trp Val Lys Thr Ser Ala Leu Val Lys Pro	
145 150 155 160	
gca ggt gac acc aat gtt aag act tac cca gta atg gtt gac tca aga	528
Ala Gly Asp Thr Asn Val Lys Thr Tyr Pro Val Met Val Asp Ser Arg	
165 170 175	
gct tac gac aag aac ggt aac tac tta ggt cac atg tac tat gca tat	576
Ala Tyr Asp Lys Asn Gly Asn Tyr Leu Gly His Met Tyr Tyr Ala Tyr	
180 185 190	
gac aac att gac atc gtt cca act gtt gta acc atc aac ggc aag act	624
Asp Asn Ile Asp Ile Val Pro Thr Val Val Thr Ile Asn Gly Lys Thr	
195 200 205	
tac tac aag gtt gct aac aag gat gaa tac gtt cgt gta act aac att	672

```

Tyr Tyr Lys Val Ala Asn Lys Asp Glu Tyr Val Arg Val Thr Asn Ile
  210                215                220

act ggt aac caa cgt acc ttg aag cac aac gct tac att tac tgg tca 720
Thr Gly Asn Gln Arg Thr Leu Lys His Asn Ala Tyr Ile Tyr Trp Ser
225                230                235                240

tca tac cgt cgt act cca ggt act ggt aag atg tat aga ggt caa act 768
Ser Tyr Arg Arg Thr Pro Gly Thr Gly Lys Met Tyr Arg Gly Gln Thr
                245                250                255

gta act act tac ggt cca caa atg aaa ttc aag aac ggt aag aag tac 816
Val Thr Thr Tyr Gly Pro Gln Met Lys Phe Lys Asn Gly Lys Lys Tyr
                260                265                270

tac aga att gaa ggc tgc aga aat aac aac aag cgt tac atc aag gct 864
Tyr Arg Ile Glu Gly Cys Arg Asn Asn Lys Arg Tyr Ile Lys Ala
                275                280                285

gta aac ttc tat
Val Asn Phe Tyr
290

```

```

<210> 70
<211> 292
<212> PRT
<213> Lactobacillus acidophilus

```

```

<400> 70
Met Asn Gly Gln Val Phe Gln Val Ala Val Gly Ser Asn Phe Asn Pro
  1                5                10                15
Leu Asn Phe Thr Asn Ser Asn Gly Glu Asn Ile Ile Val Ser Ala Gln
                20                25                30
Gln Ser Lys Asn Asn Thr Thr Phe Ala Ser Ile Glu Ala Thr Ser Asn
                35                40                45
Pro Val Asn Thr Ser Glu Ala Gly Arg Tyr Tyr Asn Val Thr Leu Thr
                50                55                60
Ala Thr Gly Asn Thr Gly Lys Lys Thr Thr Ala Thr Tyr Thr Val Leu
65                70                75                80
Ile Thr Ser Ser Gln Lys Gln Thr Leu Tyr Gly Asn Gly Glu Ser Thr
                85                90                95
Ile Ser Thr Tyr Ser Ile Tyr Gly Asn Asn Val Leu Ser Asn Ser Thr
                100                105                110
Thr Phe Lys Asp Gly Asp Gln Val Tyr Val Ser Asp Gln Thr Lys Thr
                115                120                125
Val Gly Gly Val Ser Tyr Ser Gln Val Ser Pro Lys Ser Lys Asn Asp
                130                135                140
Ala Asn Ser Ser Asn Ile Trp Val Lys Thr Ser Ala Leu Val Lys Pro
145                150                155                160
Ala Gly Asp Thr Asn Val Lys Thr Tyr Pro Val Met Val Asp Ser Arg
                165                170                175
Ala Tyr Asp Lys Asn Gly Asn Tyr Leu Gly His Met Tyr Tyr Ala Tyr
                180                185                190
Asp Asn Ile Asp Ile Val Pro Thr Val Val Thr Ile Asn Gly Lys Thr
                195                200                205
Tyr Tyr Lys Val Ala Asn Lys Asp Glu Tyr Val Arg Val Thr Asn Ile

```

210	215	220
Thr Gly Asn Gln Arg	Thr Leu Lys His Asn Ala	Tyr Ile Tyr Trp Ser
225	230	235
Ser Tyr Arg Arg Thr	Pro Gly Thr Gly Lys Met	Tyr Arg Gly Gln Thr
245	250	255
Val Thr Thr Tyr Gly	Pro Gln Met Lys Phe	Lys Asn Gly Lys Lys Tyr
260	265	270
Tyr Arg Ile Glu Gly	Cys Arg Asn Asn Asn	Lys Arg Tyr Ile Lys Ala
275	280	285
Val Asn Phe Tyr		
290		

<210> 71

<211> 648

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1455 - surface layer protein

<220>

<221> CDS

<222> (1)...(648)

<400> 71

atg gtc tgg cgt ggt cat aaa aaa gca tcg ttt tat aat att ggt ggt	48
Met Val Trp Arg Gly His Lys Lys Ala Ser Phe Tyr Asn Ile Gly Gly	
1 5 10 15	
aat cgt tat ctc tta ggc tat aat gtt gct tcg ctt aat gat aaa gga	96
Asn Arg Tyr Leu Leu Gly Tyr Asn Val Ala Ser Leu Asn Asp Lys Gly	
20 25 30	
acg ttg agt ata tat cgt gat tcg tat att tat gat aag act ggt aaa	144
Thr Leu Ser Ile Tyr Arg Asp Ser Tyr Ile Tyr Asp Lys Thr Gly Lys	
35 40 45	
aga gtt gaa aaa aat act gta ctt aga aaa ggc aca gca att aat tat	192
Arg Val Glu Lys Asn Thr Val Leu Arg Lys Gly Thr Ala Ile Asn Tyr	
50 55 60	
gta gat aaa tta aac gaa aaa atc gaa aca gaa aag aat tta cct aag	240
Val Asp Lys Leu Asn Glu Lys Ile Glu Thr Glu Lys Asn Leu Pro Lys	
65 70 75 80	
ttt tat tac tat aat atg gcg att caa cgt acg cat gaa ggt atg tta	288
Phe Tyr Tyr Tyr Asn Met Ala Ile Gln Arg Thr His Glu Gly Met Leu	
85 90 95	
tgg gta aaa tat agt gta ttg tcg gta aaa tat cat att att aat gga	336
Trp Val Lys Tyr Ser Val Leu Ser Val Lys Tyr His Ile Ile Asn Gly	
100 105 110	

aaa gaa tat tat aaa att gca aat aat aaa tat att aga gca act aat 384
 Lys Glu Tyr Tyr Lys Ile Ala Asn Asn Lys Tyr Ile Arg Ala Thr Asn
 115 120 125

 atc ggt tac ata aac ggt agg cag tta ttt aca act gaa gct aca gtt 432
 Ile Gly Tyr Ile Asn Gly Arg Gln Leu Phe Thr Thr Glu Ala Thr Val
 130 135 140

 aca atg gga aaa gca acg act aaa gat gga aaa tac tat gct aga aat 480
 Thr Met Gly Lys Ala Thr Thr Lys Asp Gly Lys Tyr Tyr Ala Arg Asn
 145 150 155 160

 atg aat ggg aaa att act aaa act att ttg cct tat aag ccg gga caa 528
 Met Asn Gly Lys Ile Thr Lys Thr Ile Leu Pro Tyr Lys Pro Gly Gln
 165 170 175

 aaa gtg gtt gta gat agg tct ttc caa cat tct tct aaa tcg ttt tgg 576
 Lys Val Val Val Asp Arg Ser Phe Gln His Ser Ser Lys Ser Phe Trp
 180 185 190

 aga ata aag gga aca aat tat tat att ttt gga cca gac att aaa aag 624
 Arg Ile Lys Gly Thr Asn Tyr Tyr Ile Phe Gly Pro Asp Ile Lys Lys
 195 200 205

 ttc cca ata cag gca tta cgc cgg 648
 Phe Pro Ile Gln Ala Leu Arg Arg
 210 215

<210> 72

<211> 216

<212> PRT

<213> Lactobacillus acidophilus

<400> 72

Met Val Trp Arg Gly His Lys Lys Ala Ser Phe Tyr Asn Ile Gly Gly
 1 5 10 15
 Asn Arg Tyr Leu Gly Tyr Asn Val Ala Ser Leu Asn Asp Lys Gly
 20 25 30
 Thr Leu Ser Ile Tyr Arg Asp Ser Tyr Ile Tyr Asp Lys Thr Gly Lys
 35 40 45
 Arg Val Glu Lys Asn Thr Val Leu Arg Lys Gly Thr Ala Ile Asn Tyr
 50 55 60
 Val Asp Lys Leu Asn Glu Lys Ile Glu Thr Glu Lys Asn Leu Pro Lys
 65 70 75 80
 Phe Tyr Tyr Tyr Asn Met Ala Ile Gln Arg Thr His Glu Gly Met Leu
 85 90 95
 Trp Val Lys Tyr Ser Val Leu Ser Val Lys Tyr His Ile Ile Asn Gly
 100 105 110
 Lys Glu Tyr Tyr Lys Ile Ala Asn Lys Tyr Ile Arg Ala Thr Asn
 115 120 125
 Ile Gly Tyr Ile Asn Gly Arg Gln Leu Phe Thr Thr Glu Ala Thr Val
 130 135 140
 Thr Met Gly Lys Ala Thr Thr Lys Asp Gly Lys Tyr Tyr Ala Arg Asn
 145 150 155 160
 Met Asn Gly Lys Ile Thr Lys Thr Ile Leu Pro Tyr Lys Pro Gly Gln
 165 170 175

Lys Val Val Val Asp Arg Ser Phe Gln His Ser Ser Lys Ser Phe Trp
 180 185 190
 Arg Ile Lys Gly Thr Asn Tyr Tyr Ile Phe Gly Pro Asp Ile Lys Lys
 195 200 205
 Phe Pro Ile Gln Ala Leu Arg Arg
 210 215

<210> 73

<211> 1077

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1029 - surface layer protein

<220>

<221> CDS

<222> (1)...(1077)

<400> 73

atg caa agt aat gat gct aat gta gtt caa gct gcc act agt aat aag	48
Met Gln Ser Asn Asp Ala Asn Val Val Gln Ala Ala Thr Ser Asn Lys	
1 5 10 15	
aaa aat acg att aag tta att agt act aac aat aat atc aaa att cct	96
Lys Asn Thr Ile Lys Leu Ile Ser Thr Asn Asn Asn Ile Lys Ile Pro	
20 25 30	
gtg tat gac cgt caa ggt aag caa att aat gga ttt aca gtt gaa tca	144
Val Tyr Asp Arg Gln Gly Lys Gln Ile Asn Gly Phe Thr Val Glu Ser	
35 40 45	
ggt gcc aat gta act gtt atc ggc aaa cca att att gtt caa caa aag	192
Gly Ala Asn Val Thr Val Ile Gly Lys Pro Ile Ile Val Gln Gln Lys	
50 55 60	
tat aga aaa gat gtc ttt gaa ggt ata aaa att aat ggt aaa act tat	240
Tyr Arg Lys Asp Val Phe Glu Gly Ile Lys Ile Asn Gly Lys Thr Tyr	
65 70 75 80	
gca tcc cta ggc gat gga ggt tat att cca ata aat gct aca ggt gtt	288
Ala Ser Leu Gly Asp Gly Gly Tyr Ile Pro Ile Asn Ala Thr Gly Val	
85 90 95	
att aca tct aaa gga atg aaa att aca cgt gat act gcc gtt tat aac	336
Ile Thr Ser Lys Gly Met Lys Ile Thr Arg Asp Thr Ala Val Tyr Asn	
100 105 110	
aaa aac ggt aaa aaa ttg agt aca tat cgc gga cac acg gct act tta	384
Lys Asn Gly Lys Lys Leu Ser Thr Tyr Arg Gly His Thr Ala Thr Leu	
115 120 125	
aaa aag gat tca atc gta aaa tac ggt ggc gca act acc tat aca ata	432

Lys	Lys	Asp	Ser	Ile	Val	Lys	Tyr	Gly	Gly	Ala	Thr	Thr	Tyr	Thr	Ile		
130						135					140						
ccg	gta	tct	tac	ttc	aac	att	ggg	aat	ggg	cgt	tat	gta	aga	gcc	agc	480	
Pro	Val	Ser	Tyr	Phe	Asn	Ile	Gly	Asn	Gly	Arg	Tyr	Val	Arg	Ala	Ser		
145					150					155					160		
tat	gtt	caa	gaa	tat	aat	ggg	caa	aca	gtt	tta	act	ttg	aat	tat	aat	528	
Tyr	Val	Gln	Glu	Tyr	Asn	Gly	Gln	Thr	Val	Leu	Thr	Leu	Asn	Tyr	Asn		
				165					170					175			
act	ttt	gtt	tat	aac	aaa	aag	ggg	aaa	cgt	atc	aac	tac	gat	ggc	caa	576	
Thr	Phe	Val	Tyr	Asn	Lys	Lys	Gly	Lys	Arg	Ile	Asn	Tyr	Asp	Gly	Gln		
			180					185					190				
cgt	aaa	tta	atg	aac	ggg	ggc	gta	gta	act	act	aat	agt	aaa	att	aga	624	
Arg	Lys	Leu	Met	Asn	Gly	Gly	Val	Val	Thr	Thr	Asn	Ser	Lys	Ile	Arg		
		195					200					205					
gaa	gct	aag	tct	tca	gat	caa	aac	tac	ttc	tat	agt	agt	gct	aat	tat	672	
Glu	Ala	Lys	Ser	Ser	Asp	Gln	Asn	Tyr	Phe	Tyr	Ser	Ser	Ala	Asn	Tyr		
	210					215					220						
act	gat	aaa	aat	aaa	tta	gct	ttt	acg	act	aca	aaa	att	aag	ggc	caa	720	
Thr	Asp	Lys	Asn	Lys	Leu	Ala	Phe	Thr	Thr	Thr	Lys	Ile	Lys	Gly	Gln		
	225				230					235					240		
gat	tat	ctt	tca	att	ggg	aaa	ggg	gaa	tat	att	aaa	att	gct	aat	gta	768	
Asp	Tyr	Leu	Ser	Ile	Gly	Lys	Gly	Glu	Tyr	Ile	Lys	Ile	Ala	Asn	Val		
			245					250						255			
aaa	aca	gct	aat	gga	atg	att	tta	ttt	act	aaa	ggg	cct	atc	act	att	816	
Lys	Thr	Ala	Asn	Gly	Met	Ile	Leu	Phe	Thr	Lys	Gly	Pro	Ile	Thr	Ile		
		260						265					270				
act	ttg	cct	agt	gac	act	act	att	tac	agc	tct	aat	ttc	aag	gaa	acg	864	
Thr	Leu	Pro	Ser	Asp	Thr	Thr	Ile	Tyr	Ser	Ser	Asn	Phe	Lys	Glu	Thr		
		275					280					285					
aag	aaa	caa	att	gct	gct	ggg	aag	aaa	gta	att	ttg	gat	aaa	act	gaa	912	
Lys	Lys	Gln	Ile	Ala	Ala	Gly	Lys	Lys	Val	Ile	Leu	Asp	Lys	Thr	Glu		
	290					295					300						
att	gat	aat	agt	tta	agt	gat	cca	caa	tta	tat	ttc	aga	att	aag	ggg	960	
Ile	Asp	Asn	Ser	Leu	Ser	Asp	Pro	Gln	Leu	Tyr	Phe	Arg	Ile	Lys	Gly		
	305				310					315					320		
act	aat	gaa	ttg	atc	tac	tgg	ggc	gat	ttg	gga	gaa	tat	cct	ggg	gtt	1008	
Thr	Asn	Glu	Leu	Ile	Tyr	Trp	Gly	Asp	Leu	Gly	Glu	Tyr	Pro	Gly	Val		
			325					330						335			
gat	cac	act	gct	gtt	tac	gat	cca	aat	tat	tat	agt	att	tat	tca	ttc	1056	
Asp	His	Thr	Ala	Val	Tyr	Asp	Pro	Asn	Tyr	Tyr	Ser	Ile	Tyr	Ser	Phe		
			340					345					350				
cca	ctt	aga	caa	ttt	atg	gaa										1077	
Pro	Leu	Arg	Gln	Phe	Met	Glu											

355

<210> 74

<211> 359

<212> PRT

<213> Lactobacillus acidophilus

<400> 74

```

Met Gln Ser Asn Asp Ala Asn Val Val Gln Ala Ala Thr Ser Asn Lys
 1          5          10          15
Lys Asn Thr Ile Lys Leu Ile Ser Thr Asn Asn Asn Ile Lys Ile Pro
          20          25          30
Val Tyr Asp Arg Gln Gly Lys Gln Ile Asn Gly Phe Thr Val Glu Ser
          35          40          45
Gly Ala Asn Val Thr Val Ile Gly Lys Pro Ile Ile Val Gln Gln Lys
 50          55          60
Tyr Arg Lys Asp Val Phe Glu Gly Ile Lys Ile Asn Gly Lys Thr Tyr
 65          70          75          80
Ala Ser Leu Gly Asp Gly Gly Tyr Ile Pro Ile Asn Ala Thr Gly Val
          85          90          95
Ile Thr Ser Lys Gly Met Lys Ile Thr Arg Asp Thr Ala Val Tyr Asn
          100          105          110
Lys Asn Gly Lys Lys Leu Ser Thr Tyr Arg Gly His Thr Ala Thr Leu
          115          120          125
Lys Lys Asp Ser Ile Val Lys Tyr Gly Gly Ala Thr Thr Tyr Thr Ile
          130          135          140
Pro Val Ser Tyr Phe Asn Ile Gly Asn Gly Arg Tyr Val Arg Ala Ser
          145          150          155          160
Tyr Val Gln Glu Tyr Asn Gly Gln Thr Val Leu Thr Leu Asn Tyr Asn
          165          170          175
Thr Phe Val Tyr Asn Lys Lys Gly Lys Arg Ile Asn Tyr Asp Gly Gln
          180          185          190
Arg Lys Leu Met Asn Gly Gly Val Val Thr Thr Asn Ser Lys Ile Arg
          195          200          205
Glu Ala Lys Ser Ser Asp Gln Asn Tyr Phe Tyr Ser Ser Ala Asn Tyr
          210          215          220
Thr Asp Lys Asn Lys Leu Ala Phe Thr Thr Thr Lys Ile Lys Gly Gln
          225          230          235          240
Asp Tyr Leu Ser Ile Gly Lys Gly Glu Tyr Ile Lys Ile Ala Asn Val
          245          250          255
Lys Thr Ala Asn Gly Met Ile Leu Phe Thr Lys Gly Pro Ile Thr Ile
          260          265          270
Thr Leu Pro Ser Asp Thr Thr Ile Tyr Ser Ser Asn Phe Lys Glu Thr
          275          280          285
Lys Lys Gln Ile Ala Ala Gly Lys Lys Val Ile Leu Asp Lys Thr Glu
          290          295          300
Ile Asp Asn Ser Leu Ser Asp Pro Gln Leu Tyr Phe Arg Ile Lys Gly
          305          310          315          320
Thr Asn Glu Leu Ile Tyr Trp Gly Asp Leu Gly Glu Tyr Pro Gly Val
          325          330          335
Asp His Thr Ala Val Tyr Asp Pro Asn Tyr Tyr Ser Ile Tyr Ser Phe
          340          345          350
Pro Leu Arg Gln Phe Met Glu
          355

```

<210> 75
 <211> 5028
 <212> DNA
 <213> *Lactobacillus acidophilus*

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1633 - surface protein

<220>
 <221> CDS
 <222> (1)...(5028)

<400> 75
 atg gga acg ggt caa agt aaa tct gtt aag gcc gat tct gtg caa gat 48
 Met Gly Thr Gly Gln Ser Lys Ser Val Lys Ala Asp Ser Val Gln Asp
 1 5 10 15
 gac atg att acg caa aca gat gaa gat gaa gca tta tcg gat gaa gtg 96
 Asp Met Ile Thr Gln Thr Asp Glu Asp Glu Ala Leu Ser Asp Glu Val
 20 25 30
 aaa ata gat act acg gat act tca acc gaa gaa gta agt aat cca gct 144
 Lys Ile Asp Thr Thr Asp Thr Ser Thr Glu Glu Val Ser Asn Pro Ala
 35 40 45
 aca gac act tca acc gaa gaa gtg aat ggt ccg tct tcg gat agt tta 192
 Thr Asp Thr Ser Thr Glu Glu Val Asn Gly Pro Ser Ser Asp Ser Leu
 50 55 60
 acg gta gtg gat ccg aca atg gaa aca cag tct cct gtt gaa gat act 240
 Thr Val Val Asp Pro Thr Met Glu Thr Gln Ser Pro Val Glu Asp Thr
 65 70 75 80
 ata aca aca gaa ccg gat aat tca gca gtt aat gat aca aac cat tca 288
 Ile Thr Thr Glu Pro Asp Asn Ser Ala Val Asn Asp Thr Asn His Ser
 85 90 95
 act gcc gat act tcg gaa gtt gaa act aat acg tct act act gat aac 336
 Thr Ala Asp Thr Ser Glu Val Glu Thr Asn Thr Ser Thr Thr Asp Asn
 100 105 110
 gta gca gct gaa acg act aat aca gct gca agt act aca aca aat gcg 384
 Val Ala Ala Glu Thr Thr Asn Thr Ala Ala Ser Thr Thr Thr Asn Ala
 115 120 125
 gat gat tca gtt aat gct gca gac aca agc aca atg act gtg gtt aag 432
 Asp Asp Ser Val Asn Ala Ala Asp Thr Ser Thr Met Thr Val Val Lys
 130 135 140
 aca act gaa gaa aaa tct gat gaa aat gat cag act aaa gaa gcc gta 480
 Thr Thr Glu Glu Lys Ser Asp Glu Asn Asp Gln Thr Lys Glu Ala Val
 145 150 155 160
 gat aag tta act gtt ggt gca act aag gcc aaa gct ttg gcc gct gca 528

Asp Lys Leu Thr Val Gly Ala Thr Lys Ala Lys Ala Leu Ala Ala Ala	165	170	175	
gca gaa gga cag act gtt tcg gta aca gat tat cag aca ttt tta gat	180	185	190	576
Ala Glu Gly Gln Thr Val Ser Val Thr Asp Tyr Gln Thr Phe Leu Asp				
gct tta cgc aat aaa gat gta agc act att gat ttt gca aat gat att	195	200	205	624
Ala Leu Arg Asn Lys Asp Val Ser Thr Ile Asp Phe Ala Asn Asp Ile				
gat ttc agt gat gcg tta ttt aaa cgt gga ctt att aat tac aaa aat	210	215	220	672
Asp Phe Ser Asp Ala Leu Phe Lys Arg Gly Leu Ile Asn Tyr Lys Asn				
gtg att ttg aat gaa tca act gat gaa gat att gct cgt gca gtg acg	225	230	235	720
Val Ile Leu Asn Glu Thr Asp Glu Asp Ile Ala Arg Ala Val Thr				
att aat ggt aac ggt aat aaa tta att atg agt gac cgt tac att caa	245	250	255	768
Ile Asn Gly Asn Gly Asn Lys Leu Ile Met Ser Asp Arg Tyr Ile Gln				
ttt act agt agg aat caa aag act gat ggt aaa aat tgg gat att gaa	260	265	270	816
Phe Thr Ser Arg Asn Gln Lys Thr Asp Gly Lys Asn Trp Asp Ile Glu				
tta aaa gat tta acc cta caa act acc agt ggc tat ggt ccc ttc tgg	275	280	285	864
Leu Lys Asp Leu Thr Leu Gln Thr Thr Ser Gly Tyr Gly Pro Phe Trp				
ttt gat aat act gct aag caa gct gct ggc aat acc att acc ttt aat	290	295	300	912
Phe Asp Asn Thr Ala Lys Gln Ala Ala Gly Asn Thr Ile Thr Phe Asn				
ggg gtt aac acc aca gca gat tca cgt gaa att atg tgg tat aag agt	305	310	315	960
Gly Val Asn Thr Thr Ala Asp Ser Arg Glu Ile Met Trp Tyr Lys Ser				
ggt gcc att tat agt tcg aca gct aat gta gtc ttt aaa gga aat aat	325	330	335	1008
Gly Ala Ile Tyr Ser Ser Thr Ala Asn Val Val Phe Lys Gly Asn Asn				
gta att aac agt act ctt aag ggg gat act gct gca att tac gct tac	340	345	350	1056
Val Ile Asn Ser Thr Leu Lys Gly Asp Thr Ala Ala Ile Tyr Ala Tyr				
agc gtc aaa gca gaa gaa ggt agc act act aca ttt aat gta att gat	355	360	365	1104
Ser Val Lys Ala Glu Glu Gly Ser Thr Thr Thr Phe Asn Val Ile Asp				
gaa tca cct gcc aat tct ggc tat gat cga gca gta att gtg att cct	370	375	380	1152
Glu Ser Pro Ala Asn Ser Gly Tyr Asp Arg Ala Val Ile Val Ile Pro				
gat aat aaa aat tct gga aat gtt acg gtt gct aaa ggt gct act tta				1200
Asp Asn Lys Asn Ser Gly Asn Val Thr Val Ala Lys Gly Ala Thr Leu				

385	390	395	400	
aat att aat gcg gat aat aaa gta act gtg gaa gga atg gac ggc tcg	1248			
Asn Ile Asn Ala Asp Asn Lys Val Thr Val Glu Gly Met Asp Gly Ser				
405	410	415		
aat tcc tat ggt acg atg ggt atc cgt ttt aaa ggc tgg gca caa aat	1296			
Asn Ser Tyr Gly Thr Met Gly Ile Arg Phe Lys Gly Trp Ala Gln Asn				
420	425	430		
gca gat ata gat aca gct gcg act agt gtg gtt cag gta tta ggt aac	1344			
Ala Asp Ile Asp Thr Ala Ala Thr Ser Val Val Gln Val Leu Gly Asn				
435	440	445		
ttg aat atg aat atg gga tca ggc ggt tct act gcc att ctt ggg tca	1392			
Leu Asn Met Asn Met Gly Ser Gly Gly Ser Thr Ala Ile Leu Gly Ser				
450	455	460		
tat gtt gat gtt caa aac gtt gga aat gtt aat att gaa acg gct caa	1440			
Tyr Val Asp Val Gln Asn Val Gly Asn Val Asn Ile Glu Thr Ala Gln				
465	470	475	480	
gat ggt aat aat ggt aat act ggt act tta gaa gta gaa cat aat ggt	1488			
Asp Gly Asn Asn Gly Asn Thr Gly Thr Leu Glu Val Glu His Asn Gly				
485	490	495		
act cac ttt ggt gta att aca ggt gga tta gct ggt agt gat aac tat	1536			
Thr His Phe Gly Val Ile Thr Gly Gly Leu Ala Gly Ser Asp Asn Tyr				
500	505	510		
gca ggt ata aga att gct gat ggt ggt act ttg aaa att gtt cgt tcg	1584			
Ala Gly Ile Arg Ile Ala Asp Gly Gly Thr Leu Lys Ile Val Arg Ser				
515	520	525		
gta gat aat gaa aac ggc aat aaa tct aca caa ccg tta att tca tat	1632			
Val Asp Asn Glu Asn Gly Asn Lys Ser Thr Gln Pro Leu Ile Ser Tyr				
530	535	540		
ggg gat atc act act tca aac ggt aaa act ttt act att gat gtt aaa	1680			
Gly Asp Ile Thr Thr Ser Asn Gly Lys Thr Phe Thr Ile Asp Val Lys				
545	550	555	560	
cca ggc ggt acg ctt gat tta caa gat aat gca cag aac cct aat gaa	1728			
Pro Gly Gly Thr Leu Asp Leu Gln Asp Asn Ala Gln Asn Pro Asn Glu				
565	570	575		
tgg gaa cct aat act ggt acg cct tta gca gga tta att aca atg tgg	1776			
Trp Glu Pro Asn Thr Gly Thr Pro Leu Ala Gly Leu Ile Thr Met Trp				
580	585	590		
ggt act agt ggt aca aac att gtt aaa att aat gat cct aag tat gtg	1824			
Gly Thr Ser Gly Thr Asn Ile Val Lys Ile Asn Asp Pro Lys Tyr Val				
595	600	605		
aac ttc caa cgt act ggc agt caa cca ggt tca atg tta cgg ttg gaa	1872			
Asn Phe Gln Arg Thr Gly Ser Gln Pro Gly Ser Met Leu Arg Leu Glu				
610	615	620		

ggt act act aat agt gtt tct att aat ggc gat ggt aat gct gta act	1920
Gly Thr Thr Asn Ser Val Ser Ile Asn Gly Asp Gly Asn Ala Val Thr	
625 630 635 640	
cct gtt gca caa tgg gat gta ggc aat act ggt aat gaa cca tca tac	1968
Pro Val Ala Gln Trp Asp Val Gly Asn Thr Gly Asn Glu Pro Ser Tyr	
645 650 655	
tac tgg tat att ttg aat gaa act aat cag aat aat tgg gga aca aat	2016
Tyr Trp Tyr Ile Leu Asn Glu Thr Asn Gln Asn Asn Trp Gly Thr Asn	
660 665 670	
gca aat ggg ttt act caa aag ggt gaa act aaa cca gtt aat aaa gat	2064
Ala Asn Gly Phe Thr Gln Lys Gly Glu Thr Lys Pro Val Asn Lys Asp	
675 680 685	
ggt gaa gct aaa ttc ctt aat tcc aac ggt agt gtt gaa cta gct cct	2112
Gly Glu Ala Lys Phe Leu Asn Ser Asn Gly Ser Val Glu Leu Ala Pro	
690 695 700	
aat caa tca ggt tct aca gca tca agt tat aac aat ggg act ata acc	2160
Asn Gln Ser Gly Ser Thr Ala Ser Ser Tyr Asn Asn Gly Thr Ile Thr	
705 710 715 720	
gaa tca tct gat caa act atg tac cta aac cag ttc tta aat aac ttt	2208
Glu Ser Ser Asp Gln Thr Met Tyr Leu Asn Gln Phe Leu Asn Asn Phe	
725 730 735	
aac tgg tgg act cca cag aga atc gct atg ggt agc atg tta aag gat	2256
Asn Trp Trp Thr Pro Gln Arg Ile Ala Met Gly Ser Met Leu Lys Asp	
740 745 750	
gta gct acc aat gcc caa gaa tat aaa cct gaa gta aaa gaa att act	2304
Val Ala Thr Asn Ala Gln Glu Tyr Lys Pro Glu Val Lys Glu Ile Thr	
755 760 765	
gca ggt gct aat gat gtc ctc aaa gac gtc gat cca tta gaa ggt att	2352
Ala Gly Ala Asn Asp Val Leu Lys Asp Val Asp Pro Leu Glu Gly Ile	
770 775 780	
acg ggg tta act gat agc aat ggt aac ccg gtt gaa aat gga ttg agt	2400
Thr Gly Leu Thr Asp Ser Asn Gly Asn Pro Val Glu Asn Gly Leu Ser	
785 790 795 800	
tat atc caa ggt gtg act tgg cta gat tca agt act gat gcg gag aac	2448
Tyr Ile Gln Gly Val Thr Trp Leu Asp Ser Ser Thr Asp Ala Glu Asn	
805 810 815	
tgg aag aaa tta atg agc aat gag aaa gtt cca acg aat ccg acc ggt	2496
Trp Lys Lys Leu Met Ser Asn Glu Lys Val Pro Thr Asn Pro Thr Gly	
820 825 830	
aaa tta gga gat tta gca ccg gat gaa aaa ttt gct tgg gct aag gta	2544
Lys Leu Gly Asp Leu Ala Pro Asp Glu Lys Phe Ala Trp Ala Lys Val	
835 840 845	

act tac aaa gat gat tca att gat ttc gtt aag att ccg ttg aat gta	2592
Thr Tyr Lys Asp Asp Ser Ile Asp Phe Val Lys Ile Pro Leu Asn Val	
850 855 860	
ggt act gat cca atg aag gat aat tac acg cca gca tat gaa gat gtg	2640
Val Thr Asp Pro Met Lys Asp Asn Tyr Thr Pro Ala Tyr Glu Asp Val	
865 870 875 880	
agt gtg gaa caa gga aaa gac aat agt gca caa cct gca aat ccg aca	2688
Ser Val Glu Gln Gly Lys Asp Asn Ser Ala Gln Pro Ala Asn Pro Thr	
885 890 895	
ttt act gat aag aat ggt gac aca tta gat acc att cca gaa gga act	2736
Phe Thr Asp Lys Asn Gly Asp Thr Leu Asp Thr Ile Pro Glu Gly Thr	
900 905 910	
aca ttc gct cct acc gct gat act cca act tgg gta gaa att gat cca	2784
Thr Phe Ala Pro Thr Ala Asp Thr Pro Thr Trp Val Glu Ile Asp Pro	
915 920 925	
aca aca ggt caa tta att gct aag cca ccg gta gat gta gaa gct aaa	2832
Thr Thr Gly Gln Leu Ile Ala Lys Pro Pro Val Asp Val Glu Ala Lys	
930 935 940	
gat tat gaa att ccg gtg aca gta act tac caa gat gga aca acc gat	2880
Asp Tyr Glu Ile Pro Val Thr Val Thr Tyr Gln Asp Gly Thr Thr Asp	
945 950 955 960	
aca gtt ttg gca aaa gta act gta aca cca aca gaa act aaa gaa gac	2928
Thr Val Leu Ala Lys Val Thr Val Thr Pro Thr Glu Thr Lys Glu Asp	
965 970 975	
agt aat aaa tac aca cct gtt tat agt gaa ggc gtt gga gaa gct ggt	2976
Ser Asn Lys Tyr Thr Pro Val Tyr Ser Glu Gly Val Gly Glu Ala Gly	
980 985 990	
aaa gac ttc aac gta gat agt cca aca ttt aca gat gaa gac gga aac	3024
Lys Asp Phe Asn Val Asp Ser Pro Thr Phe Thr Asp Glu Asp Gly Asn	
995 1000 1005	
aag gtt act act cca cca gtt act gtc ttt gaa aaa ggt gaa gga gct	3072
Lys Val Thr Thr Pro Pro Val Thr Val Phe Glu Lys Gly Glu Gly Ala	
1010 1015 1020	
cca gat tgg gtt aaa gta gat ccg aac acc ggt gca tta act ggt act	3120
Pro Asp Trp Val Lys Val Asp Pro Asn Thr Gly Ala Leu Thr Gly Thr	
1025 1030 1035 1040	
gta cca gaa gga acc act gga gat gtt gta att ccg gtt aaa gta aca	3168
Val Pro Glu Gly Thr Thr Gly Asp Val Val Ile Pro Val Lys Val Thr	
1045 1050 1055	
tac caa gac ggt tca agt gag gta gtg aat gca aca gtt aaa gtt aca	3216
Tyr Gln Asp Gly Ser Ser Glu Val Val Asn Ala Thr Val Lys Val Thr	
1060 1065 1070	
gaa cca acg aca cca ggt caa aca gct gat gat cat aat cca aaa tat	3264

Glu Pro Thr Thr Pro Gly Gln Thr Ala Asp Asp His Asn Pro Lys Tyr	
1075 1080 1085	
gaa gat gtc gat gtt aaa cca ggt gag acg aat aag gta act cca acc	3312
Glu Asp Val Asp Val Lys Pro Gly Glu Thr Asn Lys Val Thr Pro Thr	
1090 1095 1100	
aat acc gat aaa gat ggc aat cta gcg aat atc cca gac gga act aag	3360
Asn Thr Asp Lys Asp Gly Asn Leu Ala Asn Ile Pro Asp Gly Thr Lys	
1105 1110 1115 1120	
ttt gag aaa gat ccg gat gct cca agt tgg gta gag gta gat ccg aat	3408
Phe Glu Lys Asp Pro Asp Ala Pro Ser Trp Val Glu Val Asp Pro Asn	
1125 1130 1135	
acc ggt gaa ttg act gta gcg cca ccg gaa ggc acg cca tcg ggt gaa	3456
Thr Gly Glu Leu Thr Val Ala Pro Pro Glu Gly Thr Pro Ser Gly Glu	
1140 1145 1150	
cat gaa att aaa gta aag gta acg tac cca gac ggt tca acg gat gaa	3504
His Glu Ile Lys Val Lys Val Thr Tyr Pro Asp Gly Ser Thr Asp Glu	
1155 1160 1165	
gta ccg gta acg gta aaa gta agt gaa cca acg aca cca ggt caa acg	3552
Val Pro Val Thr Val Lys Val Ser Glu Pro Thr Thr Pro Gly Gln Thr	
1170 1175 1180	
gct gat gat cat aat cca aaa tat gaa gat gtc gat gtt aaa cca ggt	3600
Ala Asp Asp His Asn Pro Lys Tyr Glu Asp Val Asp Val Lys Pro Gly	
1185 1190 1195 1200	
gag acg aat aag gta act cca acc aat acc gat aaa gat ggc aat cca	3648
Glu Thr Asn Lys Val Thr Pro Thr Asn Thr Asp Lys Asp Gly Asn Pro	
1205 1210 1215	
gcg aat atc cca gac gga act aag ttt gag aaa gat ccg gat gct cca	3696
Ala Asn Ile Pro Asp Gly Thr Lys Phe Glu Lys Asp Pro Asp Ala Pro	
1220 1225 1230	
agt tgg gta gag gta gat ccg aat acc ggt gaa ttg act gta gcg cca	3744
Ser Trp Val Glu Val Asp Pro Asn Thr Gly Glu Leu Thr Val Ala Pro	
1235 1240 1245	
ccg gaa ggc acg cca tcg ggt gga cat gaa att aaa gta aag gta acg	3792
Pro Glu Gly Thr Pro Ser Gly Gly His Glu Ile Lys Val Lys Val Thr	
1250 1255 1260	
tac cca gac ggt tca acg gat gaa gta ccg gta acg gta aaa gta agc	3840
Tyr Pro Asp Gly Ser Thr Asp Glu Val Pro Val Thr Val Lys Val Ser	
1265 1270 1275 1280	
gac cca acg aca ccg ggt caa aca gat gcc gat aag tac acg cca gag	3888
Asp Pro Thr Thr Pro Gly Gln Thr Asp Ala Asp Lys Tyr Thr Pro Glu	
1285 1290 1295	
gca aag gat att acc gtt act cca ggc cca act cca gat cca gca gaa	3936
Ala Lys Asp Ile Thr Val Thr Pro Gly Pro Thr Pro Asp Pro Ala Glu	

1300	1305	1310	
ggc atc ggt aat aag gac aca tta cca tca ggt act aag tat gag tgg Gly Ile Gly Asn Lys Asp Thr Leu Pro Ser Gly Thr Lys Tyr Glu Trp 1315 1320 1325			3984
aaa gat cca gtt gat aca act act ccg ggt gac aag aca ggc aca att Lys Asp Pro Val Asp Thr Thr Thr Pro Gly Asp Lys Thr Gly Thr Ile 1330 1335 1340			4032
gta gta agt tac cca gat gga tca aca gac gag att caa gta aca gta Val Val Ser Tyr Pro Asp Gly Ser Thr Asp Glu Ile Gln Val Thr Val 1345 1350 1355 1360			4080
aag gtt acg gac cca acg acg ccg ggt caa aca gat gcc gat aag tac Lys Val Thr Asp Pro Thr Thr Pro Gly Gln Thr Asp Ala Asp Lys Tyr 1365 1370 1375			4128
acg ccg gag gca aag gat att acc gtt acc cta ggc caa acc cca gat Thr Pro Glu Ala Lys Asp Ile Thr Val Thr Leu Gly Gln Thr Pro Asp 1380 1385 1390			4176
cca gca gaa ggc atc ggt aat aag gac aca tta cca tca ggt act aag Pro Ala Glu Gly Ile Gly Asn Lys Asp Thr Leu Pro Ser Gly Thr Lys 1395 1400 1405			4224
tat gag tgg aaa gat cca gtt gat aca act act ccg ggt gac aag aca Tyr Glu Trp Lys Asp Pro Val Asp Thr Thr Thr Pro Gly Asp Lys Thr 1410 1415 1420			4272
ggc aca att gta gta agt tac cca gat gga tca aca gac gag att caa Gly Thr Ile Val Val Ser Tyr Pro Asp Gly Ser Thr Asp Glu Ile Gln 1425 1430 1435 1440			4320
gta aca gta aag gtt gca gaa cca acg aca cca ggt cca aca gat gct Val Thr Val Lys Val Ala Glu Pro Thr Thr Pro Gly Pro Thr Asp Ala 1445 1450 1455			4368
gac aag cat act cct gaa gct aaa gat gta aca gta gtt caa ggc caa Asp Lys His Thr Pro Glu Ala Lys Asp Val Thr Val Val Gln Gly Gln 1460 1465 1470			4416
acc cca gat cca gcg gaa ggc atc ggc aat aag gat aca tta cca cca Thr Pro Asp Pro Ala Glu Gly Ile Gly Asn Lys Asp Thr Leu Pro Pro 1475 1480 1485			4464
ggc act agg tat gca tgg aaa gat cca gtt gat aca act act ccg ggt Gly Thr Arg Tyr Ala Trp Lys Asp Pro Val Asp Thr Thr Thr Pro Gly 1490 1495 1500			4512
gac aag aca ggc aca att gta gta acc tac cca gat gga tca aca gac Asp Lys Thr Gly Thr Ile Val Val Thr Tyr Pro Asp Gly Ser Thr Asp 1505 1510 1515 1520			4560
gaa gtc tct gta acg tta cat gtt act cct tct gaa agt ggc aca aca Glu Val Ser Val Thr Leu His Val Thr Pro Ser Glu Ser Gly Thr Thr 1525 1530 1535			4608

gat aca tca acg acg cca cct acc gat act tca ggt agt gac act gac 4656
Asp Thr Ser Thr Thr Pro Pro Thr Asp Thr Ser Gly Ser Asp Thr Asp
1540 1545 1550

act act tca aaa ggt gaa acg cca gct gat aca cca cca acg gat aca 4704
Thr Thr Ser Lys Gly Glu Thr Pro Ala Asp Thr Pro Pro Thr Asp Thr
1555 1560 1565

gct tct gat tcg aca gat acc act cca aaa gat gaa aat act gat aat 4752
Ala Ser Asp Ser Thr Asp Thr Pro Lys Asp Glu Asn Thr Asp Asn
1570 1575 1580

aca ggt ggt act cat aaa tcc acc aat act gac tct agt caa agt ggt 4800
Thr Gly Gly Thr His Lys Ser Thr Asn Thr Asp Ser Ser Gln Ser Gly
1585 1590 1595 1600

gcg aca ggc aat act tct agt ggt gcg aat gca agt agt aat acc gaa 4848
Ala Thr Gly Asn Thr Ser Ser Gly Ala Asn Ala Ser Ser Asn Thr Glu
1605 1610 1615

att cat gct agt gat gta act act gac caa tac aca acg gta aac gac 4896
Ile His Ala Ser Asp Val Thr Thr Asp Gln Tyr Thr Thr Val Asn Asp
1620 1625 1630

aat act gca gat atg aat act ctt cca caa aca ggc gaa aca gac cgc 4944
Asn Thr Ala Asp Met Asn Thr Leu Pro Gln Thr Gly Glu Thr Asp Arg
1635 1640 1645

aac gtt gga gta tgg ggt atg att att gca gca gta ggt agt cta ttt 4992
Asn Val Gly Val Trp Gly Met Ile Ile Ala Ala Val Gly Ser Leu Phe
1650 1655 1660

ggt tta ggc cac ggt aag aaa cgt aga aag gat gaa 5028
Gly Leu Gly His Gly Lys Lys Arg Arg Lys Asp Glu
1665 1670 1675

<210> 76

<211> 1676

<212> PRT

<213> Lactobacillus acidophilus

<400> 76

Met Gly Thr Gly Gln Ser Lys Ser Val Lys Ala Asp Ser Val Gln Asp
1 5 10 15
Asp Met Ile Thr Gln Thr Asp Glu Asp Glu Ala Leu Ser Asp Glu Val
20 25 30
Lys Ile Asp Thr Thr Asp Thr Ser Thr Glu Glu Val Ser Asn Pro Ala
35 40 45
Thr Asp Thr Ser Thr Glu Glu Val Asn Gly Pro Ser Ser Asp Ser Leu
50 55 60
Thr Val Val Asp Pro Thr Met Glu Thr Gln Ser Pro Val Glu Asp Thr
65 70 75 80
Ile Thr Thr Glu Pro Asp Asn Ser Ala Val Asn Asp Thr Asn His Ser
85 90 95
Thr Ala Asp Thr Ser Glu Val Glu Thr Asn Thr Ser Thr Thr Asp Asn

- 202 -

Pro Gly Gly Thr Leu Asp Leu Gln Asp Asn Ala Gln Asn Pro Asn Glu
 565 570 575
 Trp Glu Pro Asn Thr Gly Thr Pro Leu Ala Gly Leu Ile Thr Met Trp
 580 585 590
 Gly Thr Ser Gly Thr Asn Ile Val Lys Ile Asn Asp Pro Lys Tyr Val
 595 600 605
 Asn Phe Gln Arg Thr Gly Ser Gln Pro Gly Ser Met Leu Arg Leu Glu
 610 615 620
 Gly Thr Thr Asn Ser Val Ser Ile Asn Gly Asp Gly Asn Ala Val Thr
 625 630 635 640
 Pro Val Ala Gln Trp Asp Val Gly Asn Thr Gly Asn Glu Pro Ser Tyr
 645 650 655
 Tyr Trp Tyr Ile Leu Asn Glu Thr Asn Gln Asn Asn Trp Gly Thr Asn
 660 665 670
 Ala Asn Gly Phe Thr Gln Lys Gly Glu Thr Lys Pro Val Asn Lys Asp
 675 680 685
 Gly Glu Ala Lys Phe Leu Asn Ser Asn Gly Ser Val Glu Leu Ala Pro
 690 695 700
 Asn Gln Ser Gly Ser Thr Ala Ser Ser Tyr Asn Asn Gly Thr Ile Thr
 705 710 715 720
 Glu Ser Ser Asp Gln Thr Met Tyr Leu Asn Gln Phe Leu Asn Asn Phe
 725 730 735
 Asn Trp Trp Thr Pro Gln Arg Ile Ala Met Gly Ser Met Leu Lys Asp
 740 745 750
 Val Ala Thr Asn Ala Gln Glu Tyr Lys Pro Glu Val Lys Glu Ile Thr
 755 760 765
 Ala Gly Ala Asn Asp Val Leu Lys Asp Val Asp Pro Leu Glu Gly Ile
 770 775 780
 Thr Gly Leu Thr Asp Ser Asn Gly Asn Pro Val Glu Asn Gly Leu Ser
 785 790 795 800
 Tyr Ile Gln Gly Val Thr Trp Leu Asp Ser Ser Thr Asp Ala Glu Asn
 805 810 815
 Trp Lys Lys Leu Met Ser Asn Glu Lys Val Pro Thr Asn Pro Thr Gly
 820 825 830
 Lys Leu Gly Asp Leu Ala Pro Asp Glu Lys Phe Ala Trp Ala Lys Val
 835 840 845
 Thr Tyr Lys Asp Asp Ser Ile Asp Phe Val Lys Ile Pro Leu Asn Val
 850 855 860
 Val Thr Asp Pro Met Lys Asp Asn Tyr Thr Pro Ala Tyr Glu Asp Val
 865 870 875 880
 Ser Val Glu Gln Gly Lys Asp Asn Ser Ala Gln Pro Ala Asn Pro Thr
 885 890 895
 Phe Thr Asp Lys Asn Gly Asp Thr Leu Asp Thr Ile Pro Glu Gly Thr
 900 905 910
 Thr Phe Ala Pro Thr Ala Asp Thr Pro Thr Trp Val Glu Ile Asp Pro
 915 920 925
 Thr Thr Gly Gln Leu Ile Ala Lys Pro Pro Val Asp Val Glu Ala Lys
 930 935 940
 Asp Tyr Glu Ile Pro Val Thr Val Thr Tyr Gln Asp Gly Thr Thr Asp
 945 950 955 960
 Thr Val Leu Ala Lys Val Thr Val Thr Pro Thr Glu Thr Lys Glu Asp
 965 970 975
 Ser Asn Lys Tyr Thr Pro Val Tyr Ser Glu Gly Val Gly Glu Ala Gly
 980 985 990
 Lys Asp Phe Asn Val Asp Ser Pro Thr Phe Thr Asp Glu Asp Gly Asn
 995 1000 1005
 Lys Val Thr Thr Pro Pro Val Thr Val Phe Glu Lys Gly Glu Gly Ala

1010	1015	1020
Pro Asp Trp Val Lys Val Asp Pro Asn Thr Gly Ala Leu Thr Gly Thr		
1025	1030	1035
Val Pro Glu Gly Thr Thr Gly Asp Val Val Ile Pro Val Lys Val Thr		
1045	1050	1055
Tyr Gln Asp Gly Ser Ser Glu Val Val Asn Ala Thr Val Lys Val Thr		
1060	1065	1070
Glu Pro Thr Thr Pro Gly Gln Thr Ala Asp Asp His Asn Pro Lys Tyr		
1075	1080	1085
Glu Asp Val Asp Val Lys Pro Gly Glu Thr Asn Lys Val Thr Pro Thr		
1090	1095	1100
Asn Thr Asp Lys Asp Gly Asn Leu Ala Asn Ile Pro Asp Gly Thr Lys		
1105	1110	1115
Phe Glu Lys Asp Pro Asp Ala Pro Ser Trp Val Glu Val Asp Pro Asn		
1125	1130	1135
Thr Gly Glu Leu Thr Val Ala Pro Pro Glu Gly Thr Pro Ser Gly Glu		
1140	1145	1150
His Glu Ile Lys Val Lys Val Thr Tyr Pro Asp Gly Ser Thr Asp Glu		
1155	1160	1165
Val Pro Val Thr Val Lys Val Ser Glu Pro Thr Thr Pro Gly Gln Thr		
1170	1175	1180
Ala Asp Asp His Asn Pro Lys Tyr Glu Asp Val Asp Val Lys Pro Gly		
1185	1190	1195
Glu Thr Asn Lys Val Thr Pro Thr Asn Thr Asp Lys Asp Gly Asn Pro		
1205	1210	1215
Ala Asn Ile Pro Asp Gly Thr Lys Phe Glu Lys Asp Pro Asp Ala Pro		
1220	1225	1230
Ser Trp Val Glu Val Asp Pro Asn Thr Gly Glu Leu Thr Val Ala Pro		
1235	1240	1245
Pro Glu Gly Thr Pro Ser Gly Gly His Glu Ile Lys Val Lys Val Thr		
1250	1255	1260
Tyr Pro Asp Gly Ser Thr Asp Glu Val Pro Val Thr Val Lys Val Ser		
1265	1270	1275
Asp Pro Thr Thr Pro Gly Gln Thr Asp Ala Asp Lys Tyr Thr Pro Glu		
1285	1290	1295
Ala Lys Asp Ile Thr Val Thr Pro Gly Pro Thr Pro Asp Pro Ala Glu		
1300	1305	1310
Gly Ile Gly Asn Lys Asp Thr Leu Pro Ser Gly Thr Lys Tyr Glu Trp		
1315	1320	1325
Lys Asp Pro Val Asp Thr Thr Pro Gly Asp Lys Thr Gly Thr Ile		
1330	1335	1340
Val Val Ser Tyr Pro Asp Gly Ser Thr Asp Glu Ile Gln Val Thr Val		
1345	1350	1355
Lys Val Thr Asp Pro Thr Thr Pro Gly Gln Thr Asp Ala Asp Lys Tyr		
1365	1370	1375
Thr Pro Glu Ala Lys Asp Ile Thr Val Thr Leu Gly Gln Thr Pro Asp		
1380	1385	1390
Pro Ala Glu Gly Ile Gly Asn Lys Asp Thr Leu Pro Ser Gly Thr Lys		
1395	1400	1405
Tyr Glu Trp Lys Asp Pro Val Asp Thr Thr Thr Pro Gly Asp Lys Thr		
1410	1415	1420
Gly Thr Ile Val Val Ser Tyr Pro Asp Gly Ser Thr Asp Glu Ile Gln		
1425	1430	1435
Val Thr Val Lys Val Ala Glu Pro Thr Thr Pro Gly Pro Thr Asp Ala		
1445	1450	1455
Asp Lys His Thr Pro Glu Ala Lys Asp Val Thr Val Val Gln Gly Gln		
1460	1465	1470

Thr Pro Asp Pro Ala Glu Gly Ile Gly Asn Lys Asp Thr Leu Pro Pro
 1475 1480 1485
 Gly Thr Arg Tyr Ala Trp Lys Asp Pro Val Asp Thr Thr Thr Pro Gly
 1490 1495 1500
 Asp Lys Thr Gly Thr Ile Val Val Thr Tyr Pro Asp Gly Ser Thr Asp
 1505 1510 1515 1520
 Glu Val Ser Val Thr Leu His Val Thr Pro Ser Glu Ser Gly Thr Thr
 1525 1530 1535
 Asp Thr Ser Thr Thr Pro Pro Thr Asp Thr Ser Gly Ser Asp Thr Asp
 1540 1545 1550
 Thr Thr Ser Lys Gly Glu Thr Pro Ala Asp Thr Pro Pro Thr Asp Thr
 1555 1560 1565
 Ala Ser Asp Ser Thr Asp Thr Thr Pro Lys Asp Glu Asn Thr Asp Asn
 1570 1575 1580
 Thr Gly Gly Thr His Lys Ser Thr Asn Thr Asp Ser Ser Gln Ser Gly
 1585 1590 1595 1600
 Ala Thr Gly Asn Thr Ser Ser Gly Ala Asn Ala Ser Ser Asn Thr Glu
 1605 1610 1615
 Ile His Ala Ser Asp Val Thr Thr Asp Gln Tyr Thr Thr Val Asn Asp
 1620 1625 1630
 Asn Thr Ala Asp Met Asn Thr Leu Pro Gln Thr Gly Glu Thr Asp Arg
 1635 1640 1645
 Asn Val Gly Val Trp Gly Met Ile Ile Ala Ala Val Gly Ser Leu Phe
 1650 1655 1660
 Gly Leu Gly His Gly Lys Lys Arg Arg Lys Asp Glu
 1665 1670 1675

<210> 77

<211> 5772

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1634 - surface protein

<220>

<221> CDS

<222> (1)...(5772)

<400> 77

atg tta tcc aag aat aat ttc aaa gaa aga tta aga aag atg gaa ccg 48
 Met Leu Ser Lys Asn Asn Phe Lys Glu Arg Leu Arg Lys Met Glu Pro
 1 5 10 15
 aga aaa gaa cgg ttt tcc att cgt aag ttt tct att gga gca gct tca 96
 Arg Lys Glu Arg Phe Ser Ile Arg Lys Phe Ser Ile Gly Ala Ala Ser
 20 25 30
 gtt ttg att ggc ttc agc ttt atg agc atg gct gga aat caa aaa gtt 144
 Val Leu Ile Gly Phe Ser Phe Met Ser Met Ala Gly Asn Gln Lys Val
 35 40 45
 caa gct gct act gaa gag gag cct gta gta gcg act aaa aat act gag 192

Gln	Ala	Ala	Thr	Glu	Glu	Glu	Pro	Val	Val	Ala	Thr	Lys	Asn	Thr	Glu	
50						55					60					
caa	caa	tca	aag	act	gat	ggt	act	caa	agt	gct	gaa	gaa	caa	tca	agt	240
Gln	Gln	Ser	Lys	Thr	Asp	Gly	Thr	Gln	Ser	Ala	Glu	Glu	Gln	Ser	Ser	
65					70					75					80	
gca	gat	gca	ggt	aat	gct	caa	aat	aat	aaa	tca	gct	aag	gca	aat	gca	288
Ala	Asp	Ala	Gly	Asn	Ala	Gln	Asn	Asn	Lys	Ser	Ala	Lys	Ala	Asn	Ala	
				85				90						95		
act	aca	cca	agt	aat	caa	aat	gct	act	gat	agc	aaa	ctt	act	caa	tct	336
Thr	Thr	Pro	Ser	Asn	Gln	Asn	Ala	Thr	Asp	Ser	Lys	Leu	Thr	Gln	Ser	
			100					105					110			
tct	gct	caa	gat	tta	tca	aag	gat	aat	gtt	aat	tca	gac	tca	aag	aat	384
Ser	Ala	Gln	Asp	Leu	Ser	Lys	Asp	Asn	Val	Asn	Ser	Asp	Ser	Lys	Asn	
			115				120					125				
gca	tca	gat	tct	aca	agt	gaa	gta	aag	caa	aac	aat	caa	gca	att	caa	432
Ala	Ser	Asp	Ser	Thr	Ser	Glu	Val	Lys	Gln	Asn	Asn	Gln	Ala	Ile	Gln	
						135						140				
ccc	gaa	act	tct	aag	ccc	tca	aga	gaa	gtt	gag	aat	aat	gag	act	gct	480
Pro	Glu	Thr	Ser	Lys	Pro	Ser	Arg	Glu	Val	Glu	Asn	Asn	Glu	Thr	Ala	
145					150					155					160	
aag	aat	gct	tca	gct	agt	caa	acg	act	aat	aca	tta	aat	gtt	aat	aaa	528
Lys	Asn	Ala	Ser	Ala	Ser	Gln	Thr	Thr	Asn	Thr	Leu	Asn	Val	Asn	Lys	
					165				170					175		
gca	tca	gaa	act	caa	gct	aaa	tca	ggt	agt	gag	tca	gtt	acc	tct	cct	576
Ala	Ser	Glu	Thr	Gln	Ala	Lys	Ser	Gly	Ser	Glu	Ser	Val	Thr	Ser	Pro	
				180				185					190			
aat	aaa	ggt	cta	gtt	tct	gag	aat	aaa	gca	aaa	gta	gaa	gtt	aag	agt	624
Asn	Lys	Gly	Leu	Val	Ser	Glu	Asn	Lys	Ala	Lys	Val	Glu	Val	Lys	Ser	
			195				200					205				
agt	aca	caa	cct	aaa	gct	gca	atg	cta	tca	ttg	gtt	caa	gag	tca	aat	672
Ser	Thr	Gln	Pro	Lys	Ala	Ala	Met	Leu	Ser	Leu	Val	Gln	Glu	Ser	Asn	
			210			215					220					
cct	gct	act	caa	act	gaa	aca	gta	aca	gac	tac	tca	acg	ttt	ctt	aat	720
Pro	Ala	Thr	Gln	Thr	Glu	Thr	Val	Thr	Asp	Tyr	Ser	Thr	Phe	Leu	Asn	
225					230					235					240	
gct	ttg	cgt	aat	gct	aat	act	ggc	act	att	aat	tta	caa	aat	gat	att	768
Ala	Leu	Arg	Asn	Ala	Asn	Thr	Gly	Thr	Ile	Asn	Leu	Gln	Asn	Asp	Ile	
				245				250						255		
gac	ttt	agt	aat	gca	aat	tta	aag	cat	ggt	cct	aat	aat	gga	tta	tct	816
Asp	Phe	Ser	Asn	Ala	Asn	Leu	Lys	His	Gly	Pro	Asn	Asn	Gly	Leu	Ser	
			260					265					270			
gga	aag	tat	gaa	cgc	ctt	aat	aat	act	gga	att	gca	cgt	gct	ata	act	864
Gly	Lys	Tyr	Glu	Arg	Leu	Asn	Asn	Thr	Gly	Ile	Ala	Arg	Ala	Ile	Thr	

275	280	285	
att aat ggt aac ggc cac gag cta aag atg gga gac cgt tac att gaa			912
Ile Asn Gly Asn Gly His Glu Leu Lys Met Gly Asp Arg Tyr Ile Glu			
290	295	300	
ttt acc agt gct aat caa aaa aat act aat agt aat tgg gat att caa			960
Phe Thr Ser Ala Asn Gln Lys Asn Thr Asn Ser Asn Trp Asp Ile Gln			
305	310	315	320
tta aag gat ctt acc tta caa act acc agt gga tat gga cca ttc tgg			1008
Leu Lys Asp Leu Thr Leu Gln Thr Thr Ser Gly Tyr Gly Pro Phe Trp			
	325	330	335
ttt gat aat aca gca gat gaa gcg gct aaa aat act att act ttt aac			1056
Phe Asp Asn Thr Ala Asp Glu Ala Ala Lys Asn Thr Ile Thr Phe Asn			
	340	345	350
ggg gta act act act act gat tca cat gaa att atg tgg tat aac ggc			1104
Gly Val Thr Thr Thr Thr Asp Ser His Glu Ile Met Trp Tyr Asn Gly			
	355	360	365
ggg ggt gcc tca act act cat gtt aaa ttc gaa ggc aat aat act atc			1152
Gly Gly Ala Ser Thr Thr His Val Lys Phe Glu Gly Asn Asn Thr Ile			
	370	375	380
aac agt acg ctt aat ggt aat act gca gcc atc tat gct tat agt gtt			1200
Asn Ser Thr Leu Asn Gly Asn Thr Ala Ala Ile Tyr Ala Tyr Ser Val			
385	390	395	400
gaa gca gta aat gga aat aca acc ttt aac gta att gat agc tca cca			1248
Glu Ala Val Asn Gly Asn Thr Thr Phe Asn Val Ile Asp Ser Ser Pro			
	405	410	415
gat aat gca ggt gct aat aga tca gca att ttg att tca att gat gca			1296
Asp Asn Ala Gly Ala Asn Arg Ser Ala Ile Leu Ile Ser Ile Asp Ala			
	420	425	430
gct cat gcg ggt aaa gtc atc gtt gat aaa ggt gct aca tta act att			1344
Ala His Ala Gly Lys Val Ile Val Asp Lys Gly Ala Thr Leu Thr Ile			
	435	440	445
aat gga gat aat caa gtt aat gtt ccg aaa atg aat agt gct gat tct			1392
Asn Gly Asp Asn Gln Val Asn Val Pro Lys Met Asn Ser Ala Asp Ser			
	450	455	460
tat ggt acg atg gga att cgt ttc caa aac tgg gct aaa aca gat atc			1440
Tyr Gly Thr Met Gly Ile Arg Phe Gln Asn Trp Ala Lys Thr Asp Ile			
465	470	475	480
gat aaa gct aag acc agt gtt gtt caa gtt aac ggt aat tta aac ttg			1488
Asp Lys Ala Lys Thr Ser Val Val Gln Val Asn Gly Asn Leu Asn Leu			
	485	490	495
aat atg ggt aaa ggt ggt tca acc gct att tta ggt tct tat gtc gat			1536
Asn Met Gly Lys Gly Gly Ser Thr Ala Ile Leu Gly Ser Tyr Val Asp			
	500	505	510

gta caa cca gac ggt aat gtt act att aac acg caa caa aat ggt act	1584
Val Gln Pro Asp Gly Asn Val Thr Ile Asn Thr Gln Gln Asn Gly Thr	
515 520 525	
agc act gtt gct ggt gac ttg gct cta ggt cat aga ggt act cac ttt	1632
Ser Thr Val Ala Gly Asp Leu Ala Leu Gly His Arg Gly Thr His Phe	
530 535 540	
ggg gta att gct ggg ggt atc gaa gtt agt gat gat tat gct ggc ttg	1680
Gly Val Ile Ala Gly Gly Ile Glu Val Ser Asp Asp Tyr Ala Gly Leu	
545 550 555 560	
aga atc gct aat ggt ggt agt tta aag att gtt cgt cca acc gat gta	1728
Arg Ile Ala Asn Gly Gly Ser Leu Lys Ile Val Arg Pro Thr Asp Val	
565 570 575	
aac tct act cag ccc tta att tca tat ggt gat gca ggt tct tct ggt	1776
Asn Ser Thr Gln Pro Leu Ile Ser Tyr Gly Asp Ala Gly Ser Ser Gly	
580 585 590	
ggg aaa aca ttt aca gta aat gtt gaa aat ggt ggt act ctt gat tta	1824
Gly, Lys Thr Phe Thr Val Asn Val Glu Asn Gly Gly Thr Leu Asp Leu	
595 600 605	
caa gat ggt gct act gat cca caa act tgg agc ttt agt aat act agt	1872
Gln Asp Gly Ala Thr Asp Pro Gln Thr Trp Ser Phe Ser Asn Thr Ser	
610 615 620	
agc acg ggt aat act aat atg cca tgg gct ggt ttg att act atg tgg	1920
Ser Thr Gly Asn Thr Asn Met Pro Trp Ala Gly Leu Ile Thr Met Trp	
625 630 635 640	
gga acc agt ggt aca aat act att aaa att aat aat cct aag tat att	1968
Gly Thr Ser Gly Thr Asn Thr Ile Lys Ile Asn Asn Pro Lys Tyr Ile	
645 650 655	
aat ttg caa cgt acc ggc aac caa act gga tca tta atg cgc ctt gaa	2016
Asn Leu Gln Arg Thr Gly Asn Gln Thr Gly Ser Leu Met Arg Leu Glu	
660 665 670	
ggg act aca aat aat gtt tca att aat ggc gat att aat aat gtt att	2064
Gly Thr Thr Asn Asn Val Ser Ile Asn Gly Asp Ile Asn Asn Val Ile	
675 680 685	
acc cca tta gct caa tgg gat gaa ggt gca aag aat aat cct tca tac	2112
Thr Pro Leu Ala Gln Trp Asp Glu Gly Ala Lys Asn Asn Pro Ser Tyr	
690 695 700	
tac tgg tat att gag aat gaa gct aac cag aat aac tgg ggt aat tat	2160
Tyr Trp Tyr Ile Glu Asn Glu Ala Asn Gln Asn Asn Trp Gly Asn Tyr	
705 710 715 720	
gca aat cgc ttt gta caa agt gga aag aat cct cag ccc gct gca aat	2208
Ala Asn Arg Phe Val Gln Ser Gly Lys Asn Pro Gln Pro Ala Ala Asn	
725 730 735	

gcc gga gtt act aca ttt atg cat tca agc ggt agt gta cag atg gct	2256
Ala Gly Val Thr Thr Phe Met His Ser Ser Gly Ser Val Gln Met Ala	
740 745 750	
cct aac cag gca gga act aat tca tcc aag ttt agc aat gga gaa gtt	2304
Pro Asn Gln Ala Gly Thr Asn Ser Ser Lys Phe Ser Asn Gly Glu Val	
755 760 765	
gcc caa act cta aat gaa gct ata aat tat caa gct cca tat ttg aat	2352
Ala Gln Thr Leu Asn Glu Ala Ile Asn Tyr Gln Ala Pro Tyr Leu Asn	
770 775 780	
caa ttc ttg aat cac ttt agt tgg tgg gca cca caa aga att gcc atg	2400
Gln Phe Leu Asn His Phe Ser Trp Trp Ala Pro Gln Arg Ile Ala Met	
785 790 795 800	
gga agc ggc tta gag gat gta gta aaa cca act gat gct gaa aag tat	2448
Gly Ser Gly Leu Glu Asp Val Val Lys Pro Thr Asp Ala Glu Lys Tyr	
805 810 815	
caa cca gaa gtt aaa act att aat ggt aat act aaa caa act tta aag	2496
Gln Pro Glu Val Lys Thr Ile Asn Gly Asn Thr Lys Gln Thr Leu Lys	
820 825 830	
gac tta act gct aaa gat ggt att aaa ggc ttg ctt tct agt gat ggt	2544
Asp Leu Thr Ala Lys Asp Gly Ile Lys Gly Leu Leu Ser Ser Asp Gly	
835 840 845	
acc gag aca act gat ctt tct tct gtt aag agc gta agc tgg tat gat	2592
Thr Glu Thr Thr Asp Leu Ser Ser Val Lys Ser Val Ser Trp Tyr Asp	
850 855 860	
aca gct act gat gcc act ggt tgg aag agc tta atg gga gat gaa aca	2640
Thr Ala Thr Asp Ala Thr Gly Trp Lys Ser Leu Met Gly Asp Glu Thr	
865 870 875 880	
gag cca act aat cca act ggt gat tta aag acc act gat aaa tca gct	2688
Glu Pro Thr Asn Pro Thr Gly Asp Leu Lys Thr Thr Asp Lys Ser Ala	
885 890 895	
tgg gca aaa gta act tat caa gat gga tgg att gac ttt gca aat atc	2736
Trp Ala Lys Val Thr Tyr Gln Asp Gly Ser Ile Asp Phe Ala Asn Ile	
900 905 910	
cca ttg aat att act gaa cca aca gca aat ctt tac act cca tca tat	2784
Pro Leu Asn Ile Thr Glu Pro Thr Ala Asn Leu Tyr Thr Pro Ser Tyr	
915 920 925	
aag cca gta act gtt gaa caa ggc caa tct gct act gat gat cca gca	2832
Lys Pro Val Thr Val Glu Gln Gly Gln Ser Ala Thr Asp Asp Pro Ala	
930 935 940	
ttt act gat caa gct ggt aag gat gct act gct cca act gga act aca	2880
Phe Thr Asp Gln Ala Gly Lys Asp Ala Thr Ala Pro Thr Gly Thr Thr	
945 950 955 960	
ttt act aca ggt act gat acg cca gat tgg gca acc att aat tca tca	2928

Phe Thr Thr Gly Thr Asp Thr Pro Asp Trp Ala Thr Ile Asn Ser Ser	
965 970 975	
act ggt act gta act gtt aaa cca ggt gcc aat gta act gta ggt gct	2976
Thr Gly Thr Val Thr Val Lys Pro Gly Ala Asn Val Thr Val Gly Ala	
980 985 990	
tac aat gtt cca gta act gta act tac cca gac aag agt act gat gag	3024
Tyr Asn Val Pro Val Thr Val Thr Tyr Pro Asp Lys Ser Thr Asp Glu	
995 1000 1005	
act act gtt cca gta att gtc act aag gct ggc caa aca gta act tgg	3072
Thr Thr Val Pro Val Ile Val Thr Lys Ala Gly Gln Thr Val Thr Trp	
1010 1015 1020	
ggt gat aag ggt gca gtt gta act agc gtt gat act tct aaa ctt aac	3120
Gly Asp Lys Gly Ala Val Thr Ser Val Thr Ser Lys Leu Asn	
1025 1030 1035 1040	
gct cat gaa act act gaa aat tca caa gtt ctt tct gct ggt ggc gtt	3168
Ala His Glu Thr Thr Glu Asn Ser Gln Val Leu Ser Ala Gly Gly Val	
1045 1050 1055	
gta act gca gaa ggt tac gaa tta aca gat ggt aaa ctt tca act aca	3216
Val Thr Ala Glu Gly Tyr Glu Leu Thr Asp Gly Lys Leu Ser Thr Thr	
1060 1065 1070	
gct act cca att acg att gac cca tca act gta agt tgg act aca acg	3264
Ala Thr Pro Ile Thr Ile Asp Pro Ser Thr Val Ser Trp Thr Thr	
1075 1080 1085	
cca gat act aac gtt gat acc gca act gca act ggt aag aaa att gaa	3312
Pro Asp Thr Asn Val Asp Thr Ala Thr Ala Thr Gly Lys Lys Ile Glu	
1090 1095 1100	
aac agc act att aag att gac ttc act aac aat gat gca gct aag aat	3360
Asn Ser Thr Ile Lys Ile Asp Phe Thr Asn Asn Asp Ala Ala Lys Asn	
1105 1110 1115 1120	
agc cta ggc tca aag aat ggt gtt gta act act aat cca ttt acc att	3408
Ser Leu Gly Ser Lys Asn Gly Val Val Thr Thr Asn Pro Phe Thr Ile	
1125 1130 1135	
gat gct aaa ggt gct ggt gct aag gct gta act gct cca gtt gat att	3456
Asp Ala Lys Gly Ala Gly Ala Lys Ala Val Thr Ala Pro Val Asp Ile	
1140 1145 1150	
aaa ctt ggc tca gat tta aat agt gaa caa ttt gat caa tta gta gat	3504
Lys Leu Gly Ser Asp Leu Asn Ser Glu Gln Phe Asp Gln Leu Val Asp	
1155 1160 1165	
aac aac atc cca att gat gag att gca tct acc act tgg gca acc atg	3552
Asn Asn Ile Pro Ile Asp Glu Ile Ala Ser Thr Thr Trp Ala Thr Met	
1170 1175 1180	
cct aat gaa aaa ggt caa ggc gga gta atc aag att acc ttt act gat	3600
Pro Asn Glu Lys Gly Gln Gly Gly Val Ile Lys Ile Thr Phe Thr Asp	

1185	1190	1195	1200	
aag gat gct aat ggt aat cca act tac ttg aac att aat att cca gca				3648
Lys Asp Ala Asn Gly Asn Pro Thr Tyr Leu Asn Ile Asn Ile Pro Ala				
1205		1210	1215	
agt tca atc aag gta act act gat gca gaa acc aat acc cca caa ggt				3696
Ser Ser Ile Lys Val Thr Thr Asp Ala Glu Thr Asn Thr Pro Gln Gly				
1220		1225	1230	
caa aac gtt tca act aag gtc ggc gaa gtt cca gat cca gca gaa ggc				3744
Gln Asn Val Ser Thr Lys Val Gly Glu Val Pro Asp Pro Ala Glu Gly				
1235		1240	1245	
atc agg aac aag agc gac tta cca gat gaa act aag tac act tgg caa				3792
Ile Arg Asn Lys Ser Asp Leu Pro Asp Glu Thr Lys Tyr Thr Trp Gln				
1250		1255	1260	
gac act cca gat acc act aaa cca ggt aag aaa cca gca gtt gtt gtc				3840
Asp Thr Pro Asp Thr Thr Lys Pro Gly Lys Lys Pro Ala Val Val Val				
1265		1270	1275	1280
gta act tat cca gat ggc tca aaa gat aca gtt tca act aat gta att				3888
Val Thr Tyr Pro Asp Gly Ser Lys Asp Thr Val Ser Thr Asn Val Ile				
1285		1290	1295	
gtt gat gct aag cca gag att aag acg att act aca act gtt ggt gga				3936
Val Asp Ala Lys Pro Glu Ile Lys Thr Ile Thr Thr Thr Val Gly Gly				
1300		1305	1310	
gat cca gtt gct act gaa ggt att gct aac ttg aat aat ggt ggt aat				3984
Asp Pro Val Ala Thr Glu Gly Ile Ala Asn Leu Asn Asn Gly Gly Asn				
1315		1320	1325	
act cca gtt gat ggt tat cca aca agt gca act tgg act act aaa cca				4032
Thr Pro Val Asp Gly Tyr Pro Thr Ser Ala Thr Trp Thr Thr Lys Pro				
1330		1335	1340	
gat act tca aag tca ggt aca act act ggc act gcg act gtt aca tat				4080
Asp Thr Ser Lys Ser Gly Thr Thr Thr Gly Thr Ala Thr Val Thr Tyr				
1345		1350	1355	1360
cca gat ggt act aag gaa act gta act att ccg gta acc gtg aat aag				4128
Pro Asp Gly Thr Lys Glu Thr Val Thr Ile Pro Val Thr Val Asn Lys				
1365		1370	1375	
agt agt caa gta aca atg act tat gac ttc tac tca acg gtt act atc				4176
Ser Ser Gln Val Thr Met Thr Tyr Asp Phe Tyr Ser Thr Val Thr Ile				
1380		1385	1390	
gat aac cca gat ggc aca tca aca act gag cca agg cag cac ata agt				4224
Asp Asn Pro Asp Gly Thr Ser Thr Thr Glu Pro Arg Gln His Ile Ser				
1395		1400	1405	
ttt act tat ctg ggt att cca act gat gca gat gta aat gtt gaa ttt				4272
Phe Thr Tyr Leu Gly Ile Pro Thr Asp Ala Asp Val Asn Val Glu Phe				
1410		1415	1420	

- 212 -

cca aca aca cca acc act cca act act cca act act cca act gat gcc	4992
Pro Thr Thr Pro Thr Thr Pro Thr Thr Pro Thr Thr Pro Thr Asp Ala	
1650 1655 1660	
gat aag tat act cca gaa ggt caa gat gtg aac acc aag acc ggc gtt	5040
Asp Lys Tyr Thr Pro Glu Gly Gln Asp Val Asn Thr Lys Thr Gly Val	
1665 1670 1675 1680	
gta cca gat cca gca gaa ggc atc aag aac aag ggt gac tta cca aat	5088
Val Pro Asp Pro Ala Glu Gly Ile Lys Asn Lys Gly Asp Leu Pro Asn	
1685 1690 1695	
ggg aca act tat act tgg aaa gct acc cca gat gta act act cca ggt	5136
Gly Thr Thr Tyr Thr Trp Lys Ala Thr Pro Asp Val Thr Thr Pro Gly	
1700 1705 1710	
gac aag cca gta aca gtt gtt gta act tac cca gac ggc tca aaa gat	5184
Asp Lys Pro Val Thr Val Val Thr Tyr Pro Asp Gly Ser Lys Asp	
1715 1720 1725	
gaa gtt cca att aca att cac gtg att gac aat act cca aat caa cca	5232
Glu Val Pro Ile Thr Ile His Val Ile Asp Asn Thr Pro Asn Gln Pro	
1730 1735 1740	
tca tct aag gat gac aac aat act cct aaa aag agt gat gct gat aag	5280
Ser Ser Lys Asp Asp Asn Asn Thr Pro Lys Lys Ser Asp Ala Asp Lys	
1745 1750 1755 1760	
aat act cca aag ggt aaa gac att act gta aaa caa ggt gaa aca cca	5328
Asn Thr Pro Lys Gly Lys Asp Ile Thr Val Lys Gln Gly Glu Thr Pro	
1765 1770 1775	
aat cca gcc gac ggc att aag aac aaa ggt gat tta cca agt ggt acc	5376
Asn Pro Ala Asp Gly Ile Lys Asn Lys Gly Asp Leu Pro Ser Gly Thr	
1780 1785 1790	
aag tat act tgg aag aat act ccg gat act tca act cca ggt aga aga	5424
Lys Tyr Thr Trp Lys Asn Thr Pro Asp Thr Ser Thr Pro Gly Arg Arg	
1795 1800 1805	
act gca aca ata gtt gta act tac cca gat ggt tca caa gat gag gta	5472
Thr Ala Thr Ile Val Val Thr Tyr Pro Asp Gly Ser Gln Asp Glu Val	
1810 1815 1820	
aca atc aac ata aat gtt atg gct gaa aat agt gct aat aat aac agt	5520
Thr Ile Asn Ile Asn Val Met Ala Glu Asn Ser Ala Asn Asn Asn Ser	
1825 1830 1835 1840	
aat act aat gtt cat gat gat gtt gcc aag caa aat aat gca cca caa	5568
Asn Thr Asn Val His Asp Asp Val Ala Lys Gln Asn Asn Ala Pro Gln	
1845 1850 1855	
gct caa gat atg acc gtg cct tca atc aat agt gct act aat ggc act	5616
Ala Gln Asp Met Thr Val Pro Ser Ile Asn Ser Ala Thr Asn Gly Thr	
1860 1865 1870	
aac gta aag gca caa aca ggt gca caa gta tct cat aaa aat tca ctt	5664

```

Asn Val Lys Ala Gln Thr Gly Ala Gln Val Ser His Lys Asn Ser Leu
1875                      1880                      1885

cca caa act gga tca aat gat aat aaa gct ggt atc ttt ggt tta gct 5712
Pro Gln Thr Gly Ser Asn Asp Asn Lys Ala Gly Ile Phe Gly Leu Ala
1890                      1895                      1900

atc gca act gta ggc agt ttg ttt gga ctt gcc ttt ggt aaa aaa cgt 5760
Ile Ala Thr Val Gly Ser Leu Phe Gly Leu Ala Phe Gly Lys Lys Arg
1905                      1910                      1915                      1920

aag gaa gat gaa 5772
Lys Glu Asp Glu

```

<210> 78
 <211> 1924
 <212> PRT
 <213> Lactobacillus acidophilus

```

<400> 78
Met Leu Ser Lys Asn Asn Phe Lys Glu Arg Leu Arg Lys Met Glu Pro
1      5      10      15
Arg Lys Glu Arg Phe Ser Ile Arg Lys Phe Ser Ile Gly Ala Ala Ser
20     25     30
Val Leu Ile Gly Phe Ser Phe Met Ser Met Ala Gly Asn Gln Lys Val
35     40     45
Gln Ala Ala Thr Glu Glu Glu Pro Val Val Ala Thr Lys Asn Thr Glu
50     55     60
Gln Gln Ser Lys Thr Asp Gly Thr Gln Ser Ala Glu Glu Gln Ser Ser
65     70     75     80
Ala Asp Ala Gly Asn Ala Gln Asn Asn Lys Ser Ala Lys Ala Asn Ala
85     90     95
Thr Thr Pro Ser Asn Gln Asn Ala Thr Asp Ser Lys Leu Thr Gln Ser
100    105    110
Ser Ala Gln Asp Leu Ser Lys Asp Asn Val Asn Ser Asp Ser Lys Asn
115    120    125
Ala Ser Asp Ser Thr Ser Glu Val Lys Gln Asn Asn Gln Ala Ile Gln
130    135    140
Pro Glu Thr Ser Lys Pro Ser Arg Glu Val Glu Asn Asn Glu Thr Ala
145    150    155    160
Lys Asn Ala Ser Ala Ser Gln Thr Thr Asn Thr Leu Asn Val Asn Lys
165    170    175
Ala Ser Glu Thr Gln Ala Lys Ser Gly Ser Glu Ser Val Thr Ser Pro
180    185    190
Asn Lys Gly Leu Val Ser Glu Asn Lys Ala Lys Val Glu Val Lys Ser
195    200    205
Ser Thr Gln Pro Lys Ala Ala Met Leu Ser Leu Val Gln Glu Ser Asn
210    215    220
Pro Ala Thr Gln Thr Glu Thr Val Thr Asp Tyr Ser Thr Phe Leu Asn
225    230    235    240
Ala Leu Arg Asn Ala Asn Thr Gly Thr Ile Asn Leu Gln Asn Asp Ile
245    250    255
Asp Phe Ser Asn Ala Asn Leu Lys His Gly Pro Asn Asn Gly Leu Ser
260    265    270
Gly Lys Tyr Glu Arg Leu Asn Asn Thr Gly Ile Ala Arg Ala Ile Thr

```

- 215 -

Ala Gly Val Thr Thr Phe Met His Ser Ser Gly Ser Val Gln Met Ala
 740 745 750
 Pro Asn Gln Ala Gly Thr Asn Ser Ser Lys Phe Ser Asn Gly Glu Val
 755 760 765
 Ala Gln Thr Leu Asn Glu Ala Ile Asn Tyr Gln Ala Pro Tyr Leu Asn
 770 775 780
 Gln Phe Leu Asn His Phe Ser Trp Trp Ala Pro Gln Arg Ile Ala Met
 785 790 795 800
 Gly Ser Gly Leu Glu Asp Val Val Lys Pro Thr Asp Ala Glu Lys Tyr
 805 810 815
 Gln Pro Glu Val Lys Thr Ile Asn Gly Asn Thr Lys Gln Thr Leu Lys
 820 825 830
 Asp Leu Thr Ala Lys Asp Gly Ile Lys Gly Leu Leu Ser Ser Asp Gly
 835 840 845
 Thr Glu Thr Thr Asp Leu Ser Ser Val Lys Ser Val Ser Trp Tyr Asp
 850 855 860
 Thr Ala Thr Asp Ala Thr Gly Trp Lys Ser Leu Met Gly Asp Glu Thr
 865 870 875 880
 Glu Pro Thr Asn Pro Thr Gly Asp Leu Lys Thr Thr Asp Lys Ser Ala
 885 890 895
 Trp Ala Lys Val Thr Tyr Gln Asp Gly Ser Ile Asp Phe Ala Asn Ile
 900 905 910
 Pro Leu Asn Ile Thr Glu Pro Thr Ala Asn Leu Tyr Thr Pro Ser Tyr
 915 920 925
 Lys Pro Val Thr Val Glu Gln Gly Gln Ser Ala Thr Asp Asp Pro Ala
 930 935 940
 Phe Thr Asp Gln Ala Gly Lys Asp Ala Thr Ala Pro Thr Gly Thr Thr
 945 950 955 960
 Phe Thr Thr Gly Thr Asp Thr Pro Asp Trp Ala Thr Ile Asn Ser Ser
 965 970 975
 Thr Gly Thr Val Thr Val Lys Pro Gly Ala Asn Val Thr Val Gly Ala
 980 985 990
 Tyr Asn Val Pro Val Thr Val Thr Tyr Pro Asp Lys Ser Thr Asp Glu
 995 1000 1005
 Thr Thr Val Pro Val Ile Val Thr Lys Ala Gly Gln Thr Val Thr Trp
 1010 1015 1020
 Gly Asp Lys Gly Ala Val Val Thr Ser Val Asp Thr Ser Lys Leu Asn
 1025 1030 1035 1040
 Ala His Glu Thr Thr Glu Asn Ser Gln Val Leu Ser Ala Gly Gly Val
 1045 1050 1055
 Val Thr Ala Glu Gly Tyr Glu Leu Thr Asp Gly Lys Leu Ser Thr Thr
 1060 1065 1070
 Ala Thr Pro Ile Thr Ile Asp Pro Ser Thr Val Ser Trp Thr Thr Thr
 1075 1080 1085
 Pro Asp Thr Asn Val Asp Thr Ala Thr Ala Thr Gly Lys Lys Ile Glu
 1090 1095 1100
 Asn Ser Thr Ile Lys Ile Asp Phe Thr Asn Asn Asp Ala Ala Lys Asn
 1105 1110 1115 1120
 Ser Leu Gly Ser Lys Asn Gly Val Val Thr Thr Asn Pro Phe Thr Ile
 1125 1130 1135
 Asp Ala Lys Gly Ala Gly Ala Lys Ala Val Thr Ala Pro Val Asp Ile
 1140 1145 1150
 Lys Leu Gly Ser Asp Leu Asn Ser Glu Gln Phe Asp Gln Leu Val Asp
 1155 1160 1165
 Asn Asn Ile Pro Ile Asp Glu Ile Ala Ser Thr Thr Trp Ala Thr Met
 1170 1175 1180
 Pro Asn Glu Lys Gly Gln Gly Gly Val Ile Lys Ile Thr Phe Thr Asp

1185		1190		1195		1200
Lys Asp Ala Asn Gly Asn Pro Thr Tyr Leu Asn Ile Asn Ile Pro Ala						
	1205			1210		1215
Ser Ser Ile Lys Val Thr Thr Asp Ala Glu Thr Asn Thr Pro Gln Gly						
	1220			1225		1230
Gln Asn Val Ser Thr Lys Val Gly Glu Val Pro Asp Pro Ala Glu Gly						
	1235			1240		1245
Ile Arg Asn Lys Ser Asp Leu Pro Asp Glu Thr Lys Tyr Thr Trp Gln						
	1250			1255		1260
Asp Thr Pro Asp Thr Thr Lys Pro Gly Lys Lys Pro Ala Val Val Val						
	1265			1270		1275
Val Thr Tyr Pro Asp Gly Ser Lys Asp Thr Val Ser Thr Asn Val Ile						
	1285			1290		1295
Val Asp Ala Lys Pro Glu Ile Lys Thr Ile Thr Thr Thr Val Gly Gly						
	1300			1305		1310
Asp Pro Val Ala Thr Glu Gly Ile Ala Asn Leu Asn Asn Gly Gly Asn						
	1315			1320		1325
Thr Pro Val Asp Gly Tyr Pro Thr Ser Ala Thr Trp Thr Thr Lys Pro						
	1330			1335		1340
Asp Thr Ser Lys Ser Gly Thr Thr Thr Gly Thr Ala Thr Val Thr Tyr						
	1345			1350		1355
Pro Asp Gly Thr Lys Glu Thr Val Thr Ile Pro Val Thr Val Asn Lys						
	1365			1370		1375
Ser Ser Gln Val Thr Met Thr Tyr Asp Phe Tyr Ser Thr Val Thr Ile						
	1380			1385		1390
Asp Asn Pro Asp Gly Thr Ser Thr Thr Glu Pro Arg Gln His Ile Ser						
	1395			1400		1405
Phe Thr Tyr Leu Gly Ile Pro Thr Asp Ala Asp Val Asn Val Glu Phe						
	1410			1415		1420
Lys Asn Val Ala Ile Pro Ser Phe Asp Gly Tyr Thr Pro Glu Val Ser						
	1425			1430		1435
Leu Thr Thr Pro Ser Ala Glu Gly Thr Pro Met Ala Thr Leu Glu Lys						
	1445			1450		1455
Gly Val Asp Gly Lys Trp Thr Leu Lys Leu Pro Lys Pro Glu Leu Ser						
	1460			1465		1470
Tyr Pro Tyr Tyr Asn Tyr Thr Ile Ser Tyr Lys Lys Ser Gly Ser Glu						
	1475			1480		1485
Thr Pro Thr Asp Ala Asp Lys Tyr Thr Pro Glu Gly Gln Asp Val Asn						
	1490			1495		1500
Thr Lys Thr Gly Val Val Pro Asp Pro Ala Glu Gly Ile Lys Asn Lys						
	1505			1510		1515
Ser Asp Leu Pro Glu Gly Thr Lys Tyr Thr Trp Lys Asp Thr Pro Asp						
	1525			1530		1535
Val Thr Thr Ser Gly Asn Lys Pro Ala Thr Val Val Val Thr Tyr Pro						
	1540			1545		1550
Asp Asp Ser Lys Asp Glu Val Pro Val Thr Ile His Val Thr Asn Pro						
	1555			1560		1565
Thr Thr Pro Thr Asp Ala Asp Lys Tyr Thr Pro Glu Gly Gln Asp Val						
	1570			1575		1580
Asn Thr Lys Thr Gly Val Val Pro Asp Pro Ala Glu Gly Ile Lys Asn						
	1585			1590		1595
Lys Gly Asp Leu Pro Asp Gly Thr Lys Tyr Thr Trp Gln Asp Thr Pro						
	1605			1610		1615
Asp Val Thr Thr Ser Gly Asp Lys Pro Val Thr Val Val Val Thr Tyr						
	1620			1625		1630
Pro Asp Gly Ser Lys Asp Glu Val Ser Val Thr Ile His Val Thr Asn						
	1635			1640		1645

Pro Thr Thr Pro Thr Thr Pro Thr Thr Pro Thr Thr Pro Thr Asp Ala
 1650 1655 1660
 Asp Lys Tyr Thr Pro Glu Gly Gln Asp Val Asn Thr Lys Thr Gly Val
 1665 1670 1675 1680
 Val Pro Asp Pro Ala Glu Gly Ile Lys Asn Lys Gly Asp Leu Pro Asn
 1685 1690 1695
 Gly Thr Thr Tyr Thr Trp Lys Ala Thr Pro Asp Val Thr Thr Pro Gly
 1700 1705 1710
 Asp Lys Pro Val Thr Val Val Val Thr Tyr Pro Asp Gly Ser Lys Asp
 1715 1720 1725
 Glu Val Pro Ile Thr Ile His Val Ile Asp Asn Thr Pro Asn Gln Pro
 1730 1735 1740
 Ser Ser Lys Asp Asp Asn Asn Thr Pro Lys Lys Ser Asp Ala Asp Lys
 1745 1750 1755 1760
 Asn Thr Pro Lys Gly Lys Asp Ile Thr Val Lys Gln Gly Glu Thr Pro
 1765 1770 1775
 Asn Pro Ala Asp Gly Ile Lys Asn Lys Gly Asp Leu Pro Ser Gly Thr
 1780 1785 1790
 Lys Tyr Thr Trp Lys Asn Thr Pro Asp Thr Ser Thr Pro Gly Arg Arg
 1795 1800 1805
 Thr Ala Thr Ile Val Val Thr Tyr Pro Asp Gly Ser Gln Asp Glu Val
 1810 1815 1820
 Thr Ile Asn Ile Asn Val Met Ala Glu Asn Ser Ala Asn Asn Asn Ser
 1825 1830 1835 1840
 Asn Thr Asn Val His Asp Asp Val Ala Lys Gln Asn Asn Ala Pro Gln
 1845 1850 1855
 Ala Gln Asp Met Thr Val Pro Ser Ile Asn Ser Ala Thr Asn Gly Thr
 1860 1865 1870
 Asn Val Lys Ala Gln Thr Gly Ala Gln Val Ser His Lys Asn Ser Leu
 1875 1880 1885
 Pro Gln Thr Gly Ser Asn Asp Asn Lys Ala Gly Ile Phe Gly Leu Ala
 1890 1895 1900
 Ile Ala Thr Val Gly Ser Leu Phe Gly Leu Ala Phe Gly Lys Lys Arg
 1905 1910 1915 1920
 Lys Glu Asp Glu

<210> 79
 <211> 1059
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1568 - surface protein

<220>
 <221> CDS
 <222> (1)...(1059)

<400> 79
 ttg ttt tcg gag att ttt att tta att tta gca ctt atg aaa gtg tta 48
 Met Phe Ser Glu Ile Phe Ile Leu Ile Leu Ala Leu Met Lys Val Leu
 1 5 10 15

aaa tca act tgt agg ttt cat tat aag gag aat att atg aag aat aaa	96
Lys Ser Thr Cys Arg Phe His Tyr Lys Glu Asn Ile Met Lys Asn Lys	
20 25 30	
aaa tta gta gct att gca gcg aca ctt tta atc agc gct tct cca gta	144
Lys Leu Val Ala Ile Ala Ala Thr Leu Leu Ile Ser Ala Ser Pro Val	
35 40 45	
gtt gca ctg att aat caa cca atc cat cca gtt caa gcc gtt aat caa	192
Val Ala Leu Ile Asn Gln Pro Ile His Pro Val Gln Ala Val Asn Gln	
50 55 60	
aca cta aaa gat aaa atc aaa tta aaa aag act ttt aac aac act att	240
Thr Leu Lys Asp Lys Ile Lys Leu Lys Lys Thr Phe Asn Asn Thr Ile	
65 70 75 80	
caa gtt ttc aac agc aaa ggt aac gct tct aca act acc aag act att	288
Gln Val Phe Asn Ser Lys Gly Asn Ala Ser Thr Thr Thr Lys Thr Ile	
85 90 95	
aat ggt aaa aag atg acc gaa gcc tca aca gtt aaa gct ggt caa act	336
Asn Gly Lys Lys Met Thr Glu Ala Ser Thr Val Lys Ala Gly Gln Thr	
100 105 110	
ttt aaa tat tat ggc agt cca gta ctg atc caa ggt aaa aag ata act	384
Phe Lys Tyr Tyr Gly Ser Pro Val Leu Ile Gln Gly Lys Lys Ile Thr	
115 120 125	
gat agt acc aat aag aat tat cac tac gca acc gct tct tat atc aat	432
Asp Ser Thr Asn Lys Asn Tyr His Tyr Ala Thr Ala Ser Tyr Ile Asn	
130 135 140	
att ggt aaa aaa cgt tat att aaa tca ata aat gtt agt tca atg gat	480
Ile Gly Lys Lys Arg Tyr Ile Lys Ser Ile Asn Val Ser Ser Met Asp	
145 150 155 160	
gga caa aat gtc tta gtc tta agt gct aat tca cgt atc tat gat aaa	528
Gly Gln Asn Val Leu Val Leu Ser Ala Asn Ser Arg Ile Tyr Asp Lys	
165 170 175	
aat gga cat cgt act acc ttt aac ggg ctt aca tta att cca aaa tat	576
Asn Gly His Arg Thr Thr Phe Asn Gly Leu Thr Leu Ile Pro Lys Tyr	
180 185 190	
atg tta ctt aag aca cct gat aaa aca cat gtg aca acc aaa aat gat	624
Met Leu Leu Lys Thr Pro Asp Lys Thr His Val Thr Thr Lys Asn Asp	
195 200 205	
atg ttt tac tat ttt tca aat ctt aat ggt tct aaa aaa aga agc tta	672
Met Phe Tyr Tyr Phe Ser Asn Leu Asn Gly Ser Lys Lys Arg Ser Leu	
210 215 220	
aat aca aca act att aat ggc aaa ttg tat tat tca tta ggt aag gat	720
Asn Thr Thr Thr Ile Asn Gly Lys Leu Tyr Tyr Ser Leu Gly Lys Asp	
225 230 235 240	

```

gct tat att aga gct tca aat gtt ggc tac atc aat ggt aat act gta 768
Ala Tyr Ile Arg Ala Ser Asn Val Gly Tyr Ile Asn Gly Asn Thr Val
245 250 255

tat caa gcc tct ggt aca act act gcc act att ttg aat aag att cac 816
Tyr Gln Ala Ser Gly Thr Thr Thr Ala Thr Ile Leu Asn Lys Ile His
260 265 270

gtt ttg gat aat aaa tta aaa aca act aac aag gcc tta aaa gtt ggt 864
Val Leu Asp Asn Lys Leu Lys Thr Thr Asn Lys Ala Leu Lys Val Gly
275 280 285

aaa aag gtt aag gtt gat gca aca aaa gtt act gga caa ggc gat agt 912
Lys Lys Val Lys Val Asp Ala Thr Lys Val Thr Gly Gln Gly Asp Ser
290 295 300

gct gcc ctt tac ttt aga att gct ggt act aaa ggt aac aat gct caa 960
Ala Ala Leu Tyr Phe Arg Ile Ala Gly Thr Lys Gly Asn Asn Ala Gln
305 310 315 320

tat atc tat tgg ggc gac tat tcc gaa tat ggt atg gat cag gag agt 1008
Tyr Ile Tyr Trp Gly Asp Tyr Ser Glu Tyr Gly Met Asp Gln Glu Ser
325 330 335

act acc gat gaa ttt caa ggt aac ttc aac tta gca aat cat tta gca 1056
Thr Thr Asp Glu Phe Gln Gly Asn Phe Asn Leu Ala Asn His Leu Ala
340 345 350

aat 1059
Asn

```

<210> 80

<211> 353

<212> PRT

<213> Lactobacillus acidophilus

<400> 80

```

Met Phe Ser Glu Ile Phe Ile Leu Ile Leu Ala Leu Met Lys Val Leu
1 5 10 15
Lys Ser Thr Cys Arg Phe His Tyr Lys Glu Asn Ile Met Lys Asn Lys
20 25 30
Lys Leu Val Ala Ile Ala Ala Thr Leu Leu Ile Ser Ala Ser Pro Val
35 40 45
Val Ala Leu Ile Asn Gln Pro Ile His Pro Val Gln Ala Val Asn Gln
50 55 60
Thr Leu Lys Asp Lys Ile Lys Leu Lys Lys Thr Phe Asn Asn Thr Ile
65 70 75 80
Gln Val Phe Asn Ser Lys Gly Asn Ala Ser Thr Thr Thr Lys Thr Ile
85 90 95
Asn Gly Lys Lys Met Thr Glu Ala Ser Thr Val Lys Ala Gly Gln Thr
100 105 110
Phe Lys Tyr Tyr Gly Ser Pro Val Leu Ile Gln Gly Lys Lys Ile Thr
115 120 125
Asp Ser Thr Asn Lys Asn Tyr His Tyr Ala Thr Ala Ser Tyr Ile Asn
130 135 140

```

Ile Gly Lys Lys Arg Tyr Ile Lys Ser Ile Asn Val Ser Ser Met Asp
 145 150 155 160
 Gly Gln Asn Val Leu Val Leu Ser Ala Asn Ser Arg Ile Tyr Asp Lys
 165 170 175
 Asn Gly His Arg Thr Thr Phe Asn Gly Leu Thr Leu Ile Pro Lys Tyr
 180 185 190
 Met Leu Leu Lys Thr Pro Asp Lys Thr His Val Thr Thr Lys Asn Asp
 195 200 205
 Met Phe Tyr Tyr Phe Ser Asn Leu Asn Gly Ser Lys Lys Arg Ser Leu
 210 215 220
 Asn Thr Thr Thr Ile Asn Gly Lys Leu Tyr Tyr Ser Leu Gly Lys Asp
 225 230 235 240
 Ala Tyr Ile Arg Ala Ser Asn Val Gly Tyr Ile Asn Gly Asn Thr Val
 245 250 255
 Tyr Gln Ala Ser Gly Thr Thr Thr Ala Thr Ile Leu Asn Lys Ile His
 260 265 270
 Val Leu Asp Asn Lys Leu Lys Thr Thr Asn Lys Ala Leu Lys Val Gly
 275 280 285
 Lys Lys Val Lys Val Asp Ala Thr Lys Val Thr Gly Gln Gly Asp Ser
 290 295 300
 Ala Ala Leu Tyr Phe Arg Ile Ala Gly Thr Lys Gly Asn Asn Ala Gln
 305 310 315 320
 Tyr Ile Tyr Trp Gly Asp Tyr Ser Glu Tyr Gly Met Asp Gln Glu Ser
 325 330 335
 Thr Thr Asp Glu Phe Gln Gly Asn Phe Asn Leu Ala Asn His Leu Ala
 340 345 350
 Asn

<210> 81

<211> 1092

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 177 - autolysin; amidase

<220>

<221> CDS

<222> (1)...(1092)

<400> 81

gtg aag tta agg aag aag tta ata acc tta att gcg gca ata agt tta 48

Met Lys Leu Arg Lys Lys Leu Ile Thr Leu Ile Ala Ala Ile Ser Leu

1

5

10

15

aca ggt gtt gcg aca aat aca ggc gtt aac att gtt caa gcc gac tca 96

Thr Gly Val Ala Thr Asn Thr Gly Val Asn Ile Val Gln Ala Asp Ser

20

25

30

att aat gta caa gct aaa aaa tat caa tat agc ggt gtt acc tat tta 144

Ile Asn Val Gln Ala Lys Lys Tyr Gln Tyr Ser Gly Val Thr Tyr Leu

35

40

45

tat aag atg ctc aag ctt gaa ggg att aag tat aat aaa ttc cca ggt	192
Tyr Lys Met Leu Lys Leu Glu Gly Ile Lys Tyr Asn Lys Phe Pro Gly	
50 55 60	
ggt gaa tat aaa act ggt aaa ccg gaa gga att gta att cac gaa act	240
Val Glu Tyr Lys Thr Gly Lys Pro Glu Gly Ile Val Ile His Glu Thr	
65 70 75 80	
gat gat cct ggt gca aca gcc cac gat gaa gca att tat ttt aat cgt	288
Asp Asp Pro Gly Ala Thr Ala His Asp Glu Ala Ile Tyr Phe Asn Arg	
85 90 95	
gaa tgg cct aaa gta aag gct tat gtt cat gcc ttt gtt gat gat gac	336
Glu Trp Pro Lys Val Lys Ala Tyr Val His Ala Phe Val Asp Asp Asp	
100 105 110	
cat gtc atc cag atg aga tca cct gag atg ggt act tgg ggc gct gga	384
His Val Ile Gln Met Arg Ser Pro Glu Met Gly Thr Trp Gly Ala Gly	
115 120 125	
cct aat gct aac gat cgt ttc att cag att gag ctt tgt gaa gag aac	432
Pro Asn Ala Asn Asp Arg Phe Ile Gln Ile Glu Leu Cys Glu Glu Asn	
130 135 140	
act cgt gat gct ttt att aaa tca att aac aat gat gcg att tat gta	480
Thr Arg Asp Ala Phe Ile Lys Ser Ile Asn Asn Asp Ala Ile Tyr Val	
145 150 155 160	
gct aag ttg ctt cat cgc tat gat ctc aag cct gat aat gct tgt gat	528
Ala Lys Leu Leu His Arg Tyr Asp Leu Lys Pro Asp Asn Ala Cys Asp	
165 170 175	
gat ggt gaa gga acg att tgg tca cac cat gcc gta agt act tat ctt	576
Asp Gly Glu Gly Thr Ile Trp Ser His His Ala Val Ser Thr Tyr Leu	
180 185 190	
gga gga acc gat cac gtt gat cct gat ggt tac ttc gaa aag tgg ggc	624
Gly Gly Thr Asp His Val Asp Pro Asp Gly Tyr Phe Glu Lys Trp Gly	
195 200 205	
tac agt atg gat caa ttc ttt gac ttg att cag tat tac tat gat ttg	672
Tyr Ser Met Asp Gln Phe Phe Asp Leu Ile Gln Tyr Tyr Tyr Asp Leu	
210 215 220	
caa gct aag gat act gat gct aag gaa aag gat cca gct aag agt aag	720
Gln Ala Lys Asp Thr Asp Ala Lys Glu Lys Asp Pro Ala Lys Ser Lys	
225 230 235 240	
aaa gat gtc gaa gca att caa ggt gca gta act tta ggt cat gat gct	768
Lys Asp Val Glu Ala Ile Gln Gly Ala Val Thr Leu Gly His Asp Ala	
245 250 255	
tat att tat gat gct aaa ggc aag aac acc aag aaa ctt aag aag gct	816
Tyr Ile Tyr Asp Ala Lys Gly Lys Asn Thr Lys Lys Leu Lys Lys Ala	
260 265 270	

```

ggt ggt cct gtt gtt gtc atg ggt tac aag gct atg aat aat aag aag      864
Gly Gly Pro Val Val Val Met Gly Tyr Lys Ala Met Asn Asn Lys Lys
      275                      280                      285

tac tac caa att ggt aag aat caa tat gta gtt gcc tct aac att gac      912
Tyr Tyr Gln Ile Gly Lys Asn Gln Tyr Val Val Ala Ser Asn Ile Asp
      290                      295                      300

gct aca gat aga gta gtt aag aaa aat act tac tta cga act aat act      960
Ala Thr Asp Arg Val Val Lys Lys Asn Thr Tyr Leu Arg Thr Asn Thr
      305                      310                      315                      320

ggg cga atc gaa ccg gaa aac aaa gtc aag aag ggg agc cga gta tta      1008
Gly Arg Ile Glu Pro Glu Asn Lys Val Lys Lys Gly Ser Arg Val Leu
      325                      330                      335

act tat ggt agt cgt gtc aca att aaa ggc caa aag tac tat gca ctt      1056
Thr Tyr Gly Ser Arg Val Thr Ile Lys Gly Gln Lys Tyr Tyr Ala Leu
      340                      345                      350

aac gcc aca caa ttt att ttg gca agt gat ata gaa                      1092
Asn Ala Thr Gln Phe Ile Leu Ala Ser Asp Ile Glu
      355                      360

```

<210> 82

<211> 364

<212> PRT

<213> Lactobacillus acidophilus

<400> 82

```

Met Lys Leu Arg Lys Lys Leu Ile Thr Leu Ile Ala Ala Ile Ser Leu
  1           5           10           15
Thr Gly Val Ala Thr Asn Thr Gly Val Asn Ile Val Gln Ala Asp Ser
      20           25           30
Ile Asn Val Gln Ala Lys Lys Tyr Gln Tyr Ser Gly Val Thr Tyr Leu
      35           40           45
Tyr Lys Met Leu Lys Leu Glu Gly Ile Lys Tyr Asn Lys Phe Pro Gly
      50           55           60
Val Glu Tyr Lys Thr Gly Lys Pro Glu Gly Ile Val Ile His Glu Thr
      65           70           75           80
Asp Asp Pro Gly Ala Thr Ala His Asp Glu Ala Ile Tyr Phe Asn Arg
      85           90           95
Glu Trp Pro Lys Val Lys Ala Tyr Val His Ala Phe Val Asp Asp Asp
      100          105          110
His Val Ile Gln Met Arg Ser Pro Glu Met Gly Thr Trp Gly Ala Gly
      115          120          125
Pro Asn Ala Asn Asp Arg Phe Ile Gln Ile Glu Leu Cys Glu Glu Asn
      130          135          140
Thr Arg Asp Ala Phe Ile Lys Ser Ile Asn Asn Asp Ala Ile Tyr Val
      145          150          155          160
Ala Lys Leu Leu His Arg Tyr Asp Leu Lys Pro Asp Asn Ala Cys Asp
      165          170          175
Asp Gly Glu Gly Thr Ile Trp Ser His His Ala Val Ser Thr Tyr Leu
      180          185          190
Gly Gly Thr Asp His Val Asp Pro Asp Gly Tyr Phe Glu Lys Trp Gly
      195          200          205

```

```

Tyr Ser Met Asp Gln Phe Phe Asp Leu Ile Gln Tyr Tyr Tyr Asp Leu
 210                215                220
Gln Ala Lys Asp Thr Asp Ala Lys Glu Lys Asp Pro Ala Lys Ser Lys
 225                230                235                240
Lys Asp Val Glu Ala Ile Gln Gly Ala Val Thr Leu Gly His Asp Ala
                245                250                255
Tyr Ile Tyr Asp Ala Lys Gly Lys Asn Thr Lys Lys Leu Lys Lys Ala
 260                265                270
Gly Gly Pro Val Val Val Met Gly Tyr Lys Ala Met Asn Asn Lys Lys
 275                280                285
Tyr Tyr Gln Ile Gly Lys Asn Gln Tyr Val Val Ala Ser Asn Ile Asp
 290                295                300
Ala Thr Asp Arg Val Val Lys Lys Asn Thr Tyr Leu Arg Thr Asn Thr
 305                310                315                320
Gly Arg Ile Glu Pro Glu Asn Lys Val Lys Lys Gly Ser Arg Val Leu
                325                330                335
Thr Tyr Gly Ser Arg Val Thr Ile Lys Gly Gln Lys Tyr Tyr Ala Leu
 340                345                350
Asn Ala Thr Gln Phe Ile Leu Ala Ser Asp Ile Glu
 355                360

```

```

<210> 83
<211> 1002
<212> DNA
<213> Lactobacillus acidophilus

```

```

<220>
<221> misc_feature
<222> (0)...(0)
<223> ORF 798 - rod shape-det. prot. MreB

```

```

<220>
<221> CDS
<222> (1)...(1002)

```

```

<400> 83
gtg ttt gga tta ggt aca aaa aat att ggt atc gat tta ggt aca gcc 48
Met Phe Gly Leu Gly Thr Lys Asn Ile Gly Ile Asp Leu Gly Thr Ala
 1                5                10                15

aat aca ctc gtt tat atg gaa ggt aaa ggt att gtt tta aga gaa cct 96
Asn Thr Leu Val Tyr Met Glu Gly Lys Gly Ile Val Leu Arg Glu Pro
                20                25                30

tcc gta gta gca aag aac aca caa aca ggt gaa gta att gca gtg ggt 144
Ser Val Val Ala Lys Asn Thr Gln Thr Gly Glu Val Ile Ala Val Gly
 35                40                45

tca gaa gcc aaa gaa atg att ggt aga aca cca ggt act atc gta gct 192
Ser Glu Ala Lys Glu Met Ile Gly Arg Thr Pro Gly Thr Ile Val Ala
 50                55                60

atc cgt cct atg aaa gac ggt gta att gct gat tac gat acg act gct 240
Ile Arg Pro Met Lys Asp Gly Val Ile Ala Asp Tyr Asp Thr Thr Ala
 65                70                75                80

```

gct atg ctt aaa tac ttt atg gaa aag act gtt ggt aat tct aag cct	288
Ala Met Leu Lys Tyr Phe Met Glu Lys Thr Val Gly Asn Ser Lys Pro	
85 90 95	
tca gta atg gta tgt gtt cct tca ggt gtt act gaa gtt gaa aag cgt	336
Ser Val Met Val Cys Val Pro Ser Gly Val Thr Glu Val Glu Lys Arg	
100 105 110	
gct gtt att gat gca gct aga gta gct ggt gca cgt gaa gca ttt gtg	384
Ala Val Ile Asp Ala Ala Arg Val Ala Gly Ala Arg Glu Ala Phe Val	
115 120 125	
att gaa gaa cca ttt gct gca gct att ggt gca gga ctt cca gtt atg	432
Ile Glu Glu Pro Phe Ala Ala Ala Ile Gly Ala Gly Leu Pro Val Met	
130 135 140	
gat cct act ggt tca atg gtt gtt gat att ggt ggt ggt act act gat	480
Asp Pro Thr Gly Ser Met Val Val Asp Ile Gly Gly Gly Thr Thr Asp	
145 150 155 160	
gtt gct aca att tca tta ggt ggt atc gtg tca tca act tca att cgt	528
Val Ala Thr Ile Ser Leu Gly Gly Ile Val Ser Ser Thr Ser Ile Arg	
165 170 175	
caa gca ggt gac aag ttt aat aat tca atc atc aat tac att cac tca	576
Gln Ala Gly Asp Lys Phe Asn Asn Ser Ile Ile Asn Tyr Ile His Ser	
180 185 190	
aac ttt aac tta tta att ggt gaa aga act gct gaa gat att aag att	624
Asn Phe Asn Leu Leu Ile Gly Glu Arg Thr Ala Glu Asp Ile Lys Ile	
195 200 205	
caa att ggt tca gct tct att gaa aag gcc aaa gat atc gaa tca atg	672
Gln Ile Gly Ser Ala Ser Ile Glu Lys Ala Lys Asp Ile Glu Ser Met	
210 215 220	
aat atc cgt ggt cgt gat tta gtt act ggt tta cca aag tca gtt gat	720
Asn Ile Arg Gly Arg Asp Leu Val Thr Gly Leu Pro Lys Ser Val Asp	
225 230 235 240	
gtt gat gca gtt gat att gct aag gca att caa gat gtt gtt caa gat	768
Val Asp Ala Val Asp Ile Ala Lys Ala Ile Gln Asp Val Val Gln Asp	
245 250 255	
att att gtt gca atc aaa gag act ttg gaa caa act tca cct gaa att	816
Ile Ile Val Ala Ile Lys Glu Thr Leu Glu Gln Thr Ser Pro Glu Ile	
260 265 270	
gct gcc gat gtt atc gat cat ggt atc gta tta act ggt ggt gga gct	864
Ala Ala Asp Val Ile Asp His Gly Ile Val Leu Thr Gly Gly Gly Ala	
275 280 285	
ctt ctt aag aac ttg cca gaa gtt att tct gaa gca acc aag gtt cct	912
Leu Leu Lys Asn Leu Pro Glu Val Ile Ser Glu Ala Thr Lys Val Pro	
290 295 300	

gta ttt att gct caa gat cca ctt gat tgt gta gca att ggt act ggt 960
 Val Phe Ile Ala Gln Asp Pro Leu Asp Cys Val Ala Ile Gly Thr Gly
 305 310 315 320

gaa tca ctt aaa aat att gaa gta atg cgt aga agt cgc aaa 1002
 Glu Ser Leu Lys Asn Ile Glu Val Met Arg Arg Ser Arg Lys
 325 330

<210> 84

<211> 334

<212> PRT

<213> Lactobacillus acidophilus

<400> 84

Met Phe Gly Leu Gly Thr Lys Asn Ile Gly Ile Asp Leu Gly Thr Ala
 1 5 10 15
 Asn Thr Leu Val Tyr Met Glu Gly Lys Gly Ile Val Leu Arg Glu Pro
 20 25 30
 Ser Val Val Ala Lys Asn Thr Gln Thr Gly Glu Val Ile Ala Val Gly
 35 40 45
 Ser Glu Ala Lys Glu Met Ile Gly Arg Thr Pro Gly Thr Ile Val Ala
 50 55 60
 Ile Arg Pro Met Lys Asp Gly Val Ile Ala Asp Tyr Asp Thr Thr Ala
 65 70 75 80
 Ala Met Leu Lys Tyr Phe Met Glu Lys Thr Val Gly Asn Ser Lys Pro
 85 90 95
 Ser Val Met Val Cys Val Pro Ser Gly Val Thr Glu Val Glu Lys Arg
 100 105 110
 Ala Val Ile Asp Ala Ala Arg Val Ala Gly Ala Arg Glu Ala Phe Val
 115 120 125
 Ile Glu Glu Pro Phe Ala Ala Ile Gly Ala Gly Leu Pro Val Met
 130 135 140
 Asp Pro Thr Gly Ser Met Val Val Asp Ile Gly Gly Thr Thr Asp
 145 150 155 160
 Val Ala Thr Ile Ser Leu Gly Gly Ile Val Ser Ser Thr Ser Ile Arg
 165 170 175
 Gln Ala Gly Asp Lys Phe Asn Asn Ser Ile Ile Asn Tyr Ile His Ser
 180 185 190
 Asn Phe Asn Leu Leu Ile Gly Glu Arg Thr Ala Glu Asp Ile Lys Ile
 195 200 205
 Gln Ile Gly Ser Ala Ser Ile Glu Lys Ala Lys Asp Ile Glu Ser Met
 210 215 220
 Asn Ile Arg Gly Arg Asp Leu Val Thr Gly Leu Pro Lys Ser Val Asp
 225 230 235 240
 Val Asp Ala Val Asp Ile Ala Lys Ala Ile Gln Asp Val Val Gln Asp
 245 250 255
 Ile Ile Val Ala Ile Lys Glu Thr Leu Glu Gln Thr Ser Pro Glu Ile
 260 265 270
 Ala Ala Asp Val Ile Asp His Gly Ile Val Leu Thr Gly Gly Gly Ala
 275 280 285
 Leu Leu Lys Asn Leu Pro Glu Val Ile Ser Glu Ala Thr Lys Val Pro
 290 295 300
 Val Phe Ile Ala Gln Asp Pro Leu Asp Cys Val Ala Ile Gly Thr Gly
 305 310 315 320
 Glu Ser Leu Lys Asn Ile Glu Val Met Arg Arg Ser Arg Lys

325

330

<210> 85
 <211> 987
 <212> DNA
 <213> Lactobacillus acidophilus

 <220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 780 - cell shape det. prot. MreB

<220>
 <221> CDS
 <222> (1)...(987)

<400> 85
 gtg gca cga gat ata gga atc gat tta ggg aca gct aat gta cta atc 48
 Met Ala Arg Asp Ile Gly Ile Asp Leu Gly Thr Ala Asn Val Leu Ile
 1 5 10 15

 aat gtt tct ggt aag ggt atc gtt tta aac gaa cct tca gtt gtt gct 96
 Asn Val Ser Gly Lys Gly Ile Val Leu Asn Glu Pro Ser Val Val Ala
 20 25 30

 gtg aat act gat aca aat aaa gta gtt gca gtt ggc tcg gat gca tat 144
 Val Asn Thr Asp Thr Asn Lys Val Val Ala Val Gly Ser Asp Ala Tyr
 35 40 45

 gaa atg gta ggt aga act cct ggt aat att cgt gta att cgc cca tta 192
 Glu Met Val Gly Arg Thr Pro Gly Asn Ile Arg Val Ile Arg Pro Leu
 50 55 60

 aaa aat ggg gta att gca gac ttt gat att aca gaa gaa atg ctg tct 240
 Lys Asn Gly Val Ile Ala Asp Phe Asp Ile Thr Glu Glu Met Leu Ser
 65 70 75 80

 tac ttt att gaa aaa tta aac gtt aaa ggc ttt atg tcc aag cca aat 288
 Tyr Phe Ile Glu Lys Leu Asn Val Lys Gly Phe Met Ser Lys Pro Asn
 85 90 95

 att tta att tgt gct cct aca gga gtt act tca att gaa caa aag gca 336
 Ile Leu Ile Cys Ala Pro Thr Gly Val Thr Ser Ile Glu Gln Lys Ala
 100 105 110

 att att caa gca gct gaa aaa tca ggt gga gga aaa gtt tac ctt gat 384
 Ile Ile Gln Ala Ala Glu Lys Ser Gly Gly Gly Lys Val Tyr Leu Asp
 115 120 125

 ttt gaa cca aag gtt gca gct gta ggt gcc ggc ttg gat att ttt aag 432
 Phe Glu Pro Lys Val Ala Ala Val Gly Ala Gly Leu Asp Ile Phe Lys
 130 135 140

 cca caa ggt aat atg gta atc gac atc ggt ggt gga aca act gat gtt 480
 Pro Gln Gly Asn Met Val Ile Asp Ile Gly Gly Gly Thr Thr Asp Val

145	150	155	160	
gca gtt tta tct atg ggt gaa att gta act tct cgt tct tta cgt tat				528
Ala Val Leu Ser Met Gly Glu Ile Val Thr Ser Arg Ser Leu Arg Tyr	165	170	175	
gct ggt gat cga atg aat caa gct gtt att agt tat att aag aac aag				576
Ala Gly Asp Arg Met Asn Gln Ala Val Ile Ser Tyr Ile Lys Asn Lys	180	185	190	
cat aat ttg tta att ggt tct aga act gct gaa caa atc aaa att gaa				624
His Asn Leu Leu Ile Gly Ser Arg Thr Ala Glu Gln Ile Lys Ile Glu	195	200	205	
att ggt agt gca ttc gaa cca gaa gaa gat aag caa att act gta cgt				672
Ile Gly Ser Ala Phe Glu Pro Glu Glu Asp Lys Gln Ile Thr Val Arg	210	215	220	
ggg cgt gac gtg gtt gat ggt tta cct aag caa aca aca gtc act gcg				720
Gly Arg Asp Val Val Asp Gly Leu Pro Lys Gln Thr Thr Val Thr Ala	225	230	235	240
cca gag att caa tca gct ttg caa gat gga tta atg tct att gtt gca				768
Pro Glu Ile Gln Ser Ala Leu Gln Asp Gly Leu Met Ser Ile Val Ala	245	250	255	
gca gct aaa gaa gtt ttg gaa act aca cca cct gag ctt tct gcc gat				816
Ala Ala Lys Glu Val Leu Glu Thr Thr Pro Pro Glu Leu Ser Ala Asp	260	265	270	
atc att gat cgt ggt atc atg ctt aca ggt ggt gga gca tta tta aag				864
Ile Ile Asp Arg Gly Ile Met Leu Thr Gly Gly Gly Ala Leu Leu Lys	275	280	285	
aat att gat aag ttg atc tca tat tat ttg caa gta cca gtt tta aca				912
Asn Ile Asp Lys Leu Ile Ser Tyr Tyr Leu Gln Val Pro Val Leu Thr	290	295	300	
gct gat cat cca ctt gaa gca gtt gct tta ggt aca ggt act ttg ctt				960
Ala Asp His Pro Leu Glu Ala Val Ala Leu Gly Thr Gly Thr Leu Leu	305	310	315	320
aaa aat att gaa aag cat caa cga cac				987
Lys Asn Ile Glu Lys His Gln Arg His	325			

<210> 86

<211> 329

<212> PRT

<213> Lactobacillus acidophilus

<400> 86

Met Ala Arg Asp Ile Gly Ile Asp Leu Gly Thr Ala Asn Val Leu Ile				
1	5	10	15	
Asn Val Ser Gly Lys Gly Ile Val Leu Asn Glu Pro Ser Val Val Ala				
20	25	30		

```

Val Asn Thr Asp Thr Asn Lys Val Val Ala Val Gly Ser Asp Ala Tyr
      35      40      45
Glu Met Val Gly Arg Thr Pro Gly Asn Ile Arg Val Ile Arg Pro Leu
      50      55      60
Lys Asn Gly Val Ile Ala Asp Phe Asp Ile Thr Glu Glu Met Leu Ser
65      70      75      80
Tyr Phe Ile Glu Lys Leu Asn Val Lys Gly Phe Met Ser Lys Pro Asn
      85      90      95
Ile Leu Ile Cys Ala Pro Thr Gly Val Thr Ser Ile Glu Gln Lys Ala
      100     105     110
Ile Ile Gln Ala Ala Glu Lys Ser Gly Gly Gly Lys Val Tyr Leu Asp
      115     120     125
Phe Glu Pro Lys Val Ala Ala Val Gly Ala Gly Leu Asp Ile Phe Lys
      130     135     140
Pro Gln Gly Asn Met Val Ile Asp Ile Gly Gly Gly Thr Thr Asp Val
145     150     155     160
Ala Val Leu Ser Met Gly Glu Ile Val Thr Ser Arg Ser Leu Arg Tyr
      165     170     175
Ala Gly Asp Arg Met Asn Gln Ala Val Ile Ser Tyr Ile Lys Asn Lys
      180     185     190
His Asn Leu Leu Ile Gly Ser Arg Thr Ala Glu Gln Ile Lys Ile Glu
      195     200     205
Ile Gly Ser Ala Phe Glu Pro Glu Glu Asp Lys Gln Ile Thr Val Arg
      210     215     220
Gly Arg Asp Val Val Asp Gly Leu Pro Lys Gln Thr Thr Val Thr Ala
225     230     235     240
Pro Glu Ile Gln Ser Ala Leu Gln Asp Gly Leu Met Ser Ile Val Ala
      245     250     255
Ala Ala Lys Glu Val Leu Glu Thr Thr Pro Pro Glu Leu Ser Ala Asp
      260     265     270
Ile Ile Asp Arg Gly Ile Met Leu Thr Gly Gly Gly Ala Leu Leu Lys
      275     280     285
Asn Ile Asp Lys Leu Ile Ser Tyr Tyr Leu Gln Val Pro Val Leu Thr
      290     295     300
Ala Asp His Pro Leu Glu Ala Val Ala Leu Gly Thr Gly Thr Leu Leu
305     310     315     320
Lys Asn Ile Glu Lys His Gln Arg His
      325

```

<210> 87

<211> 849

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 799 - cell shape det. prot. MreC

<220>

<221> CDS

<222> (1)...(849)

<400> 87

atg aaa aaa ttt cta caa aac aaa aaa tta tta tca gca ttt att ata 48

Met	Lys	Lys	Phe	Leu	Gln	Asn	Lys	Lys	Leu	Leu	Ser	Ala	Phe	Ile	Ile		
1				5					10					15			
ggt	ggt	ggt	att	ttg	gcc	ggt	tta	ggg	ggg	agt	ggt	aat	ttg	cgc	aat	96	
Val	Val	Val	Ile	Leu	Ala	Val	Leu	Gly	Gly	Ser	Val	Asn	Leu	Arg	Asn		
			20					25					30				
aag	cgt	aac	acg	cca	tta	tta	att	caa	agt	tta	ggc	aat	gat	ggt	ggt	144	
Lys	Arg	Asn	Thr	Pro	Leu	Leu	Ile	Gln	Ser	Leu	Gly	Asn	Asp	Val	Val		
		35					40					45					
gct	tgg	gga	act	aga	atc	gta	gat	ggt	cct	ggt	ggc	ttt	ata	tcg	ggc	192	
Ala	Trp	Gly	Thr	Arg	Ile	Val	Asp	Val	Pro	Val	Gly	Phe	Ile	Ser	Gly		
	50					55					60						
ggt	cta	aat	agt	ggt	cat	gat	att	tta	aat	act	caa	gaa	gaa	aat	aat	240	
Gly	Leu	Asn	Ser	Val	His	Asp	Ile	Leu	Asn	Thr	Gln	Glu	Glu	Asn	Asn		
	65				70				75					80			
cat	tta	aaa	cgc	gaa	ggt	act	aac	tta	ggg	caa	act	aaa	gcg	aga	aat	288	
His	Leu	Lys	Arg	Glu	Val	Thr	Asn	Leu	Gly	Gln	Thr	Lys	Ala	Arg	Asn		
			85					90					95				
tca	gta	tta	gaa	aaa	gaa	aat	agt	caa	tta	aaa	tca	gca	tta	aaa	tta	336	
Ser	Val	Leu	Glu	Lys	Glu	Asn	Ser	Gln	Leu	Lys	Ser	Ala	Leu	Lys	Leu		
			100					105					110				
aga	gat	aca	tta	agt	ggc	tat	act	tta	ggt	aat	gcc	tca	ggt	att	tct	384	
Arg	Asp	Thr	Leu	Ser	Gly	Tyr	Thr	Leu	Val	Asn	Ala	Ser	Val	Ile	Ser		
		115					120					125					
cgt	gca	cct	gat	act	tgg	tca	gat	tta	ttg	aca	ata	gat	aaa	ggg	agt	432	
Arg	Ala	Pro	Asp	Thr	Trp	Ser	Asp	Leu	Leu	Thr	Ile	Asp	Lys	Gly	Ser		
	130					135					140						
tct	gct	gga	att	aaa	aag	aat	atg	gcc	gta	atg	tgt	ggg	ggc	ggg	gtc	480	
Ser	Ala	Gly	Ile	Lys	Lys	Asn	Met	Ala	Val	Met	Cys	Gly	Gly	Gly	Val		
	145				150				155						160		
att	ggg	aga	atc	att	gaa	acc	aat	gct	gct	tca	tcg	aag	gtg	gaa	tta	528	
Ile	Gly	Arg	Ile	Ile	Glu	Thr	Asn	Ala	Ala	Ser	Ser	Lys	Val	Glu	Leu		
			165					170					175				
att	act	aca	act	gat	gaa	tca	gct	aac	cgt	ttt	tca	ggt	caa	gca	gat	576	
Ile	Thr	Thr	Thr	Asp	Glu	Ser	Ala	Asn	Arg	Phe	Ser	Val	Gln	Ala	Asp		
			180					185					190				
gca	gct	agt	ggg	aaa	aca	ggt	cat	gga	att	att	act	gta	act	aat	aat	624	
Ala	Ala	Ser	Gly	Lys	Thr	Val	His	Gly	Ile	Ile	Thr	Val	Thr	Asn	Asn		
		195					200					205					
aat	aat	ctg	gcc	ttt	act	caa	gta	ggt	gat	ggg	caa	aaa	tta	aaa	gcc	672	
Asn	Asn	Leu	Ala	Phe	Thr	Gln	Val	Val	Asp	Gly	Gln	Lys	Leu	Lys	Ala		
		210				215					220						
ggg	aca	cgt	ggt	tat	act	agt	ggg	atg	gga	ggc	aat	tct	cct	aaa	gga	720	
Gly	Thr	Arg	Val	Tyr	Thr	Ser	Gly	Met	Gly	Gly	Asn	Ser	Pro	Lys	Gly		

225	230	235	240	
ctt ttg att ggt aca gta act act aca act cgt gat tca ttt ggt tta				768
Leu Leu Ile Gly Thr Val Thr Thr Thr Thr Arg Asp Ser Phe Gly Leu	245	250	255	
tca gat cag att aga att aag cca gca ggt aat att aat gat cca tca				816
Ser Asp Gln Ile Arg Ile Lys Pro Ala Gly Asn Ile Asn Asp Pro Ser	260	265	270	
ggt gta aca gtt att gaa aga cag gtg gct aat				849
Val Val Thr Val Ile Glu Arg Gln Val Ala Asn	275	280		

<210> 88

<211> 283

<212> PRT

<213> Lactobacillus acidophilus

<400> 88

Met Lys Lys Phe Leu Gln Asn Lys Lys Leu Leu Ser Ala Phe Ile Ile				
1 5 10 15				
Val Val Val Ile Leu Ala Val Leu Gly Gly Ser Val Asn Leu Arg Asn	20	25	30	
Lys Arg Asn Thr Pro Leu Leu Ile Gln Ser Leu Gly Asn Asp Val Val	35	40	45	
Ala Trp Gly Thr Arg Ile Val Asp Val Pro Val Gly Phe Ile Ser Gly	50	55	60	
Gly Leu Asn Ser Val His Asp Ile Leu Asn Thr Gln Glu Glu Asn Asn	65	70	75	80
His Leu Lys Arg Glu Val Thr Asn Leu Gly Gln Thr Lys Ala Arg Asn	85	90	95	
Ser Val Leu Glu Lys Glu Asn Ser Gln Leu Lys Ser Ala Leu Lys Leu	100	105	110	
Arg Asp Thr Leu Ser Gly Tyr Thr Leu Val Asn Ala Ser Val Ile Ser	115	120	125	
Arg Ala Pro Asp Thr Trp Ser Asp Leu Leu Thr Ile Asp Lys Gly Ser	130	135	140	
Ser Ala Gly Ile Lys Lys Asn Met Ala Val Met Cys Gly Gly Gly Val	145	150	155	160
Ile Gly Arg Ile Ile Glu Thr Asn Ala Ala Ser Ser Lys Val Glu Leu	165	170	175	
Ile Thr Thr Thr Asp Glu Ser Ala Asn Arg Phe Ser Val Gln Ala Asp	180	185	190	
Ala Ala Ser Gly Lys Thr Val His Gly Ile Ile Thr Val Thr Asn Asn	195	200	205	
Asn Asn Leu Ala Phe Thr Gln Val Val Asp Gly Gln Lys Leu Lys Ala	210	215	220	
Gly Thr Arg Val Tyr Thr Ser Gly Met Gly Gly Asn Ser Pro Lys Gly	225	230	235	240
Leu Leu Ile Gly Thr Val Thr Thr Thr Thr Arg Asp Ser Phe Gly Leu	245	250	255	
Ser Asp Gln Ile Arg Ile Lys Pro Ala Gly Asn Ile Asn Asp Pro Ser	260	265	270	
Val Val Thr Val Ile Glu Arg Gln Val Ala Asn	275	280		

<210> 89
 <211> 537
 <212> DNA
 <213> *Lactobacillus acidophilus*

 <220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 800 - cell shape det. protein MreD

<220>
 <221> CDS
 <222> (1)...(537)

<400> 89
 atg tct gtt ttt cgt aaa tgg gtt tta gca att agc tta ttt gtt gct 48
 Met Ser Val Phe Arg Lys Trp Val Leu Ala Ile Ser Leu Phe Val Ala
 1 5 10 15

 tta gtc tta gaa ggc gtt tgt tca ttt tat cta cac caa ttt atg act 96
 Leu Val Leu Glu Gly Val Cys Ser Phe Tyr Leu His Gln Phe Met Thr
 20 25 30

 tat ggt aac tat gga gct ttt agt gta atc ttg cca att agt att atg 144
 Tyr Gly Asn Tyr Gly Ala Phe Ser Val Ile Leu Pro Ile Ser Ile Met
 35 40 45

 tta att ggt tta ttt gat gat act aat gag aat gaa att tgg tta gct 192
 Leu Ile Gly Leu Phe Asp Asp Thr Asn Glu Asn Glu Ile Trp Leu Ala
 50 55 60

 ttg ggt aca gga att att gcc gac atc tat ttt tat gga ata atc ggt 240
 Leu Gly Thr Gly Ile Ile Ala Asp Ile Tyr Phe Tyr Gly Ile Ile Gly
 65 70 75 80

 att tat acc gta ttt ttg cca ctt agc tgt tgg gct ggc caa aaa att 288
 Ile Tyr Thr Val Phe Leu Pro Leu Ser Cys Trp Ala Gly Gln Lys Ile
 85 90 95

 gct cgt ttt tta cct gaa ata ttt tgg gca cga tta att gta gtt tta 336
 Ala Arg Phe Leu Pro Glu Ile Phe Trp Ala Arg Leu Ile Val Val Leu
 100 105 110

 ata gat acg act gcg ttt atc gtt tat agt tgg tta gta ttt aaa atg 384
 Ile Asp Thr Thr Ala Phe Ile Val Tyr Ser Trp Leu Val Phe Lys Met
 115 120 125

 att ggc ttt gcg tca att tca att cat atg ctt tta atg agt tta tta 432
 Ile Gly Phe Ala Ser Ile Ser Ile His Met Leu Leu Met Ser Leu Leu
 130 135 140

 gta aat cta ggt tgg aca att tta ttt ttt gtt ctg cta tat tgg att 480
 Val Asn Leu Gly Trp Thr Ile Leu Phe Phe Val Leu Leu Tyr Trp Ile
 145 150 155 160

tgg ggt aat tta gca caa gat tat cct ttc tta ata gat ttg aat gca 528
 Trp Gly Asn Leu Ala Gln Asp Tyr Pro Phe Leu Ile Asp Leu Asn Ala
 165 170 175

tat cga gta 537
 Tyr Arg Val

<210> 90
 <211> 179
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 90
 Met Ser Val Phe Arg Lys Trp Val Leu Ala Ile Ser Leu Phe Val Ala
 1 5 10 15
 Leu Val Leu Glu Gly Val Cys Ser Phe Tyr Leu His Gln Phe Met Thr
 20 25 30
 Tyr Gly Asn Tyr Gly Ala Phe Ser Val Ile Leu Pro Ile Ser Ile Met
 35 40 45
 Leu Ile Gly Leu Phe Asp Asp Thr Asn Glu Asn Glu Ile Trp Leu Ala
 50 55 60
 Leu Gly Thr Gly Ile Ile Ala Asp Ile Tyr Phe Tyr Gly Ile Ile Gly
 65 70 75 80
 Ile Tyr Thr Val Phe Leu Pro Leu Ser Cys Trp Ala Gly Gln Lys Ile
 85 90 95
 Ala Arg Phe Leu Pro Glu Ile Phe Trp Ala Arg Leu Ile Val Val Leu
 100 105 110
 Ile Asp Thr Thr Ala Phe Ile Val Tyr Ser Trp Leu Val Phe Lys Met
 115 120 125
 Ile Gly Phe Ala Ser Ile Ser Ile His Met Leu Leu Met Ser Leu Leu
 130 135 140
 Val Asn Leu Gly Trp Thr Ile Leu Phe Phe Val Leu Leu Tyr Trp Ile
 145 150 155 160
 Trp Gly Asn Leu Ala Gln Asp Tyr Pro Phe Leu Ile Asp Leu Asn Ala
 165 170 175
 Tyr Arg Val

<210> 91
 <211> 1191
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 782 - rod shape-det. protein RodA

<220>
 <221> CDS
 <222> (1)...(1191)

<400> 91

atg gca aaa gtt gaa aat aag acg agc tta gta gat cga tta gct tgg	48
Met Ala Lys Val Glu Asn Lys Thr Ser Leu Val Asp Arg Leu Ala Trp	
1 5 10 15	
aat atc att att cct gta gca ctt ttg gct tta att agt ttg tac tgt	96
Asn Ile Ile Ile Pro Val Ala Leu Leu Ala Leu Ile Ser Leu Tyr Cys	
20 25 30	
att tat gta gca gct tta ggt gat ccg agt cat att ggt tca cca gtt	144
Ile Tyr Val Ala Ala Leu Gly Asp Pro Ser His Ile Gly Ser Pro Val	
35 40 45	
aga gcg gtt gtt atg cag gca tta tgg tat tta att tcg gta gca att	192
Arg Ala Val Val Met Gln Ala Leu Trp Tyr Leu Ile Ser Val Ala Ile	
50 55 60	
gtt ata gtg gtc atg cag ttt gat gca gat caa ttg ttt aaa att gct	240
Val Ile Val Val Met Gln Phe Asp Ala Asp Gln Leu Phe Lys Ile Ala	
65 70 75 80	
ccg ata ttt ttt gga ata gcg ata ttc ttg ctg ata gcg gta ttg ttc	288
Pro Ile Phe Phe Gly Ile Ala Ile Phe Leu Leu Ile Ala Val Leu Phe	
85 90 95	
ttg tat aac cgt agt gtg gcc gca gat aca ggg gct aaa agt tgg ttt	336
Leu Tyr Asn Arg Ser Val Ala Ala Asp Thr Gly Ala Lys Ser Trp Phe	
100 105 110	
aaa tta ggg ccg att act ttt cag cct tcg gaa tta atg aag cct gct	384
Lys Leu Gly Pro Ile Thr Phe Gln Pro Ser Glu Leu Met Lys Pro Ala	
115 120 125	
ttt att tta atg ctg gct cgc gtg att aaa gac cat aat gac aaa tat	432
Phe Ile Leu Met Leu Ala Arg Val Ile Lys Asp His Asn Asp Lys Tyr	
130 135 140	
ggg cat acg atc cga act gac tgg ctt ctt tta ggt aag ata att gcc	480
Gly His Thr Ile Arg Thr Asp Trp Leu Leu Gly Lys Ile Ile Ala	
145 150 155 160	
tgg tta gct ccg gta gca att tta tta aaa tta caa aat gac ttt ggt	528
Trp Leu Ala Pro Val Ala Ile Leu Leu Lys Leu Gln Asn Asp Phe Gly	
165 170 175	
act atg tta gtt ttc att gcc atc gtt ggt ggt gta gtt tta gtt tcc	576
Thr Met Leu Val Phe Ile Ala Ile Val Gly Gly Val Val Leu Val Ser	
180 185 190	
ggg ata tca tgg aaa att atc att ccg att tat ggt atg gta att atc	624
Gly Ile Ser Trp Lys Ile Ile Ile Pro Ile Tyr Gly Met Val Ile Ile	
195 200 205	
ggg gca att gct ata att ttg tta gtt gta act cca ggt gga cag tca	672
Gly Ala Ile Ala Ile Ile Leu Leu Val Val Thr Pro Gly Gly Gln Ser	
210 215 220	

```

ttt ttg agt cat ttc ttc caa gct tac cag ttt gaa aga att aaa tca 720
Phe Leu Ser His Phe Phe Gln Ala Tyr Gln Phe Glu Arg Ile Lys Ser
225                230                235                240

tgg ctt gat cca tct ggc gat acg tct tct ggt gct tat caa tta tgg 768
Trp Leu Asp Pro Ser Gly Asp Thr Ser Ser Gly Ala Tyr Gln Leu Trp
                245                250                255

caa agt atg aag gcg att ggt tca gga caa ttg ttt ggt aat ggc ttt 816
Gln Ser Met Lys Ala Ile Gly Ser Gly Gln Leu Phe Gly Asn Gly Phe
                260                265                270

ggg aaa gct agc gta tat gtt cca gtt cgt gga tct gac atg gtt ttc 864
Gly Lys Ala Ser Val Tyr Val Pro Val Arg Gly Ser Asp Met Val Phe
                275                280                285

tca gtt att ggt gaa aac ttt ggt ttt gtc ggc tgt gta gtt ttg att 912
Ser Val Ile Gly Glu Asn Phe Gly Phe Val Gly Cys Val Val Leu Ile
                290                295                300

ttg att tat tta tac tta att gtc caa atg gta aga att tca ttt gat 960
Leu Ile Tyr Leu Tyr Leu Ile Val Gln Met Val Arg Ile Ser Phe Asp
305                310                315                320

aca aga aat gta ttt tat tca tat att tct acc ggt gtt atc atg atg 1008
Thr Arg Asn Val Phe Tyr Ser Tyr Ile Ser Thr Gly Val Ile Met Met
                325                330                335

att tta ttc cat gtt ttt gaa aat att ggt atg aat att gat ttg tta 1056
Ile Leu Phe His Val Phe Glu Asn Ile Gly Met Asn Ile Asp Leu Leu
                340                345                350

cca ttg act ggt att cca tta ccg ttt gta tcg caa ggt ggt tcc gct 1104
Pro Leu Thr Gly Ile Pro Leu Pro Phe Val Ser Gln Gly Gly Ser Ala
                355                360                365

ttg tta ggt aac atg atc ggt atc ggt ttg atc tta tca atg aaa ttc 1152
Leu Leu Gly Asn Met Ile Gly Ile Gly Leu Ile Leu Ser Met Lys Phe
                370                375                380

cat aat cgt gat tac atg ttt agt aca gca ggc gat ttt 1191
His Asn Arg Asp Tyr Met Phe Ser Thr Ala Gly Asp Phe
385                390                395

```

<210> 92

<211> 397

<212> PRT

<213> Lactobacillus acidophilus

<400> 92

```

Met Ala Lys Val Glu Asn Lys Thr Ser Leu Val Asp Arg Leu Ala Trp
 1          5          10          15
Asn Ile Ile Ile Pro Val Ala Leu Leu Ala Leu Ile Ser Leu Tyr Cys
          20          25          30
Ile Tyr Val Ala Ala Leu Gly Asp Pro Ser His Ile Gly Ser Pro Val
          35          40          45

```

```

Arg Ala Val Val Met Gln Ala Leu Trp Tyr Leu Ile Ser Val Ala Ile
 50          55          60
Val Ile Val Val Met Gln Phe Asp Ala Asp Gln Leu Phe Lys Ile Ala
 65          70          75          80
Pro Ile Phe Phe Gly Ile Ala Ile Phe Leu Leu Ile Ala Val Leu Phe
          85          90          95
Leu Tyr Asn Arg Ser Val Ala Ala Asp Thr Gly Ala Lys Ser Trp Phe
          100          105          110
Lys Leu Gly Pro Ile Thr Phe Gln Pro Ser Glu Leu Met Lys Pro Ala
          115          120          125
Phe Ile Leu Met Leu Ala Arg Val Ile Lys Asp His Asn Asp Lys Tyr
          130          135          140
Gly His Thr Ile Arg Thr Asp Trp Leu Leu Leu Gly Lys Ile Ile Ala
          145          150          155          160
Trp Leu Ala Pro Val Ala Ile Leu Leu Lys Leu Gln Asn Asp Phe Gly
          165          170          175
Thr Met Leu Val Phe Ile Ala Ile Val Gly Gly Val Val Leu Val Ser
          180          185          190
Gly Ile Ser Trp Lys Ile Ile Ile Pro Ile Tyr Gly Met Val Ile Ile
          195          200          205
Gly Ala Ile Ala Ile Ile Leu Leu Val Val Thr Pro Gly Gly Gln Ser
          210          215          220
Phe Leu Ser His Phe Phe Gln Ala Tyr Gln Phe Glu Arg Ile Lys Ser
          225          230          235          240
Trp Leu Asp Pro Ser Gly Asp Thr Ser Ser Gly Ala Tyr Gln Leu Trp
          245          250          255
Gln Ser Met Lys Ala Ile Gly Ser Gly Gln Leu Phe Gly Asn Gly Phe
          260          265          270
Gly Lys Ala Ser Val Tyr Val Pro Val Arg Gly Ser Asp Met Val Phe
          275          280          285
Ser Val Ile Gly Glu Asn Phe Gly Phe Val Gly Cys Val Val Leu Ile
          290          295          300
Leu Ile Tyr Leu Tyr Leu Ile Val Gln Met Val Arg Ile Ser Phe Asp
          305          310          315          320
Thr Arg Asn Val Phe Tyr Ser Tyr Ile Ser Thr Gly Val Ile Met Met
          325          330          335
Ile Leu Phe His Val Phe Glu Asn Ile Gly Met Asn Ile Asp Leu Leu
          340          345          350
Pro Leu Thr Gly Ile Pro Leu Pro Phe Val Ser Gln Gly Gly Ser Ala
          355          360          365
Leu Leu Gly Asn Met Ile Gly Ile Gly Leu Ile Leu Ser Met Lys Phe
          370          375          380
His Asn Arg Asp Tyr Met Phe Ser Thr Ala Gly Asp Phe
          385          390          395

```

<210> 93

<211> 1311

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1579 - UDP-N-acetylmuramate-alanine ligase

<220>

<221> CDS

<222> (1)...(1311)

<400> 93

atg tta gat aaa aac aaa caa att tgg ttt att ggt att aaa gga aca	48
Met Leu Asp Lys Asn Lys Gln Ile Trp Phe Ile Gly Ile Lys Gly Thr	
1 5 10 15	
ggt atg gct tca ttg gcc tta ttg ctt cac gat tta ggc tac aac gtt	96
Gly Met Ala Ser Leu Ala Leu Leu Leu His Asp Leu Gly Tyr Asn Val	
20 25 30	
gcc gga agt gat att gaa aag tac act ttt aca gaa gtt ccg ctt gaa	144
Ala Gly Ser Asp Ile Glu Lys Tyr Thr Phe Thr Glu Val Pro Leu Glu	
35 40 45	
aaa gtt ggg att gat att aag agc ttt aat cct gac aat atc aag agt	192
Lys Val Gly Ile Asp Ile Lys Ser Phe Asn Pro Asp Asn Ile Lys Ser	
50 55 60	
aat gaa gaa caa gta atc gtt aag ggt aat gcc ttc aag gaa gat aat	240
Asn Glu Glu Gln Val Ile Val Lys Gly Asn Ala Phe Lys Glu Asp Asn	
65 70 75 80	
cca gaa gtt aag gct tgt ctt gat aaa ggc gtt aag tgg caa agc tac	288
Pro Glu Val Lys Ala Cys Leu Asp Lys Gly Val Lys Trp Gln Ser Tyr	
85 90 95	
cca gat act gtt gaa gaa atc gtg caa atg cac act tca att gga att	336
Pro Asp Thr Val Glu Glu Ile Val Gln Met His Thr Ser Ile Gly Ile	
100 105 110	
tca ggt acc cac ggt aag acc tcg act act agt ctt tta gca cac gtt	384
Ser Gly Thr His Gly Lys Thr Ser Thr Thr Ser Leu Leu Ala His Val	
115 120 125	
tta ggc gaa gtt gca cca act tca tat ttg atc ggt gat ggt cgc ggt	432
Leu Gly Glu Val Ala Pro Thr Ser Tyr Leu Ile Gly Asp Gly Arg Gly	
130 135 140	
aag ggt gta gac gac tca cgt ttc ttt gtt tat gaa gct gat gaa tac	480
Lys Gly Val Asp Asp Ser Arg Phe Phe Val Tyr Glu Ala Asp Glu Tyr	
145 150 155 160	
cgt cgt cac ttc ttg gca tac cac cca gat tac caa att atg act aac	528
Arg Arg His Phe Leu Ala Tyr His Pro Asp Tyr Gln Ile Met Thr Asn	
165 170 175	
atc gat ttt gat cac cca gat tac ttc aaa gat caa gac gat tac act	576
Ile Asp Phe Asp His Pro Asp Tyr Phe Lys Asp Gln Asp Tyr Thr	
180 185 190	
agt gca ttc caa tct gca gct gat caa act aaa aag gca ttg ttt gta	624
Ser Ala Phe Gln Ser Ala Ala Asp Gln Thr Lys Lys Ala Leu Phe Val	
195 200 205	

tgg ggt gat gac aag cgt ctt caa agt ctt aag act gat att cct aaa	672
Trp Gly Asp Asp Lys Arg Leu Gln Ser Leu Lys Thr Asp Ile Pro Lys	
210 215 220	
tat act tat ggc ttt aag gat act gat gac ttc caa gca gtt gat att	720
Tyr Thr Tyr Gly Phe Lys Asp Thr Asp Asp Phe Gln Ala Val Asp Ile	
225 230 235 240	
aag aag aca act act ggt tcg agc ttt aac gtt tta gct cat ggt aag	768
Lys Lys Thr Thr Gly Ser Ser Phe Asn Val Leu Ala His Gly Lys	
245 250 255	
gat ctt ggt cgt ttt gaa att cat ttg ttt ggt gac cac agt att tta	816
Asp Leu Gly Arg Phe Glu Ile His Leu Phe Gly Asp His Ser Ile Leu	
260 265 270	
aat gct act gca gtt att gcc gtt gct tat act gaa aag gta cca atg	864
Asn Ala Thr Ala Val Ile Ala Val Ala Tyr Thr Glu Lys Val Pro Met	
275 280 285	
gat gca att aga gaa ggt ctt ctt act ttt aaa ggg gct aag cgt aga	912
Asp Ala Ile Arg Glu Gly Leu Leu Thr Phe Lys Gly Ala Lys Arg Arg	
290 295 300	
ttt agt gaa aaa gac ttt ggt gat att gcc gta atc gac gac tac gca	960
Phe Ser Glu Lys Asp Phe Gly Asp Ile Ala Val Ile Asp Asp Tyr Ala	
305 310 315 320	
cac cat cca act gaa atg cgt gca act att caa gct gct cgt caa aag	1008
His His Pro Thr Glu Met Arg Ala Thr Ile Gln Ala Ala Arg Gln Lys	
325 330 335	
ttc cca gat aag aag tta gtt gtt gtt ttc cag cca cat act ttc tca	1056
Phe Pro Asp Lys Lys Leu Val Val Phe Gln Pro His Thr Phe Ser	
340 345 350	
aga act aag aag tac caa aag gac ttt gaa gaa att tta cgt gat gta	1104
Arg Thr Lys Lys Tyr Gln Lys Asp Phe Glu Glu Ile Leu Arg Asp Val	
355 360 365	
gat aag gca tat att acc cca atc tat gct tca gct cgt gaa gca aat	1152
Asp Lys Ala Tyr Ile Thr Pro Ile Tyr Ala Ser Ala Arg Glu Ala Asn	
370 375 380	
ggc gat att acc agt gaa gat ttg gtt aag aat att cca ggt tca gaa	1200
Gly Asp Ile Thr Ser Glu Asp Leu Val Lys Asn Ile Pro Gly Ser Glu	
385 390 395 400	
gtt atc gac tta gat aat att gcc gat tta act aag aat aag aat tct	1248
Val Ile Asp Leu Asp Asn Ile Ala Asp Leu Thr Lys Asn Lys Asn Ser	
405 410 415	
gtc atc gta ttt atg ggt gct ggc gat att cct aag tat gaa gat gct	1296
Val Ile Val Phe Met Gly Ala Gly Asp Ile Pro Lys Tyr Glu Asp Ala	
420 425 430	
ttt gaa aag tta ctt	1311

Phe Glu Lys Leu Leu
435

<210> 94

<211> 437

<212> PRT

<213> Lactobacillus acidophilus

<400> 94

```

Met Leu Asp Lys Asn Lys Gln Ile Trp Phe Ile Gly Ile Lys Gly Thr
 1           5           10           15
Gly Met Ala Ser Leu Ala Leu Leu Leu His Asp Leu Gly Tyr Asn Val
          20           25           30
Ala Gly Ser Asp Ile Glu Lys Tyr Thr Phe Thr Glu Val Pro Leu Glu
          35           40           45
Lys Val Gly Ile Asp Ile Lys Ser Phe Asn Pro Asp Asn Ile Lys Ser
          50           55           60
Asn Glu Glu Gln Val Ile Val Lys Gly Asn Ala Phe Lys Glu Asp Asn
65           70           75           80
Pro Glu Val Lys Ala Cys Leu Asp Lys Gly Val Lys Trp Gln Ser Tyr
          85           90           95
Pro Asp Thr Val Glu Glu Ile Val Gln Met His Thr Ser Ile Gly Ile
          100          105          110
Ser Gly Thr His Gly Lys Thr Ser Thr Thr Ser Leu Leu Ala His Val
          115          120          125
Leu Gly Glu Val Ala Pro Thr Ser Tyr Leu Ile Gly Asp Gly Arg Gly
130          135          140
Lys Gly Val Asp Asp Ser Arg Phe Phe Val Tyr Glu Ala Asp Glu Tyr
145          150          155          160
Arg Arg His Phe Leu Ala Tyr His Pro Asp Tyr Gln Ile Met Thr Asn
          165          170          175
Ile Asp Phe Asp His Pro Asp Tyr Phe Lys Asp Gln Asp Asp Tyr Thr
          180          185          190
Ser Ala Phe Gln Ser Ala Ala Asp Gln Thr Lys Lys Ala Leu Phe Val
          195          200          205
Trp Gly Asp Asp Lys Arg Leu Gln Ser Leu Lys Thr Asp Ile Pro Lys
210          215          220
Tyr Thr Tyr Gly Phe Lys Asp Thr Asp Asp Phe Gln Ala Val Asp Ile
225          230          235          240
Lys Lys Thr Thr Thr Gly Ser Ser Phe Asn Val Leu Ala His Gly Lys
          245          250          255
Asp Leu Gly Arg Phe Glu Ile His Leu Phe Gly Asp His Ser Ile Leu
          260          265          270
Asn Ala Thr Ala Val Ile Ala Val Ala Tyr Thr Glu Lys Val Pro Met
          275          280          285
Asp Ala Ile Arg Glu Gly Leu Leu Thr Phe Lys Gly Ala Lys Arg Arg
290          295          300
Phe Ser Glu Lys Asp Phe Gly Asp Ile Ala Val Ile Asp Asp Tyr Ala
305          310          315          320
His His Pro Thr Glu Met Arg Ala Thr Ile Gln Ala Ala Arg Gln Lys
          325          330          335
Phe Pro Asp Lys Lys Leu Val Val Val Phe Gln Pro His Thr Phe Ser
          340          345          350
Arg Thr Lys Lys Tyr Gln Lys Asp Phe Glu Glu Ile Leu Arg Asp Val
          355          360          365
Asp Lys Ala Tyr Ile Thr Pro Ile Tyr Ala Ser Ala Arg Glu Ala Asn

```

```

      370      375      380
Gly Asp Ile Thr Ser Glu Asp Leu Val Lys Asn Ile Pro Gly Ser Glu
385      390      395      400
Val Ile Asp Leu Asp Asn Ile Ala Asp Leu Thr Lys Asn Lys Asn Ser
      405      410      415
Val Ile Val Phe Met Gly Ala Gly Asp Ile Pro Lys Tyr Glu Asp Ala
      420      425      430
Phe Glu Lys Leu Leu
      435

```

<210> 95

<211> 1356

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 765 - UDP-N-acetylmuramyl tripeptide
synthetase

<220>

<221> CDS

<222> (1)...(1356)

<400> 95

```

atg tac atg agt ttt aaa tca gga atc gct aaa gtt gct gga aaa tct      48
Met Tyr Met Ser Phe Lys Ser Gly Ile Ala Lys Val Ala Gly Lys Ser
  1              5              10              15

agt tat tgg ttt tta cac aat gtt tta aaa ggt ggt act agt ttt cct      96
Ser Tyr Trp Phe Leu His Asn Val Leu Lys Gly Gly Thr Ser Phe Pro
      20              25              30

ggc aaa ttt gca atg aaa atc gat cca aat gtt ctt aac tct tta gcc      144
Gly Lys Phe Ala Met Lys Ile Asp Pro Asn Val Leu Asn Ser Leu Ala
      35              40              45

aaa ggt tat gaa aca gtg att gtt aca ggt acc aat ggt aaa act atg      192
Lys Gly Tyr Glu Thr Val Ile Val Thr Gly Thr Asn Gly Lys Thr Met
      50              55              60

aca act gct ttg att gtt gaa gca ttg aag aaa aaa tat ggt gac gtt      240
Thr Thr Ala Leu Ile Val Glu Ala Leu Lys Lys Lys Tyr Gly Asp Val
      65              70              75              80

tta act aat cca tct ggt tca aac atg caa caa ggt att gtc aca gca      288
Leu Thr Asn Pro Ser Gly Ser Asn Met Gln Gln Gly Ile Val Thr Ala
      85              90              95

ttt tta gct cat aaa aat aag cat gtt aaa cgt aaa atc gct gta tta      336
Phe Leu Ala His Lys Asn Lys His Val Lys Arg Lys Ile Ala Val Leu
      100              105              110

gaa gtt gat gaa gct aac gta aaa atg gtt acg aaa ttg ctt cat ccc      384

```

Glu Val Asp	Glu Ala Asn Val	Lys Met Val Thr	Lys Leu Leu His Pro	
115		120	125	
agc gtc ttt gtt tta act aat att ttc cgt gat caa atg gat cgt tat				432
Ser Val Phe Val Leu Thr Asn Ile Phe Arg Asp Gln Met Asp Arg Tyr				
130	135	140		
ggg gaa atc tat acc act tat gaa aaa att gtt gat ggt att aaa cta				480
Gly Glu Ile Tyr Thr Thr Tyr Glu Lys Ile Val Asp Gly Ile Lys Leu				
145	150	155	160	
gca cct gac gct aca att att gcc aat ggt gac gcc agc atc ttt tca				528
Ala Pro Asp Ala Thr Ile Ile Ala Asn Gly Asp Ala Ser Ile Phe Ser				
165	170	175		
tca gta gat tta cca aat aag aaa att ttc tac ggt ttc aaa ttg cct				576
Ser Val Asp Leu Pro Asn Lys Lys Ile Phe Tyr Gly Phe Lys Leu Pro				
180	185	190		
gac gat aaa aaa gag aat gat ttt aaa gca cca gtt aat act gat ggc				624
Asp Asp Lys Lys Glu Asn Asp Phe Lys Ala Pro Val Asn Thr Asp Gly				
195	200	205		
gtt ctt tgt cca aaa tgt gat cat att tta cat tat cat gaa aga att				672
Val Leu Cys Pro Lys Cys Asp His Ile Leu His Tyr His Glu Arg Ile				
210	215	220		
tac gca aac tta ggt gac ttc ttc tgc cct aac tgc ggc tat cat cgt				720
Tyr Ala Asn Leu Gly Asp Phe Phe Cys Pro Asn Cys Gly Tyr His Arg				
225	230	235	240	
cct gat tta act ttt acc gtt aac aag att ctt gaa caa aca cct aac				768
Pro Asp Leu Thr Phe Thr Val Asn Lys Ile Leu Glu Gln Thr Pro Asn				
245	250	255		
agc gta aaa ttc caa atg ggt aat aag gat tat tcg att aat att ggt				816
Ser Val Lys Phe Gln Met Gly Asn Lys Asp Tyr Ser Ile Asn Ile Gly				
260	265	270		
ggg acc tac aat atc tat aac gct tta gct gca tat tct gtt gct cgc				864
Gly Thr Tyr Asn Ile Tyr Asn Ala Leu Ala Ala Tyr Ser Val Ala Arg				
275	280	285		
cat ttt ggt tta act gaa gca gaa gtt gca caa gca ttt gct gaa aat				912
His Phe Gly Leu Thr Glu Ala Glu Val Ala Gln Ala Phe Ala Glu Asn				
290	295	300		
aag cga atc ttt ggc cgt caa gaa ttg att cac tac ggc gga aaa gac				960
Lys Arg Ile Phe Gly Arg Gln Glu Leu Ile His Tyr Gly Gly Lys Asp				
305	310	315	320	
att gat tta atc ttg gtt aag aat ccg gtt gga ctt gat gaa gtt ctt				1008
Ile Asp Leu Ile Leu Val Lys Asn Pro Val Gly Leu Asp Glu Val Leu				
325	330	335		
cat atg ctt aac act gaa aaa gat gat tat tca tta gta gct tta tta				1056
His Met Leu Asn Thr Glu Lys Asp Asp Tyr Ser Leu Val Ala Leu Leu				

340	345	350	
aat gca aac cat gcc gat ggg att gat act tct tgg att tgg gat gca			1104
Asn Ala Asn His Ala Asp Gly Ile Asp Thr Ser Trp Ile Trp Asp Ala			
355	360	365	
gac ttt gaa gga ctt gat cgt agc aag att aag aaa gta ctt gtt ggt			1152
Asp Phe Glu Gly Leu Asp Arg Ser Lys Ile Lys Lys Val Leu Val Gly			
370	375	380	
ggc cag cgc tgg cac gac atg gga ttt aga ctt gaa atc gct ggt ttt			1200
Gly Gln Arg Trp His Asp Met Gly Phe Arg Leu Glu Ile Ala Gly Phe			
385	390	395	400
gat cca ggc aag atg agt act aat cca gat gat gat agc ttg att gaa			1248
Asp Pro Gly Lys Met Ser Thr Asn Pro Asp Asp Asp Ser Leu Ile Glu			
405	410	415	
gaa atc aag aaa tta cca acc aag aag gtt tac att ctt tca act tat			1296
Glu Ile Lys Lys Leu Pro Thr Lys Lys Val Tyr Ile Leu Ser Thr Tyr			
420	425	430	
act gca atg ctt gca ctt aga aag aaa atg gct gaa aag aaa att atc			1344
Thr Ala Met Leu Ala Leu Arg Lys Lys Met Ala Glu Lys Lys Ile Ile			
435	440	445	
aaa gct ggt atg			1356
Lys Ala Gly Met			
450			

<210> 96

<211> 452

<212> PRT

<213> Lactobacillus acidophilus

<400> 96

Met Tyr Met Ser Phe Lys Ser Gly Ile Ala Lys Val Ala Gly Lys Ser			
1	5	10	15
Ser Tyr Trp Phe Leu His Asn Val Leu Lys Gly Gly Thr Ser Phe Pro			
20	25	30	
Gly Lys Phe Ala Met Lys Ile Asp Pro Asn Val Leu Asn Ser Leu Ala			
35	40	45	
Lys Gly Tyr Glu Thr Val Ile Val Thr Gly Thr Asn Gly Lys Thr Met			
50	55	60	
Thr Thr Ala Leu Ile Val Glu Ala Leu Lys Lys Lys Tyr Gly Asp Val			
65	70	75	80
Leu Thr Asn Pro Ser Gly Ser Asn Met Gln Gln Gly Ile Val Thr Ala			
85	90	95	
Phe Leu Ala His Lys Asn Lys His Val Lys Arg Lys Ile Ala Val Leu			
100	105	110	
Glu Val Asp Glu Ala Asn Val Lys Met Val Thr Lys Leu Leu His Pro			
115	120	125	
Ser Val Phe Val Leu Thr Asn Ile Phe Arg Asp Gln Met Asp Arg Tyr			
130	135	140	
Gly Glu Ile Tyr Thr Thr Tyr Glu Lys Ile Val Asp Gly Ile Lys Leu			
145	150	155	160

Ala Pro Asp Ala Thr Ile Ile Ala Asn Gly Asp Ala Ser Ile Phe Ser
 165 170 175
 Ser Val Asp Leu Pro Asn Lys Lys Ile Phe Tyr Gly Phe Lys Leu Pro
 180 185 190
 Asp Asp Lys Lys Glu Asn Asp Phe Lys Ala Pro Val Asn Thr Asp Gly
 195 200 205
 Val Leu Cys Pro Lys Cys Asp His Ile Leu His Tyr His Glu Arg Ile
 210 215 220
 Tyr Ala Asn Leu Gly Asp Phe Phe Cys Pro Asn Cys Gly Tyr His Arg
 225 230 235 240
 Pro Asp Leu Thr Phe Thr Val Asn Lys Ile Leu Glu Gln Thr Pro Asn
 245 250 255
 Ser Val Lys Phe Gln Met Gly Asn Lys Asp Tyr Ser Ile Asn Ile Gly
 260 265 270
 Gly Thr Tyr Asn Ile Tyr Asn Ala Leu Ala Ala Tyr Ser Val Ala Arg
 275 280 285
 His Phe Gly Leu Thr Glu Ala Glu Val Ala Gln Ala Phe Ala Glu Asn
 290 295 300
 Lys Arg Ile Phe Gly Arg Gln Glu Leu Ile His Tyr Gly Gly Lys Asp
 305 310 315 320
 Ile Asp Leu Ile Leu Val Lys Asn Pro Val Gly Leu Asp Glu Val Leu
 325 330 335
 His Met Leu Asn Thr Glu Lys Asp Asp Tyr Ser Leu Val Ala Leu Leu
 340 345 350
 Asn Ala Asn His Ala Asp Gly Ile Asp Thr Ser Trp Ile Trp Asp Ala
 355 360 365
 Asp Phe Glu Gly Leu Asp Arg Ser Lys Ile Lys Lys Val Leu Val Gly
 370 375 380
 Gly Gln Arg Trp His Asp Met Gly Phe Arg Leu Glu Ile Ala Gly Phe
 385 390 395 400
 Asp Pro Gly Lys Met Ser Thr Asn Pro Asp Asp Asp Ser Leu Ile Glu
 405 410 415
 Glu Ile Lys Lys Leu Pro Thr Lys Lys Val Tyr Ile Leu Ser Thr Tyr
 420 425 430
 Thr Ala Met Leu Ala Leu Arg Lys Lys Met Ala Glu Lys Lys Ile Ile
 435 440 445
 Lys Ala Gly Met
 450

<210> 97

<211> 1596

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1818 -

UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-lysine
ligase

<220>

<221> CDS

<222> (1)...(1596)

<400> 97

atg ttt tta ata caa cga gga gaa aaa atg agt att tct tta aat acc	48
Met Phe Leu Ile Gln Arg Gly Glu Lys Met Ser Ile Ser Leu Asn Thr	
1 5 10 15	
tgt ata tta att tta aaa gag cac cat ttg ctc aag tca agc gca gtg	96
Cys Ile Leu Ile Leu Lys Glu His His Leu Leu Lys Ser Ser Ala Val	
20 25 30	
caa gat act gta gca acc aag atg gac tac gtt tct tat gac tca cgc	144
Gln Asp Thr Val Ala Thr Lys Met Asp Tyr Val Ser Tyr Asp Ser Arg	
35 40 45	
gat att caa act aac aca ttg ttt ttc tgt aag gga gca ggc ttt aga	192
Asp Ile Gln Thr Asn Thr Leu Phe Phe Cys Lys Gly Ala Gly Phe Arg	
50 55 60	
cca act tat tta tca atg gct aaa agt aat gga gca aat tgt tac gtt	240
Pro Thr Tyr Leu Ser Met Ala Lys Ser Asn Gly Ala Asn Cys Tyr Val	
65 70 75 80	
gct gaa caa cca tat cct gaa ggt aaa gga atg cac gct tta att gtt	288
Ala Glu Gln Pro Tyr Pro Glu Gly Lys Gly Met His Ala Leu Ile Val	
85 90 95	
cgc gat gtt tca aag gca atg gca tta ttg tca gcg gca ttt ttc cgt	336
Arg Asp Val Ser Lys Ala Met Ala Leu Leu Ser Ala Ala Phe Phe Arg	
100 105 110	
ttc cca caa gat gat ttg tat gtt gtt gca ttc act ggt act aag gga	384
Phe Pro Gln Asp Asp Leu Tyr Val Val Ala Phe Thr Gly Thr Lys Gly	
115 120 125	
aag act act tcg gca tac ttt ttg aag ggg atg ctt gat caa gca aac	432
Lys Thr Thr Ser Ala Tyr Phe Leu Lys Gly Met Leu Asp Gln Ala Asn	
130 135 140	
ggg ggt aga aca gct tta att tct tca gtt aat gat gtt gtt ggg cca	480
Gly Gly Arg Thr Ala Leu Ile Ser Ser Val Asn Asp Val Val Gly Pro	
145 150 155 160	
aag cca gaa gat agc ttt aaa tca agt tta act aca cca gaa agt ttg	528
Lys Pro Glu Asp Ser Phe Lys Ser Ser Leu Thr Thr Pro Glu Ser Leu	
165 170 175	
gac ttg ttc cgt gat atg cgt act gct gtt gat aac ggt atg act cac	576
Asp Leu Phe Arg Asp Met Arg Thr Ala Val Asp Asn Gly Met Thr His	
180 185 190	
ctt gta atg gaa gtt tca agt caa gct tat aag aag aac cgt gta ttt	624
Leu Val Met Glu Val Ser Ser Gln Ala Tyr Lys Lys Asn Arg Val Phe	
195 200 205	
gga tta act tat gat tta ggt ttc ttt tta aat atc agt ccg gat cat	672
Gly Leu Thr Tyr Asp Leu Gly Phe Phe Leu Asn Ile Ser Pro Asp His	
210 215 220	

att gga cca aat gaa cac cct aac ttt gcg gat tac ttg cac tgc aag	720
Ile Gly Pro Asn Glu His Pro Asn Phe Ala Asp Tyr Leu His Cys Lys	
225 230 235 240	
ttg caa ttg atg gtt aac tca cgt aaa tgt att att aac gca gaa act	768
Leu Gln Leu Met Val Asn Ser Arg Lys Cys Ile Ile Asn Ala Glu Thr	
245 250 255	
gct aac ttt aat gaa gta tat gca gca gca aca acg act act aat cca	816
Ala Asn Phe Asn Glu Val Tyr Ala Ala Ala Thr Thr Thr Thr Asn Pro	
260 265 270	
gat agc att tac ttg ttt gca aga gaa gat ttt gaa aat cca gat ttg	864
Asp Ser Ile Tyr Leu Phe Ala Arg Glu Asp Phe Glu Asn Pro Asp Leu	
275 280 285	
gat gtg cca att gac ttt aga ttt gct tcc caa gaa ttg gat atg aaa	912
Asp Val Pro Ile Asp Phe Arg Phe Ala Ser Gln Glu Leu Asp Met Lys	
290 295 300	
gaa act cgc ttt aag ttg ttc tgt gcc act gat aag gct aag aag ttg	960
Glu Thr Arg Phe Lys Leu Phe Cys Ala Thr Asp Lys Ala Lys Lys Leu	
305 310 315 320	
cct att aat ggt gat tac act tta aag atg ttg ggt gac ttt aat gaa	1008
Pro Ile Asn Gly Asp Tyr Thr Leu Lys Met Leu Gly Asp Phe Asn Glu	
325 330 335	
tca aat ggt aca gct gcc atc att ggt gca gga ctt gcc ggt ctt aac	1056
Ser Asn Gly Thr Ala Ala Ile Ile Gly Ala Gly Leu Ala Gly Leu Asn	
340 345 350	
cat gat caa tgt gct aag ggg atc cgt aat gtt act atc cct ggt cgt	1104
His Asp Gln Cys Ala Lys Gly Ile Arg Asn Val Thr Ile Pro Gly Arg	
355 360 365	
atg caa act gaa aga act aaa gaa cac ggt atg gtt gtt gtt gat tat	1152
Met Gln Thr Glu Arg Thr Lys Glu His Gly Met Val Val Val Asp Tyr	
370 375 380	
gcc cac aat aag gct tcg atg atg gct ttg atg aga ttc atg caa aat	1200
Ala His Asn Lys Ala Ser Met Met Ala Leu Met Arg Phe Met Gln Asn	
385 390 395 400	
gaa ttt aac gat cct aag atc atc gta gtt gtt ggt gca cct ggt gat	1248
Glu Phe Asn Asp Pro Lys Ile Ile Val Val Val Gly Ala Pro Gly Asp	
405 410 415	
aaa ggc gtt tca cgt cgt cca ggc ttt agt gaa agt ttg agt gca tat	1296
Lys Gly Val Ser Arg Arg Pro Gly Phe Ser Glu Ser Leu Ser Ala Tyr	
420 425 430	
gct gat aag gca ttt ttg aca act gat gat cca gga ttt gaa gat cca	1344
Ala Asp Lys Ala Phe Leu Thr Thr Asp Asp Pro Gly Phe Glu Asp Pro	
435 440 445	
aag tct att gct gaa gaa att gat gct ggt att gat cac tct aag tgt	1392

Lys Ser Ile Ala Glu Glu Ile Asp Ala Gly Ile Asp His Ser Lys Cys
 450 455 460
 gat gta aca att gaa ttg gac cgt aag aaa gct att cat gat gca att 1440
 Asp Val Thr Ile Glu Leu Asp Arg Lys Lys Ala Ile His Asp Ala Ile
 465 470 475 480
 gct tca gct ggt cca gat gat gta gtt tta atc tgt ggt aag ggt gct 1488
 Ala Ser Ala Gly Pro Asp Asp Val Val Leu Ile Cys Gly Lys Gly Ala
 485 490 495
 gac gct ttc caa aag att cgc ggc gta gac act cca tat cca tca gat 1536
 Asp Ala Phe Gln Lys Ile Arg Gly Val Asp Thr Pro Tyr Pro Ser Asp
 500 505 510
 att gtg gtt gct caa cag gta att aac gaa tta gaa ggc caa gac gag 1584
 Ile Val Val Ala Gln Gln Val Ile Asn Glu Leu Glu Gly Gln Asp Glu
 515 520 525
 cac ttt aga aaa 1596
 His Phe Arg Lys
 530

<210> 98

<211> 532

<212> PRT

<213> Lactobacillus acidophilus

<400> 98

Met Phe Leu Ile Gln Arg Gly Glu Lys Met Ser Ile Ser Leu Asn Thr
 1 5 10 15
 Cys Ile Leu Ile Leu Lys Glu His His Leu Leu Lys Ser Ser Ala Val
 20 25 30
 Gln Asp Thr Val Ala Thr Lys Met Asp Tyr Val Ser Tyr Asp Ser Arg
 35 40 45
 Asp Ile Gln Thr Asn Thr Leu Phe Phe Cys Lys Gly Ala Gly Phe Arg
 50 55 60
 Pro Thr Tyr Leu Ser Met Ala Lys Ser Asn Gly Ala Asn Cys Tyr Val
 65 70 75 80
 Ala Glu Gln Pro Tyr Pro Glu Gly Lys Gly Met His Ala Leu Ile Val
 85 90 95
 Arg Asp Val Ser Lys Ala Met Ala Leu Leu Ser Ala Ala Phe Phe Arg
 100 105 110
 Phe Pro Gln Asp Asp Leu Tyr Val Val Ala Phe Thr Gly Thr Lys Gly
 115 120 125
 Lys Thr Thr Ser Ala Tyr Phe Leu Lys Gly Met Leu Asp Gln Ala Asn
 130 135 140
 Gly Gly Arg Thr Ala Leu Ile Ser Ser Val Asn Asp Val Val Gly Pro
 145 150 155 160
 Lys Pro Glu Asp Ser Phe Lys Ser Ser Leu Thr Thr Pro Glu Ser Leu
 165 170 175
 Asp Leu Phe Arg Asp Met Arg Thr Ala Val Asp Asn Gly Met Thr His
 180 185 190
 Leu Val Met Glu Val Ser Ser Gln Ala Tyr Lys Lys Asn Arg Val Phe
 195 200 205
 Gly Leu Thr Tyr Asp Leu Gly Phe Phe Leu Asn Ile Ser Pro Asp His

210	215	220
Ile Gly Pro Asn Glu His	Pro Asn Phe Ala Asp Tyr Leu His Cys Lys	
225	230	235
Leu Gln Leu Met Val Asn Ser Arg Lys Cys Ile Ile Asn Ala Glu Thr		240
	245	250
Ala Asn Phe Asn Glu Val Tyr Ala Ala Thr Thr Thr Thr Asn Pro		255
	260	265
Asp Ser Ile Tyr Leu Phe Ala Arg Glu Asp Phe Glu Asn Pro Asp Leu		270
	275	280
Asp Val Pro Ile Asp Phe Arg Phe Ala Ser Gln Glu Leu Asp Met Lys		285
	290	295
Glu Thr Arg Phe Lys Leu Phe Cys Ala Thr Asp Lys Ala Lys Lys Leu		300
305	310	315
Pro Ile Asn Gly Asp Tyr Thr Leu Lys Met Leu Gly Asp Phe Asn Glu		320
	325	330
Ser Asn Gly Thr Ala Ala Ile Ile Gly Ala Gly Leu Ala Gly Leu Asn		335
	340	345
His Asp Gln Cys Ala Lys Gly Ile Arg Asn Val Thr Ile Pro Gly Arg		350
	355	360
Met Gln Thr Glu Arg Thr Lys Glu His Gly Met Val Val Val Asp Tyr		365
	370	375
Ala His Asn Lys Ala Ser Met Met Ala Leu Met Arg Phe Met Gln Asn		380
385	390	395
Glu Phe Asn Asp Pro Lys Ile Ile Val Val Val Gly Ala Pro Gly Asp		400
	405	410
Lys Gly Val Ser Arg Arg Pro Gly Phe Ser Glu Ser Leu Ser Ala Tyr		415
	420	425
Ala Asp Lys Ala Phe Leu Thr Thr Asp Asp Pro Gly Phe Glu Asp Pro		430
	435	440
Lys Ser Ile Ala Glu Glu Ile Asp Ala Gly Ile Asp His Ser Lys Cys		445
	450	455
Asp Val Thr Ile Glu Leu Asp Arg Lys Lys Ala Ile His Asp Ala Ile		460
465	470	475
Ala Ser Ala Gly Pro Asp Asp Val Val Leu Ile Cys Gly Lys Gly Ala		480
	485	490
Asp Ala Phe Gln Lys Ile Arg Gly Val Asp Thr Pro Tyr Pro Ser Asp		495
	500	505
Ile Val Val Ala Gln Gln Val Ile Asn Glu Leu Glu Gly Gln Asp Glu		510
	515	520
His Phe Arg Lys		525
530		

<210> 99

<211> 1377

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 808 - UDP-N-acetylmuramoylalanine-D-glutamate
ligase (murD)

<220>

<221> CDS

<222> (1)...(1377)

<400> 99

atg aaa gat att aaa act tat gat aat aag aat att tta gtt tta gga	48
Met Lys Asp Ile Lys Thr Tyr Asp Asn Lys Asn Ile Leu Val Leu Gly	
1 5 10 15	
tta gga aaa agt ggc ttt gca gtt agt gaa ctt ctt tta aaa tta ggt	96
Leu Gly Lys Ser Gly Phe Ala Val Ser Glu Leu Leu Leu Lys Leu Gly	
20 25 30	
gct aat tta act tta aac gat aaa gct gat ctt gat aaa aat gaa aag	144
Ala Asn Leu Thr Leu Asn Asp Lys Ala Asp Leu Asp Lys Asn Glu Lys	
35 40 45	
gca caa gaa tta aaa gct aaa ggt gtg cgc gta att ggc gga tat cat	192
Ala Gln Glu Leu Lys Ala Lys Gly Val Arg Val Ile Gly Gly Tyr His	
50 55 60	
cca gtt gat ttg ctt gaa gaa gaa cat ttt gat tat tta gtt aaa aat	240
Pro Val Asp Leu Leu Glu Glu Glu His Phe Asp Tyr Leu Val Lys Asn	
65 70 75 80	
cca ggt att ccg tat gaa aat cca atg gtt aaa aaa gct gaa gaa tta	288
Pro Gly Ile Pro Tyr Glu Asn Pro Met Val Lys Lys Ala Glu Glu Leu	
85 90 95	
gat att cca att atc act gaa cct gaa gtt gct tta agc tgt agt gac	336
Asp Ile Pro Ile Ile Thr Glu Pro Glu Val Ala Leu Ser Cys Ser Asp	
100 105 110	
gct cct tat gta tgt att act ggt tca aat ggt aag act act act gta	384
Ala Pro Tyr Val Cys Ile Thr Gly Ser Asn Gly Lys Thr Thr Thr Val	
115 120 125	
atg ctt aca caa aga att ttg gat cat cat tta caa aaa aca ggc cat	432
Met Leu Thr Gln Arg Ile Leu Asp His His Leu Gln Lys Thr Gly His	
130 135 140	
cat gca tat gca gtt ggt aat att ggt gtt cct att tca gaa gta gtt	480
His Ala Tyr Ala Val Gly Asn Ile Gly Val Pro Ile Ser Glu Val Val	
145 150 155 160	
cct aaa gct act aaa gat gat att tta gta gtt gaa att tca agt ttc	528
Pro Lys Ala Thr Lys Asp Asp Ile Leu Val Val Glu Ile Ser Ser Phe	
165 170 175	
caa tta tta ggt gta act gat att aag cct aag gta gca gcg att gtt	576
Gln Leu Leu Gly Val Thr Asp Ile Lys Pro Lys Val Ala Ala Ile Val	
180 185 190	
gat atc tat aat aat gtt cac ctt gat tat cat aag act ttc gaa aat	624
Asp Ile Tyr Asn Asn Val His Leu Asp Tyr His Lys Thr Phe Glu Asn	
195 200 205	
tac gtt gat gct aaa tta aac gtt act aga act caa aat agc gat gat	672
Tyr Val Asp Ala Lys Leu Asn Val Thr Arg Thr Gln Asn Ser Asp Asp	

210	215	220	
tac ttt att gct aac ttt gat caa aaa gat att ttg gca aaa gaa aaa			720
Tyr Phe Ile Ala Asn Phe Asp Gln Lys Asp Ile Leu Ala Lys Glu Lys			
225	230	235	240
gaa gta tcc cca gcc aaa atg cag act ttc tca gaa act gat cac aat			768
Glu Val Ser Pro Ala Lys Met Gln Thr Phe Ser Glu Thr Asp His Asn			
	245	250	255
gct gat tac ttt att ggt gat gag tat ctt gaa agt caa gac gaa aag			816
Ala Asp Tyr Phe Ile Gly Asp Glu Tyr Leu Glu Ser Gln Asp Glu Lys			
	260	265	270
att atg aag att gcg gat att aaa ctt cca ggc gtt cat aat tta caa			864
Ile Met Lys Ile Ala Asp Ile Lys Leu Pro Gly Val His Asn Leu Gln			
	275	280	285
aac agt ctt gta gca att gca att gct aaa ctt atg gga gca gat aat			912
Asn Ser Leu Val Ala Ile Ala Ile Ala Lys Leu Met Gly Ala Asp Asn			
	290	295	300
gaa gat att gct gct gta tta agt act ttt act ggt gct aaa cat cgt			960
Glu Asp Ile Ala Ala Val Leu Ser Thr Phe Thr Gly Ala Lys His Arg			
	305	310	315
tta caa tat gta aca aca ctt gat gga cgt aag att tat aat gat tct			1008
Leu Gln Tyr Val Thr Thr Leu Asp Gly Arg Lys Ile Tyr Asn Asp Ser			
	325	330	335
aag tcg act aat att gaa gct gct acg gta gct att cct gcg ttt aaa			1056
Lys Ser Thr Asn Ile Glu Ala Ala Thr Val Ala Ile Pro Ala Phe Lys			
	340	345	350
gaa ccc gaa gtt ttg att gca ggg gga cta gac aga gga ttt aca ttt			1104
Glu Pro Glu Val Leu Ile Ala Gly Gly Leu Asp Arg Gly Phe Thr Phe			
	355	360	365
gat gat tta gtt cca tta ttt aag aaa cat gtt aaa tca att gta ctt			1152
Asp Asp Leu Val Pro Leu Phe Lys Lys His Val Lys Ser Ile Val Leu			
	370	375	380
tat ggt gaa act aaa tat tta tta gct gat gcc gct aga aaa gca ggt			1200
Tyr Gly Glu Thr Lys Tyr Leu Leu Ala Asp Ala Ala Arg Lys Ala Gly			
	385	390	395
att aag gag att gta att gtt aat acc ctt caa gaa gca gtt cct aga			1248
Ile Lys Glu Ile Val Ile Val Asn Thr Leu Gln Glu Ala Val Pro Arg			
	405	410	415
gca tat gaa tta act gaa cca ggt gat gta ata cta ttt tca cct gca			1296
Ala Tyr Glu Leu Thr Glu Pro Gly Asp Val Ile Leu Phe Ser Pro Ala			
	420	425	430
tgt gct tca tgg gat caa ttt aga act ttc gaa gaa cgt ggc gat tac			1344
Cys Ala Ser Trp Asp Gln Phe Arg Thr Phe Glu Glu Arg Gly Asp Tyr			
	435	440	445

ttt gtt aga ttt gtt gag gaa tta aaa act aaa
 Phe Val Arg Phe Val Glu Glu Leu Lys Thr Lys
 450 455

1377

<210> 100
 <211> 459
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 100
 Met Lys Asp Ile Lys Thr Tyr Asp Asn Lys Asn Ile Leu Val Leu Gly
 1 5 10 15
 Leu Gly Lys Ser Gly Phe Ala Val Ser Glu Leu Leu Lys Leu Gly
 20 25 30
 Ala Asn Leu Thr Leu Asn Asp Lys Ala Asp Leu Asp Lys Asn Glu Lys
 35 40 45
 Ala Gln Glu Leu Lys Ala Lys Gly Val Arg Val Ile Gly Gly Tyr His
 50 55 60
 Pro Val Asp Leu Leu Glu Glu His Phe Asp Tyr Leu Val Lys Asn
 65 70 75 80
 Pro Gly Ile Pro Tyr Glu Asn Pro Met Val Lys Lys Ala Glu Glu Leu
 85 90 95
 Asp Ile Pro Ile Ile Thr Glu Pro Glu Val Ala Leu Ser Cys Ser Asp
 100 105 110
 Ala Pro Tyr Val Cys Ile Thr Gly Ser Asn Gly Lys Thr Thr Val
 115 120 125
 Met Leu Thr Gln Arg Ile Leu Asp His His Leu Gln Lys Thr Gly His
 130 135 140
 His Ala Tyr Ala Val Gly Asn Ile Gly Val Pro Ile Ser Glu Val Val
 145 150 155 160
 Pro Lys Ala Thr Lys Asp Asp Ile Leu Val Val Glu Ile Ser Ser Phe
 165 170 175
 Gln Leu Leu Gly Val Thr Asp Ile Lys Pro Lys Val Ala Ala Ile Val
 180 185 190
 Asp Ile Tyr Asn Asn Val His Leu Asp Tyr His Lys Thr Phe Glu Asn
 195 200 205
 Tyr Val Asp Ala Lys Leu Asn Val Thr Arg Thr Gln Asn Ser Asp Asp
 210 215 220
 Tyr Phe Ile Ala Asn Phe Asp Gln Lys Asp Ile Leu Ala Lys Glu Lys
 225 230 235 240
 Glu Val Ser Pro Ala Lys Met Gln Thr Phe Ser Glu Thr Asp His Asn
 245 250 255
 Ala Asp Tyr Phe Ile Gly Asp Glu Tyr Leu Glu Ser Gln Asp Glu Lys
 260 265 270
 Ile Met Lys Ile Ala Asp Ile Lys Leu Pro Gly Val His Asn Leu Gln
 275 280 285
 Asn Ser Leu Val Ala Ile Ala Ile Ala Lys Leu Met Gly Ala Asp Asn
 290 295 300
 Glu Asp Ile Ala Ala Val Leu Ser Thr Phe Thr Gly Ala Lys His Arg
 305 310 315 320
 Leu Gln Tyr Val Thr Thr Leu Asp Gly Arg Lys Ile Tyr Asn Asp Ser
 325 330 335
 Lys Ser Thr Asn Ile Glu Ala Ala Thr Val Ala Ile Pro Ala Phe Lys
 340 345 350
 Glu Pro Glu Val Leu Ile Ala Gly Gly Leu Asp Arg Gly Phe Thr Phe

```

          355          360          365
Asp Asp Leu Val Pro Leu Phe Lys Lys His Val Lys Ser Ile Val Leu
 370          375          380
Tyr Gly Glu Thr Lys Tyr Leu Leu Ala Asp Ala Arg Lys Ala Gly
385          390          395          400
Ile Lys Glu Ile Val Ile Val Asn Thr Leu Gln Glu Ala Val Pro Arg
          405          410          415
Ala Tyr Glu Leu Thr Glu Pro Gly Asp Val Ile Leu Phe Ser Pro Ala
          420          425          430
Cys Ala Ser Trp Asp Gln Phe Arg Thr Phe Glu Glu Arg Gly Asp Tyr
          435          440          445
Phe Val Arg Phe Val Glu Glu Leu Lys Thr Lys
 450          455

```

<210> 101

<211> 1104

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 809 -

p-N-acetylmuramoyl-pentapeptide-transferase (murG)

<220>

<221> CDS

<222> (1)...(1104)

<400> 101

```

atg aga gtt ata ttt aca ggt ggt ggc aca ggt ggt cac att tat cca 48
Met Arg Val Ile Phe Thr Gly Gly Gly Thr Gly Gly His Ile Tyr Pro
 1          5          10          15

atc atg gca att att gaa cgt ttg aaa gaa cgt ggc att agt aaa aac 96
Ile Met Ala Ile Ile Glu Arg Leu Lys Glu Arg Gly Ile Ser Lys Asn
          20          25          30

gat gaa atc tta ttt gta ggt aca caa aag gga tta gaa tca aaa att 144
Asp Glu Ile Leu Phe Val Gly Thr Gln Lys Gly Leu Glu Ser Lys Ile
          35          40          45

gtg cct gct gca ggt gtt aat ttt gaa aca atc caa att caa gga ttt 192
Val Pro Ala Ala Gly Val Asn Phe Glu Thr Ile Gln Ile Gln Gly Phe
          50          55          60

aat cgt aaa cac ccg tta aaa aat ttt gaa aca att aaa ttg ttc ttc 240
Asn Arg Lys His Pro Leu Lys Asn Phe Glu Thr Ile Lys Leu Phe Phe
          65          70          75          80

caa gct acc aag agc gca cgt aaa att ttg caa gaa ttt aaa ccc gat 288
Gln Ala Thr Lys Ser Ala Arg Lys Ile Leu Gln Glu Phe Lys Pro Asp
          85          90          95

gtc gtt tta ggt act ggt ggt tat gtg agt ggt gct atg gta tat gaa 336

```

Val Val Leu Gly Thr Gly Gly Tyr Val Ser Gly Ala Met Val Tyr Glu	
100 105 110	
gct gca aaa atg cat atc cct act atg att cat gaa tca aat tct gtt	384
Ala Ala Lys Met His Ile Pro Thr Met Ile His Glu Ser Asn Ser Val	
115 120 125	
gtc gga tta gct aat aaa ttc ttg ggg cat tat gtt gat aag att tgt	432
Val Gly Leu Ala Asn Lys Phe Leu Gly His Tyr Val Asp Lys Ile Cys	
130 135 140	
tat act ttt gat gac gca gct aaa gaa ttc cct gag aaa aag aaa ttg	480
Tyr Thr Phe Asp Asp Ala Ala Lys Glu Phe Pro Glu Lys Lys Lys Leu	
145 150 155 160	
gta aaa aca gga aat ccg cgt tca caa caa gtt tta ggt ctt cat gaa	528
Val Lys Thr Gly Asn Pro Arg Ser Gln Val Leu Gly Leu His Glu	
165 170 175	
gat aag gtg aac ttg caa aaa gaa tta ggc tta aat ccg caa atg cca	576
Asp Lys Val Asn Leu Gln Lys Glu Leu Gly Leu Asn Pro Gln Met Pro	
180 185 190	
act gtc tta gta ttt ggt gga tct cgt ggt gca tta gca att aac cga	624
Thr Val Leu Val Phe Gly Gly Ser Arg Gly Ala Leu Ala Ile Asn Arg	
195 200 205	
att atg ctt aaa tct ttg atg gaa ctt aag aaa aag cca tat caa att	672
Ile Met Leu Lys Ser Leu Met Glu Leu Lys Lys Lys Pro Tyr Gln Ile	
210 215 220	
att tgg gct act ggt acc tac tac ttt gat tct gtt caa aag aaa tta	720
Ile Trp Ala Thr Gly Thr Tyr Tyr Phe Asp Ser Val Gln Lys Lys Leu	
225 230 235 240	
gag ggc gtt gac tat ggt gat aac att aag att ttg cca tat att caa	768
Glu Gly Val Asp Tyr Gly Asp Asn Ile Lys Ile Leu Pro Tyr Ile Gln	
245 250 255	
aat atg cct gca tta ctt cca gaa atg aca tgt gtt gtt tca aga tct	816
Asn Met Pro Ala Leu Leu Pro Glu Met Thr Cys Val Val Ser Arg Ser	
260 265 270	
ggt gca aca agt ata gct gaa ttt act gct tta ggt gta cct gtc att	864
Gly Ala Thr Ser Ile Ala Glu Phe Thr Ala Leu Gly Val Pro Val Ile	
275 280 285	
tta att cct agt cca aat gta act cat aat cac caa atg aag aat gcg	912
Leu Ile Pro Ser Pro Asn Val Thr His Asn His Gln Met Lys Asn Ala	
290 295 300	
ctt gat tta caa aaa gca ggt gct gca tta gta att cct gaa gat gat	960
Leu Asp Leu Gln Lys Ala Gly Ala Ala Leu Val Ile Pro Glu Asp Asp	
305 310 315 320	
tta aat cct aat aat ttc gtt tct tct att gat cat att tta tta gat	1008
Leu Asn Pro Asn Asn Phe Val Ser Ser Ile Asp His Ile Leu Leu Asp	

	325		330		335	
gaa aaa tat gct aat gaa atg agt gaa gcc tca aaa gca ctt gga gta						1056
Glu Lys Tyr Ala Asn Glu Met Ser Glu Ala Ser Lys Ala Leu Gly Val						
	340		345		350	
cca gat gca tct gat caa gta att aaa gtg atg gaa gaa att tca cgc						1104
Pro Asp Ala Ser Asp Gln Val Ile Lys Val Met Glu Glu Ile Ser Arg						
	355		360		365	

<210> 102

<211> 368

<212> PRT

<213> Lactobacillus acidophilus

<400> 102

Met Arg Val Ile Phe Thr Gly Gly Gly Thr Gly Gly His Ile Tyr Pro																			
1				5					10									15	
Ile Met Ala Ile Ile Glu Arg Leu Lys Glu Arg Gly Ile Ser Lys Asn																			
			20					25										30	
Asp Glu Ile Leu Phe Val Gly Thr Gln Lys Gly Leu Glu Ser Lys Ile																			
			35				40											45	
Val Pro Ala Ala Gly Val Asn Phe Glu Thr Ile Gln Ile Gln Gly Phe																			
			50			55							60						
Asn Arg Lys His Pro Leu Lys Asn Phe Glu Thr Ile Lys Leu Phe Phe																			
					70							75							80
Gln Ala Thr Lys Ser Ala Arg Lys Ile Leu Gln Glu Phe Lys Pro Asp																			
				85					90										95
Val Val Leu Gly Thr Gly Gly Tyr Val Ser Gly Ala Met Val Tyr Glu																			
			100					105											110
Ala Ala Lys Met His Ile Pro Thr Met Ile His Glu Ser Asn Ser Val																			
			115				120												125
Val Gly Leu Ala Asn Lys Phe Leu Gly His Tyr Val Asp Lys Ile Cys																			
			130			135							140						
Tyr Thr Phe Asp Asp Ala Ala Lys Glu Phe Pro Glu Lys Lys Lys Leu																			
					150							155							160
Val Lys Thr Gly Asn Pro Arg Ser Gln Gln Val Leu Gly Leu His Glu																			
				165								170							175
Asp Lys Val Asn Leu Gln Lys Glu Leu Gly Leu Asn Pro Gln Met Pro																			
			180						185										190
Thr Val Leu Val Phe Gly Gly Ser Arg Gly Ala Leu Ala Ile Asn Arg																			
			195				200												205
Ile Met Leu Lys Ser Leu Met Glu Leu Lys Lys Lys Pro Tyr Gln Ile																			
			210				215												220
Ile Trp Ala Thr Gly Thr Tyr Tyr Phe Asp Ser Val Gln Lys Lys Leu																			
					230							235							240
Glu Gly Val Asp Tyr Gly Asp Asn Ile Lys Ile Leu Pro Tyr Ile Gln																			
				245								250							255
Asn Met Pro Ala Leu Leu Pro Glu Met Thr Cys Val Val Ser Arg Ser																			
			260						265										270
Gly Ala Thr Ser Ile Ala Glu Phe Thr Ala Leu Gly Val Pro Val Ile																			
			275				280												285
Leu Ile Pro Ser Pro Asn Val Thr His Asn His Gln Met Lys Asn Ala																			
			290				295												300
Leu Asp Leu Gln Lys Ala Gly Ala Ala Leu Val Ile Pro Glu Asp Asp																			

```

305          310          315          320
Leu Asn Pro Asn Asn Phe Val Ser Ser Ile Asp His Ile Leu Leu Asp
          325          330          335
Glu Lys Tyr Ala Asn Glu Met Ser Glu Ala Ser Lys Ala Leu Gly Val
          340          345          350
Pro Asp Ala Ser Asp Gln Val Ile Lys Val Met Glu Glu Ile Ser Arg
          355          360          365

```

<210> 103

<211> 966

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 806 -

p-N-acetylmuramoyl-pentapeptide-transferase (mraY)

<220>

<221> CDS

<222> (1)...(966)

<400> 103

```

atg agt att atg cta gca agt tgt att gct tta gtt agt tca cta gtg 48
Met Ser Ile Met Leu Ala Ser Cys Ile Ala Leu Val Ser Ser Leu Val
1          5          10          15

```

```

ttg acg gta att ttt tta cct gtc ttg att aat ttc atg cat tct cac 96
Leu Thr Val Ile Phe Leu Pro Val Leu Ile Asn Phe Met His Ser His
          20          25          30

```

```

cat gag ggg caa gaa att cgt gat gaa ggg cct aaa tgg cac caa aag 144
His Glu Gly Gln Glu Ile Arg Asp Glu Gly Pro Lys Trp His Gln Lys
          35          40          45

```

```

aag tca gga acg cct aca atg gga gga acc atc ttt gta att gcg gca 192
Lys Ser Gly Thr Pro Thr Met Gly Gly Thr Ile Phe Val Ile Ala Ala
          50          55          60

```

```

gtt atc tct gtt att tgg gta gct gcc tgg caa cat agt tta aac aaa 240
Val Ile Ser Val Ile Trp Val Ala Ala Trp Gln His Ser Leu Asn Lys
          65          70          75          80

```

```

gtt gtc tgg att tta gta atc agt tta tta gga tat gga att att ggt 288
Val Val Trp Ile Leu Val Ile Ser Leu Leu Gly Tyr Gly Ile Ile Gly
          85          90          95

```

```

ttt ctt gat gat ggt att aag ctt tac tat aag cgt aat ttg gga tta 336
Phe Leu Asp Asp Gly Ile Lys Leu Tyr Tyr Lys Arg Asn Leu Gly Leu
          100          105          110

```

```

aga gct tgg caa aag ttg gca ttg caa att att att gcc gtt gta att 384
Arg Ala Trp Gln Lys Leu Ala Leu Gln Ile Ile Ile Ala Val Val Ile
          115          120          125

```

```

gtc ttg att gcc tca agc gat cat ttt caa ttt ggt tta tat att cct 432
Val Leu Ile Ala Ser Ser Asp His Phe Gln Phe Gly Leu Tyr Ile Pro
130 135 140

ttt gca ggt gtt gtt cat agt att gca tta ttt act atc ttc att att 480
Phe Ala Gly Val Val His Ser Ile Ala Leu Phe Thr Ile Phe Ile Ile
145 150 155 160

ttc tgg ctg gtt ggt ttt tct aat gct gtt aac ctt tca gat ggt ctt 528
Phe Trp Leu Val Gly Phe Ser Asn Ala Val Asn Leu Ser Asp Gly Leu
165 170 175

gat ggt tta gca act ggt tta tca att gtg gca tat ggt aca tat gct 576
Asp Gly Leu Ala Thr Gly Leu Ser Ile Val Ala Tyr Gly Thr Tyr Ala
180 185 190

tat att gca ttt aaa caa aag aat ttt gcc gtt ttg gct ttt tgt atg 624
Tyr Ile Ala Phe Lys Gln Lys Asn Phe Ala Val Leu Ala Phe Cys Met
195 200 205

agt gtg atc ggt gga tta att gcc ttc ttt att ttt aac cat aag ccg 672
Ser Val Ile Gly Gly Leu Ile Ala Phe Phe Ile Phe Asn His Lys Pro
210 215 220

gct aaa atc ttt atg ggg gat gcg ggt tca ctt gct ctt ggt ggt gga 720
Ala Lys Ile Phe Met Gly Asp Ala Gly Ser Leu Ala Leu Gly Gly Gly
225 230 235 240

ctt gca acc gta agt att atg ctt aac aga cca tgg tca tta tta ctt 768
Leu Ala Thr Val Ser Ile Met Leu Asn Arg Pro Trp Ser Leu Leu Leu
245 250 255

atc ggt att gta ttt gtt tgt gaa act gct agt gta att tta cag gtt 816
Ile Gly Ile Val Phe Val Cys Glu Thr Ala Ser Val Ile Leu Gln Val
260 265 270

att tca ttc caa act aca ggt aag aga att ttt aag atg act cct att 864
Ile Ser Phe Gln Thr Thr Gly Lys Arg Ile Phe Lys Met Thr Pro Ile
275 280 285

cac cac cac ttt gaa atg ctt ggt tgg tca gaa tgg aaa gtt gat att 912
His His His Phe Glu Met Leu Gly Trp Ser Glu Trp Lys Val Asp Ile
290 295 300

gtc ttt tgg ctt gtt ggc tta att tgt agt att ttg tat tta gca att 960
Val Phe Trp Leu Val Gly Leu Ile Cys Ser Ile Leu Tyr Leu Ala Ile
305 310 315 320

tgg gga
Trp Gly 966

```

<210> 104

<211> 322

<212> PRT

<213> *Lactobacillus acidophilus*

<400> 104

```

Met Ser Ile Met Leu Ala Ser Cys Ile Ala Leu Val Ser Ser Leu Val
 1           5           10           15
Leu Thr Val Ile Phe Leu Pro Val Leu Ile Asn Phe Met His Ser His
 20           25           30
His Glu Gly Gln Glu Ile Arg Asp Glu Gly Pro Lys Trp His Gln Lys
 35           40           45
Lys Ser Gly Thr Pro Thr Met Gly Gly Thr Ile Phe Val Ile Ala Ala
 50           55           60
Val Ile Ser Val Ile Trp Val Ala Ala Trp Gln His Ser Leu Asn Lys
 65           70           75           80
Val Val Trp Ile Leu Val Ile Ser Leu Leu Gly Tyr Gly Ile Ile Gly
 85           90           95
Phe Leu Asp Asp Gly Ile Lys Leu Tyr Tyr Lys Arg Asn Leu Gly Leu
 100          105          110
Arg Ala Trp Gln Lys Leu Ala Leu Gln Ile Ile Ile Ala Val Val Ile
 115          120          125
Val Leu Ile Ala Ser Ser Asp His Phe Gln Phe Gly Leu Tyr Ile Pro
 130          135          140
Phe Ala Gly Val Val His Ser Ile Ala Leu Phe Thr Ile Phe Ile Ile
 145          150          155          160
Phe Trp Leu Val Gly Phe Ser Asn Ala Val Asn Leu Ser Asp Gly Leu
 165          170          175
Asp Gly Leu Ala Thr Gly Leu Ser Ile Val Ala Tyr Gly Thr Tyr Ala
 180          185          190
Tyr Ile Ala Phe Lys Gln Lys Asn Phe Ala Val Leu Ala Phe Cys Met
 195          200          205
Ser Val Ile Gly Gly Leu Ile Ala Phe Phe Ile Phe Asn His Lys Pro
 210          215          220
Ala Lys Ile Phe Met Gly Asp Ala Gly Ser Leu Ala Leu Gly Gly Gly
 225          230          235          240
Leu Ala Thr Val Ser Ile Met Leu Asn Arg Pro Trp Ser Leu Leu Leu
 245          250          255
Ile Gly Ile Val Phe Val Cys Glu Thr Ala Ser Val Ile Leu Gln Val
 260          265          270
Ile Ser Phe Gln Thr Thr Gly Lys Arg Ile Phe Lys Met Thr Pro Ile
 275          280          285
His His His Phe Glu Met Leu Gly Trp Ser Glu Trp Lys Val Asp Ile
 290          295          300
Val Phe Trp Leu Val Gly Leu Ile Cys Ser Ile Leu Tyr Leu Ala Ile
 305          310          315          320
Trp Gly

```

<210> 105

<211> 645

<212> DNA

<213> *Lactobacillus acidophilus*

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 527 - N-acetylmuramidase

<220> .

<221> CDS

<222> (1)...(645)

<400> 105

atg gca aaa aag cat aaa tca aga ata ccc aaa agt gta aaa att gtt	48
Met Ala Lys Lys His Lys Ser Arg Ile Pro Lys Ser Val Lys Ile Val	
1 5 10 15	
ggt cgc gca ttt att att ttg ttt gtc ttg ctt gta gcc ttt att ggc	96
Val Arg Ala Phe Ile Ile Leu Phe Val Leu Leu Val Ala Phe Ile Gly	
20 25 30	
ttt cgt tat tat aga aga tat gcg att caa tca gag cag att aga caa	144
Phe Arg Tyr Tyr Arg Arg Tyr Ala Ile Gln Ser Glu Gln Ile Arg Gln	
35 40 45	
gca cag ctg cag cga gaa caa gaa gca gca aaa tta tta aag cag aaa	192
Ala Gln Leu Gln Arg Glu Gln Glu Ala Ala Lys Leu Leu Lys Gln Lys	
50 55 60	
aaa gat ttt atc aaa aaa gtt ggc ccg att gca caa gca gta gat aag	240
Lys Asp Phe Ile Lys Lys Val Gly Pro Ile Ala Gln Ala Val Asp Lys	
65 70 75 80	
tca tac gat tta ttg ccg agt atc acg att gct caa gct tgc ctt gaa	288
Ser Tyr Asp Leu Leu Pro Ser Ile Thr Ile Ala Gln Ala Cys Leu Glu	
85 90 95	
agt aat tat ggt caa agt gat ttg tcg caa aaa tat aac aat ttg ttt	336
Ser Asn Tyr Gly Gln Ser Asp Leu Ser Gln Lys Tyr Asn Asn Leu Phe	
100 105 110	
ggc gtt aag ggg acc aat cca aat act tcg gct gtg atg acg acc aaa	384
Gly Val Lys Gly Thr Asn Pro Asn Thr Ser Ala Val Met Thr Thr Lys	
115 120 125	
gaa tat gtt aaa gga aag tgg atc act gtt aag gct cgt ttt caa ata	432
Glu Tyr Val Lys Gly Lys Trp Ile Thr Val Lys Ala Arg Phe Gln Ile	
130 135 140	
tat gac tca tat gag gct tca atc aga gcc cat gct aga tta ttc cag	480
Tyr Asp Ser Tyr Glu Ala Ser Ile Arg Ala His Ala Arg Leu Phe Gln	
145 150 155 160	
aat ggg aca acg tgg aat cac gac caa tat aag cac gtt tta gcg tct	528
Asn Gly Thr Thr Trp Asn His Asp Gln Tyr Lys His Val Leu Ala Ser	
165 170 175	
aaa gat tat aag aca cag gct aaa gca tta gta aca gat ggc tat gcg	576
Lys Asp Tyr Lys Thr Gln Ala Lys Ala Leu Val Thr Asp Gly Tyr Ala	
180 185 190	
acg gat cca gat tat gca gat aag ttg atc aat tta att gaa caa ttt	624
Thr Asp Pro Asp Tyr Ala Asp Lys Leu Ile Asn Leu Ile Glu Gln Phe	
195 200 205	

gat cta gaa aaa tat gat aag
 Asp Leu Glu Lys Tyr Asp Lys
 210 215

645

<210> 106
 <211> 215
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 106
 Met Ala Lys Lys His Lys Ser Arg Ile Pro Lys Ser Val Lys Ile Val
 1 5 10 15
 Val Arg Ala Phe Ile Ile Leu Phe Val Leu Leu Val Ala Phe Ile Gly
 20 25 30
 Phe Arg Tyr Tyr Arg Arg Tyr Ala Ile Gln Ser Glu Gln Ile Arg Gln
 35 40 45
 Ala Gln Leu Gln Arg Glu Gln Glu Ala Ala Lys Leu Leu Lys Gln Lys
 50 55 60
 Lys Asp Phe Ile Lys Lys Val Gly Pro Ile Ala Gln Ala Val Asp Lys
 65 70 75 80
 Ser Tyr Asp Leu Leu Pro Ser Ile Thr Ile Ala Gln Ala Cys Leu Glu
 85 90 95
 Ser Asn Tyr Gly Gln Ser Asp Leu Ser Gln Lys Tyr Asn Asn Leu Phe
 100 105 110
 Gly Val Lys Gly Thr Asn Pro Asn Thr Ser Ala Val Met Thr Thr Lys
 115 120 125
 Glu Tyr Val Lys Gly Lys Trp Ile Thr Val Lys Ala Arg Phe Gln Ile
 130 135 140
 Tyr Asp Ser Tyr Glu Ala Ser Ile Arg Ala His Ala Arg Leu Phe Gln
 145 150 155 160
 Asn Gly Thr Thr Trp Asn His Asp Gln Tyr Lys His Val Leu Ala Ser
 165 170 175
 Lys Asp Tyr Lys Thr Gln Ala Lys Ala Leu Val Thr Asp Gly Tyr Ala
 180 185 190
 Thr Asp Pro Asp Tyr Ala Asp Lys Leu Ile Asn Leu Ile Glu Gln Phe
 195 200 205
 Asp Leu Glu Lys Tyr Asp Lys
 210 215

<210> 107
 <211> 1227
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 176 - N-acetylmuramidase

<220>
 <221> CDS
 <222> (1)...(1227)

<400> 107

atg aag aag aga ctt ttg acc agc att gct agt gca gct atg ctg aca	48
Met Lys Lys Arg Leu Leu Thr Ser Ile Ala Ser Ala Ala Met Leu Thr	
1 5 10 15	
aca gta gct acc cca gta gtg aat aat gta atg atg act acc gct cat	96
Thr Val Ala Thr Pro Val Val Asn Asn Val Met Met Thr Thr Ala His	
20 25 30	
agc caa aag gtt tct gct gcc acc act gat gaa caa gct gct ttt ttg	144
Ser Gln Lys Val Ser Ala Ala Thr Asp Glu Gln Ala Ala Phe Leu	
35 40 45	
aac aag gct gcc aag caa gca gtt aaa gcc gct aag aaa tac gga act	192
Asn Lys Ala Ala Lys Gln Ala Val Lys Ala Ala Lys Lys Tyr Gly Thr	
50 55 60	
tat cca tca gtt atg att gca caa gcc atc tta gaa tct ggc tgg gga	240
Tyr Pro Ser Val Met Ile Ala Gln Ala Ile Leu Glu Ser Gly Trp Gly	
65 70 75 80	
caa tca gcc ctt gca act gaa gct aac aac ctt ttt ggt atg aag gct	288
Gln Ser Ala Leu Ala Thr Glu Ala Asn Asn Leu Phe Gly Met Lys Ala	
85 90 95	
gat gat agc tgg cca ggt gag act tat tct gct aag act aga gaa gaa	336
Asp Asp Ser Trp Pro Gly Glu Thr Tyr Ser Ala Lys Thr Arg Glu Glu	
100 105 110	
ggc acc aac ggt aag agt tac tat att gta gct aaa ttt aga aaa tat	384
Gly Thr Asn Gly Lys Ser Tyr Tyr Ile Val Ala Lys Phe Arg Lys Tyr	
115 120 125	
aac tca ttt gaa gaa tca ttt gaa gat aat ggc aag aaa ctt cgt gaa	432
Asn Ser Phe Glu Glu Ser Phe Glu Asp Asn Gly Lys Lys Leu Arg Glu	
130 135 140	
ggc gtg tct tgg caa ccg ctt cgc tat aag gga act tgg ctt gaa aat	480
Gly Val Ser Trp Gln Pro Leu Arg Tyr Lys Gly Thr Trp Leu Glu Asn	
145 150 155 160	
gcc aat act tat gct gat gca acg aag tct tta act ggt act tac gcc	528
Ala Asn Thr Tyr Ala Asp Ala Thr Lys Ser Leu Thr Gly Thr Tyr Ala	
165 170 175	
act gat agt aag tat gac agt tca ctt aac tca aga att acc gat cat	576
Thr Asp Ser Lys Tyr Asp Ser Ser Leu Asn Ser Arg Ile Thr Asp His	
180 185 190	
aat ttg aac caa tat gat cca att gtt tcg aaa act gct aag gtt tac	624
Asn Leu Asn Gln Tyr Asp Pro Ile Val Ser Lys Thr Ala Lys Val Tyr	
195 200 205	
acc gta tct aag tca ggc tca gtt tat aat tgg cca act gac cac tca	672
Thr Val Ser Lys Ser Gly Ser Val Tyr Asn Trp Pro Thr Asp His Ser	
210 215 220	

```

gta gct agc cct gtt gga act gtt aag aag ggc gag agg gtt gtt gca 720
Val Ala Ser Pro Val Gly Thr Val Lys Lys Gly Glu Arg Val Val Ala
225                230                235                240

act aag act att acc tat aat gac ggt tca act cgt atg tac ctt gaa 768
Thr Lys Thr Ile Thr Tyr Asn Asp Gly Ser Thr Arg Met Tyr Leu Glu
                245                250                255

ggg aaa ggc tgg att aac ggt act tca ctt ggt aag ggt aat tct aag 816
Gly Lys Gly Trp Ile Asn Gly Thr Ser Leu Gly Lys Gly Asn Ser Lys
                260                265                270

agt agc gaa cca atc act caa gca cct aag ggc gca act aag gta gac 864
Ser Ser Glu Pro Ile Thr Gln Ala Pro Lys Gly Ala Thr Lys Val Asp
                275                280                285

aag acc tta atg cac aat gcc tac gtt tac gat aac aag ggt aca aag 912
Lys Thr Leu Met His Asn Ala Tyr Val Tyr Asp Asn Lys Gly Thr Lys
290                295                300

att aag ggt aag atg ttc aag ctt aac gaa gaa gaa gat gtt aag atg 960
Ile Lys Gly Lys Met Phe Lys Leu Asn Glu Glu Glu Asp Val Lys Met
305                310                315                320

atc agt acc tat ggc aca aag act att aag ggt aag act tac tac cgt 1008
Ile Ser Thr Tyr Gly Thr Lys Thr Ile Lys Gly Lys Thr Tyr Tyr Arg
                325                330                335

gta ggc gag aat gaa tac att gca gcc ggc aac att gac ggt acg ctt 1056
Val Gly Glu Asn Glu Tyr Ile Ala Ala Gly Asn Ile Asp Gly Thr Leu
                340                345                350

aaa ttc tta aag cgt aat tct tac gtc tat aac caa tac ggc aat cgc 1104
Lys Phe Leu Lys Arg Asn Ser Tyr Val Tyr Asn Gln Tyr Gly Asn Arg
                355                360                365

gat aac agt ttg aag cgc aag aag aac gaa caa gtt gct acc tac ggt 1152
Asp Asn Ser Leu Lys Arg Lys Lys Asn Glu Gln Val Ala Thr Tyr Gly
                370                375                380

gca gca gtt act att aac ggt aag aag tat tac aga atc ggt att cgc 1200
Ala Ala Val Thr Ile Asn Gly Lys Lys Tyr Tyr Arg Ile Gly Ile Arg
385                390                395                400

caa tac att aaa aaa gct aac ttc atg 1227
Gln Tyr Ile Lys Lys Ala Asn Phe Met
                405

```

<210> 108

<211> 409

<212> PRT

<213> Lactobacillus acidophilus

<400> 108

```

Met Lys Lys Arg Leu Leu Thr Ser Ile Ala Ser Ala Ala Met Leu Thr
1          5          10          15

```

```

Thr Val Ala Thr Pro Val Val Asn Asn Val Met Met Thr Thr Ala His
      20      25      30
Ser Gln Lys Val Ser Ala Ala Thr Thr Asp Glu Gln Ala Ala Phe Leu
      35      40      45
Asn Lys Ala Ala Lys Gln Ala Val Lys Ala Ala Lys Lys Tyr Gly Thr
      50      55      60
Tyr Pro Ser Val Met Ile Ala Gln Ala Ile Leu Glu Ser Gly Trp Gly
      65      70      75      80
Gln Ser Ala Leu Ala Thr Glu Ala Asn Asn Leu Phe Gly Met Lys Ala
      85      90      95
Asp Asp Ser Trp Pro Gly Glu Thr Tyr Ser Ala Lys Thr Arg Glu Glu
      100      105      110
Gly Thr Asn Gly Lys Ser Tyr Tyr Ile Val Ala Lys Phe Arg Lys Tyr
      115      120      125
Asn Ser Phe Glu Glu Ser Phe Glu Asp Asn Gly Lys Lys Leu Arg Glu
      130      135      140
Gly Val Ser Trp Gln Pro Leu Arg Tyr Lys Gly Thr Trp Leu Glu Asn
      145      150      155      160
Ala Asn Thr Tyr Ala Asp Ala Thr Lys Ser Leu Thr Gly Thr Tyr Ala
      165      170      175
Thr Asp Ser Lys Tyr Asp Ser Ser Leu Asn Ser Arg Ile Thr Asp His
      180      185      190
Asn Leu Asn Gln Tyr Asp Pro Ile Val Ser Lys Thr Ala Lys Val Tyr
      195      200      205
Thr Val Ser Lys Ser Gly Ser Val Tyr Asn Trp Pro Thr Asp His Ser
      210      215      220
Val Ala Ser Pro Val Gly Thr Val Lys Lys Gly Glu Arg Val Val Ala
      225      230      235      240
Thr Lys Thr Ile Thr Tyr Asn Asp Gly Ser Thr Arg Met Tyr Leu Glu
      245      250      255
Gly Lys Gly Trp Ile Asn Gly Thr Ser Leu Gly Lys Gly Asn Ser Lys
      260      265      270
Ser Ser Glu Pro Ile Thr Gln Ala Pro Lys Gly Ala Thr Lys Val Asp
      275      280      285
Lys Thr Leu Met His Asn Ala Tyr Val Tyr Asp Asn Lys Gly Thr Lys
      290      295      300
Ile Lys Gly Lys Met Phe Lys Leu Asn Glu Glu Glu Asp Val Lys Met
      305      310      315      320
Ile Ser Thr Tyr Gly Thr Lys Thr Ile Lys Gly Lys Thr Tyr Tyr Arg
      325      330      335
Val Gly Glu Asn Glu Tyr Ile Ala Ala Gly Asn Ile Asp Gly Thr Leu
      340      345      350
Lys Phe Leu Lys Arg Asn Ser Tyr Val Tyr Asn Gln Tyr Gly Asn Arg
      355      360      365
Asp Asn Ser Leu Lys Arg Lys Lys Asn Glu Gln Val Ala Thr Tyr Gly
      370      375      380
Ala Ala Val Thr Ile Asn Gly Lys Lys Tyr Tyr Arg Ile Gly Ile Arg
      385      390      395      400
Gln Tyr Ile Lys Lys Ala Asn Phe Met
      405

```

<210> 109

<211> 459

<212> DNA

<213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 966 - N-acetylmuramidase

<220>
 <221> CDS
 <222> (1)...(459)

<400> 109
 atg gat aaa aaa tca act gga cca tac cag cat tat gaa cgg cct act 48
 Met Asp Lys Lys Ser Thr Gly Pro Tyr Gln His Tyr Glu Arg Pro Thr
 1 5 10 15

aag aag agg agc tca caa gat aag caa ccg aga ggc tca gcc cgc tgg 96
 Lys Lys Arg Ser Ser Gln Asp Lys Gln Pro Arg Gly Ser Ala Arg Trp
 20 25 30

att gca gtt att gta att tta gca gtt att ttg att act ctt att cca 144
 Ile Ala Val Ile Val Ile Leu Ala Val Ile Leu Ile Thr Leu Ile Pro
 35 40 45

gct gtt cat cgc ttg gct tca aag cac tct caa aaa gct gag gaa gtt 192
 Ala Val His Arg Leu Ala Ser Lys His Ser Gln Lys Ala Glu Glu Val
 50 55 60

caa act ctt aaa aag gtt tct tct agt tct gct aaa tca tca aaa gaa 240
 Gln Thr Leu Lys Lys Val Ser Ser Ser Ser Ala Lys Ser Ser Lys Glu
 65 70 75 80

aag aaa act tcg tct tct tca gct aaa aag agt tcg tca caa tct agt 288
 Lys Lys Thr Ser Ser Ser Ser Ala Lys Lys Ser Ser Ser Gln Ser Ser
 85 90 95

tca agc tca agc tcg tct aaa gag aca aca cct aag act tat act gtt 336
 Ser Ser Ser Ser Ser Ser Lys Glu Thr Thr Pro Lys Thr Tyr Thr Val
 100 105 110

caa aca ggt gat act tta act agt att gca gag caa tat ggt atg aca 384
 Gln Thr Gly Asp Thr Leu Thr Ser Ile Ala Glu Gln Tyr Gly Met Thr
 115 120 125

gtt gat caa tta gcc aga tta aat aat ctt gaa gac tct tca aac gtc 432
 Val Asp Gln Leu Ala Arg Leu Asn Asn Leu Glu Asp Ser Ser Asn Val
 130 135 140

aat att ggc caa aca ctt aag ttg aaa 459
 Asn Ile Gly Gln Thr Leu Lys Leu Lys
 145 150

<210> 110
 <211> 153
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 110

```

Met Asp Lys Lys Ser Thr Gly Pro Tyr Gln His Tyr Glu Arg Pro Thr
 1          5          10          15
Lys Lys Arg Ser Ser Gln Asp Lys Gln Pro Arg Gly Ser Ala Arg Trp
      20          25          30
Ile Ala Val Ile Val Ile Leu Ala Val Ile Leu Ile Thr Leu Ile Pro
 35          40          45
Ala Val His Arg Leu Ala Ser Lys His Ser Gln Lys Ala Glu Glu Val
 50          55          60
Gln Thr Leu Lys Lys Val Ser Ser Ser Ser Ala Lys Ser Ser Lys Glu
65          70          75          80
Lys Lys Thr Ser Ser Ser Ser Ala Lys Lys Ser Ser Ser Gln Ser Ser
      85          90          95
Ser Ser Ser Ser Ser Ser Lys Glu Thr Thr Pro Lys Thr Tyr Thr Val
      100          105          110
Gln Thr Gly Asp Thr Leu Thr Ser Ile Ala Glu Gln Tyr Gly Met Thr
      115          120          125
Val Asp Gln Leu Ala Arg Leu Asn Asn Leu Glu Asp Ser Ser Asn Val
      130          135          140
Asn Ile Gly Gln Thr Leu Lys Leu Lys
145          150

```

<210> 111

<211> 1080

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 137 - d-alanine-d-alanine ligase

<220>

<221> CDS

<222> (1)...(1080)

<400> 111

```

atg act aaa aaa ata caa gtc gga tta att ttt ggt ggt aac tca tca      48
Met Thr Lys Lys Ile Gln Val Gly Leu Ile Phe Gly Gly Asn Ser Ser
 1          5          10          15

gaa tat gaa gta tca atc gtt tca ggt cat aat att tat aag gca att      96
Glu Tyr Glu Val Ser Ile Val Ser Gly His Asn Ile Tyr Lys Ala Ile
      20          25          30

gat aaa gat aaa ttt gat gta cat cca att tgg att act aat gaa gga      144
Asp Lys Asp Lys Phe Asp Val His Pro Ile Trp Ile Thr Asn Glu Gly
      35          40          45

tac ttt gca agt gaa gaa gaa agc ttc aaa gtc tta gaa gat cct tcg      192
Tyr Phe Ala Ser Glu Glu Glu Ser Phe Lys Val Leu Glu Asp Pro Ser
      50          55          60

tat caa gtg gaa aat cca cat aag gta aat aat att tca aat att att      240
Tyr Gln Val Glu Asn Pro His Lys Val Asn Asn Ile Ser Asn Ile Ile

```

65	70	75	80	
gaa ttg aag aat tta cca gag att gat gta ttc ttc cca att gtt cac				288
Glu Leu Lys Asn Leu Pro Glu Ile Asp Val Phe Phe Pro Ile Val His	85	90	95	
ggt aat tta ggt gaa gat ggg gtc tta cag gga ttg ttt cgc ttg atg				336
Gly Asn Leu Gly Glu Asp Gly Val Leu Gln Gly Leu Phe Arg Leu Met	100	105	110	
aac aag cca ttt gta ggt gac gat gtc tta gct gca gct gca act atg				384
Asn Lys Pro Phe Val Gly Asp Asp Val Leu Ala Ala Ala Thr Met	115	120	125	
gat aag gaa ttt acc aag att tta gct caa aga gtt ggt gtt cca gta				432
Asp Lys Glu Phe Thr Lys Ile Leu Ala Gln Arg Val Gly Val Pro Val	130	135	140	
gct gat tgg att tca atc aag cgt ttt gaa tac gat gat aag aat aat				480
Ala Asp Trp Ile Ser Ile Lys Arg Phe Glu Tyr Asp Asp Lys Asn Asn	145	150	155	160
gat aaa ctt aat tat gaa aaa gta gct gaa aag ctt ggt cat gat atg				528
Asp Lys Leu Asn Tyr Glu Lys Val Ala Glu Lys Leu Gly His Asp Met	165	170	175	
ttt gta aaa cca tct aac caa ggt tca tca gtt ggc gtt aac cat gta				576
Phe Val Lys Pro Ser Asn Gln Gly Ser Ser Val Gly Val Asn His Val	180	185	190	
act aat gct gaa gaa tat gct gca gca tta gaa gaa gca ttc aag tac				624
Thr Asn Ala Glu Glu Tyr Ala Ala Ala Leu Glu Glu Ala Phe Lys Tyr	195	200	205	
gat gat aag gtt tta gtt gaa gaa act gtt cct ggc acc gaa gtt gaa				672
Asp Asp Lys Val Leu Val Glu Glu Thr Val Pro Gly Thr Glu Val Glu	210	215	220	
act gct gtc ctt ggc aac gat aag cca att gta gca ggt gtt gga caa				720
Thr Ala Val Leu Gly Asn Asp Lys Pro Ile Val Ala Gly Val Gly Gln	225	230	235	240
atc acc aat gca aaa ggc tca ttc tat act tac gaa aat aag tat gat				768
Ile Thr Asn Ala Lys Gly Ser Phe Tyr Thr Tyr Glu Asn Lys Tyr Asp	245	250	255	
gat aat tca act tct aag ttg caa att cct gca gat tta cca caa gat				816
Asp Asn Ser Thr Ser Lys Leu Gln Ile Pro Ala Asp Leu Pro Gln Asp	260	265	270	
att gtt gat act gtc aga gaa aat gct cgg aag gtt tac gaa att act				864
Ile Val Asp Thr Val Arg Glu Asn Ala Arg Lys Val Tyr Glu Ile Thr	275	280	285	
gaa tgt agt ggt atg gca aga att gat tct atg ctt act cca gat ggt				912
Glu Cys Ser Gly Met Ala Arg Ile Asp Ser Met Leu Thr Pro Asp Gly	290	295	300	

```

aaa gta gta tta act gaa gtg aat gca ctt cct ggt ttt act aat atc   960
Lys Val Val Leu Thr Glu Val Asn Ala Leu Pro Gly Phe Thr Asn Ile
305                      310                      315                      320

agt atg tat cct aag tta ttc gaa gaa gct ggt att cct tac act gaa   1008
Ser Met Tyr Pro Lys Leu Phe Glu Glu Ala Gly Ile Pro Tyr Thr Glu
                      325                      330                      335

ttg att act cgc tta atc caa gca ggt atg gat cgt ttt gac cac aag   1056
Leu Ile Thr Arg Leu Ile Gln Ala Gly Met Asp Arg Phe Asp His Lys
                      340                      345                      350

aag aca ttg ctt cac aag cat gat                                   1080
Lys Thr Leu Leu His Lys His Asp
                      355                      360

```

```

<210> 112
<211> 360
<212> PRT
<213> Lactobacillus acidophilus

```

```

<400> 112
Met Thr Lys Lys Ile Gln Val Gly Leu Ile Phe Gly Gly Asn Ser Ser
1                      5                      10                      15
Glu Tyr Glu Val Ser Ile Val Ser Gly His Asn Ile Tyr Lys Ala Ile
20                      25                      30
Asp Lys Asp Lys Phe Asp Val His Pro Ile Trp Ile Thr Asn Glu Gly
35                      40                      45
Tyr Phe Ala Ser Glu Glu Glu Ser Phe Lys Val Leu Glu Asp Pro Ser
50                      55                      60
Tyr Gln Val Glu Asn Pro His Lys Val Asn Asn Ile Ser Asn Ile Ile
65                      70                      75                      80
Glu Leu Lys Asn Leu Pro Glu Ile Asp Val Phe Phe Pro Ile Val His
85                      90                      95
Gly Asn Leu Gly Glu Asp Gly Val Leu Gln Gly Leu Phe Arg Leu Met
100                      105                      110
Asn Lys Pro Phe Val Gly Asp Asp Val Leu Ala Ala Ala Thr Met
115                      120                      125
Asp Lys Glu Phe Thr Lys Ile Leu Ala Gln Arg Val Gly Val Pro Val
130                      135                      140
Ala Asp Trp Ile Ser Ile Lys Arg Phe Glu Tyr Asp Asp Lys Asn Asn
145                      150                      155                      160
Asp Lys Leu Asn Tyr Glu Lys Val Ala Glu Lys Leu Gly His Asp Met
165                      170                      175
Phe Val Lys Pro Ser Asn Gln Gly Ser Ser Val Gly Val Asn His Val
180                      185                      190
Thr Asn Ala Glu Glu Tyr Ala Ala Ala Leu Glu Glu Ala Phe Lys Tyr
195                      200                      205
Asp Asp Lys Val Leu Val Glu Glu Thr Val Pro Gly Thr Glu Val Glu
210                      215                      220
Thr Ala Val Leu Gly Asn Asp Lys Pro Ile Val Ala Gly Val Gly Gln
225                      230                      235                      240
Ile Thr Asn Ala Lys Gly Ser Phe Tyr Thr Tyr Glu Asn Lys Tyr Asp
245                      250                      255
Asp Asn Ser Thr Ser Lys Leu Gln Ile Pro Ala Asp Leu Pro Gln Asp

```

```

                260                265                270
Ile Val Asp Thr Val Arg Glu Asn Ala Arg Lys Val Tyr Glu Ile Thr
                275                280                285
Glu Cys Ser Gly Met Ala Arg Ile Asp Ser Met Leu Thr Pro Asp Gly
                290                295                300
Lys Val Val Leu Thr Glu Val Asn Ala Leu Pro Gly Phe Thr Asn Ile
305                310                315                320
Ser Met Tyr Pro Lys Leu Phe Glu Glu Ala Gly Ile Pro Tyr Thr Glu
                325                330                335
Leu Ile Thr Arg Leu Ile Gln Ala Gly Met Asp Arg Phe Asp His Lys
                340                345                350
Lys Thr Leu Leu His Lys His Asp
                355                360

```

<210> 113

<211> 981

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1852 - d-ala,d-ala ligase

<220>

<221> CDS

<222> (1)...(981)

<400> 113

```

atg gca cat atg tct agg cga gaa tat cgc atg aaa aaa gaa cat gga      48
Met Ala His Met Ser Arg Arg Glu Tyr Arg Met Lys Lys Glu His Gly
  1                5                10                15

caa tct ggt gct agt caa tcg cga att aat tat tct aaa aat aag ata      96
Gln Ser Gly Ala Ser Gln Ser Arg Ile Asn Tyr Ser Lys Asn Lys Ile
                20                25                30

act agt cgt gaa gaa ttt aga agt aaa aag att agc aat cct gcg cca      144
Thr Ser Arg Glu Glu Phe Arg Ser Lys Lys Ile Ser Asn Pro Ala Pro
                35                40                45

att aac aat gtg aat gtg gct aat gct aca aga gaa aat tat aat cat      192
Ile Asn Asn Val Asn Val Ala Asn Ala Thr Arg Glu Asn Tyr Asn His
                50                55                60

gtc aaa ctt aac ttt tgg aat att ttc tct gat agg cca tat gtc tct      240
Val Lys Leu Asn Phe Trp Asn Ile Phe Ser Asp Arg Pro Tyr Val Ser
        65                70                75                80

gta aca ata att gtg ttg gct ttg ttc ttt att atg atc aaa ctg tgg      288
Val Thr Ile Ile Val Leu Ala Leu Phe Phe Ile Met Ile Lys Leu Trp
                85                90                95

tgg gga ctc att gtg ctg ctt att gct gtc ata gct ggt att tat gtg      336
Trp Gly Leu Ile Val Leu Leu Ile Ala Val Ile Ala Gly Ile Tyr Val

```

100	105	110	
ata gga cgt agt cat cat cct aac cgt gtg ctg agt cta gag ttt cat			384
Ile Gly Arg Ser His His Pro Asn Arg Val Leu Ser Leu Glu Phe His			
115	120	125	
atg aaa gct tct aga aaa ctt agt atg ctt aga gcc ttt gaa tta ggt			432
Met Lys Ala Ser Arg Lys Leu Ser Met Leu Arg Ala Phe Glu Leu Gly			
130	135	140	
ggc tct gtt gtt atg ttt tta gca act tat atg aaa caa gtg gtt tct			480
Gly Ser Val Val Met Phe Leu Ala Thr Tyr Met Lys Gln Val Val Ser			
145	150	155	160
gta gat ttc tca tca gca gga tca acc gat agt ttc caa att att caa			528
Val Asp Phe Ser Ser Ala Gly Ser Thr Asp Ser Phe Gln Ile Ile Gln			
	165	170	175
ggg atg ctg tct aat aat ggt ggt tat tat ggt caa cgt gga tca tat			576
Gly Met Leu Ser Asn Asn Gly Gly Tyr Tyr Gly Gln Arg Gly Ser Tyr			
	180	185	190
ttc ttg aat ttg ctt aat aca gta act ggt ggg cag tta tgg agc tct			624
Phe Leu Asn Leu Leu Asn Thr Val Thr Gly Gly Gln Leu Trp Ser Ser			
	195	200	205
tat cgg tat gca acc aat agt gca caa atg atg agt agt aat tca gga			672
Tyr Arg Tyr Ala Thr Asn Ser Ala Gln Met Met Ser Ser Asn Ser Gly			
210	215	220	
aga tgg att att att tgg atc atg ctt ttg atg att gct cca gca ttt			720
Arg Trp Ile Ile Ile Trp Ile Met Leu Leu Met Ile Ala Pro Ala Phe			
225	230	235	240
tgt gtg ttg gca cag ttc ttt aaa gag cca tat tca aga aat gca aca			768
Cys Val Leu Ala Gln Phe Phe Lys Glu Pro Tyr Ser Arg Asn Ala Thr			
	245	250	255
tta gtt act tca ttg atc act acg gta agt ttt gta tta act cct gtt			816
Leu Val Thr Ser Leu Ile Thr Thr Val Ser Phe Val Leu Thr Pro Val			
	260	265	270
tta atg aga aga tgg gta gta ggt tat gca atg gaa aat caa atg gca			864
Leu Met Arg Arg Trp Val Val Gly Tyr Ala Met Glu Asn Gln Met Ala			
	275	280	285
aga gaa gca gcc aac aat gca gtt cat att ggt acc atg gcg tat gtt			912
Arg Glu Ala Ala Asn Asn Ala Val His Ile Gly Thr Met Ala Tyr Val			
	290	295	300
ggg atg ggg tgc tca att atg gtt ttg att att gca att tat cgt ttt			960
Gly Met Gly Cys Ser Ile Met Val Leu Ile Ile Ala Ile Tyr Arg Phe			
305	310	315	320
gtt aaa caa gat aat ttt gaa			981
Val Lys Gln Asp Asn Phe Glu			
	325		

<210> 114
 <211> 327
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 114
 Met Ala His Met Ser Arg Arg Glu Tyr Arg Met Lys Lys Glu His Gly
 1 5 10 15
 Gln Ser Gly Ala Ser Gln Ser Arg Ile Asn Tyr Ser Lys Asn Lys Ile
 20 25 30
 Thr Ser Arg Glu Glu Phe Arg Ser Lys Lys Ile Ser Asn Pro Ala Pro
 35 40 45
 Ile Asn Asn Val Asn Val Ala Asn Ala Thr Arg Glu Asn Tyr Asn His
 50 55 60
 Val Lys Leu Asn Phe Trp Asn Ile Phe Ser Asp Arg Pro Tyr Val Ser
 65 70 75 80
 Val Thr Ile Ile Val Leu Ala Leu Phe Phe Ile Met Ile Lys Leu Trp
 85 90 95
 Trp Gly Leu Ile Val Leu Leu Ile Ala Val Ile Ala Gly Ile Tyr Val
 100 105 110
 Ile Gly Arg Ser His His Pro Asn Arg Val Leu Ser Leu Glu Phe His
 115 120 125
 Met Lys Ala Ser Arg Lys Leu Ser Met Leu Arg Ala Phe Glu Leu Gly
 130 135 140
 Gly Ser Val Val Met Phe Leu Ala Thr Tyr Met Lys Gln Val Val Ser
 145 150 155 160
 Val Asp Phe Ser Ser Ala Gly Ser Thr Asp Ser Phe Gln Ile Ile Gln
 165 170 175
 Gly Met Leu Ser Asn Asn Gly Gly Tyr Tyr Gly Gln Arg Gly Ser Tyr
 180 185 190
 Phe Leu Asn Leu Leu Asn Thr Val Thr Gly Gly Gln Leu Trp Ser Ser
 195 200 205
 Tyr Arg Tyr Ala Thr Asn Ser Ala Gln Met Met Ser Ser Asn Ser Gly
 210 215 220
 Arg Trp Ile Ile Ile Trp Ile Met Leu Leu Met Ile Ala Pro Ala Phe
 225 230 235 240
 Cys Val Leu Ala Gln Phe Phe Lys Glu Pro Tyr Ser Arg Asn Ala Thr
 245 250 255
 Leu Val Thr Ser Leu Ile Thr Thr Val Ser Phe Val Leu Thr Pro Val
 260 265 270
 Leu Met Arg Arg Trp Val Val Gly Tyr Ala Met Glu Asn Gln Met Ala
 275 280 285
 Arg Glu Ala Ala Asn Asn Ala Val His Ile Gly Thr Met Ala Tyr Val
 290 295 300
 Gly Met Gly Cys Ser Ile Met Val Leu Ile Ile Ala Ile Tyr Arg Phe
 305 310 315 320
 Val Lys Gln Asp Asn Phe Glu
 325

<210> 115
 <211> 1365
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 266 - d-ala-d-ala adding enzyme

<220>
 <221> CDS
 <222> (1)...(1365)

<400> 115
 atg aaa atg caa atg gct gaa att gcc aaa gct tta gat aag act tgt 48
 Met Lys Met Gln Met Ala Glu Ile Ala Lys Ala Leu Asp Lys Thr Cys
 1 5 10 15
 gaa ggt gac gat aaa aca gtt att act tct gtt gcc ttt gac tcc aga 96
 Glu Gly Asp Asp Lys Thr Val Ile Thr Ser Val Ala Phe Asp Ser Arg
 20 25 30
 aag atc aca aat ggt gga tta ttt gta cca ctt gaa ggt gaa cgt gat 144
 Lys Ile Thr Asn Gly Gly Leu Phe Val Pro Leu Glu Gly Glu Arg Asp
 35 40 45
 gga cat gat ttt gtg gct ggt gct att agt aat ggt gct tct gct act 192
 Gly His Asp Phe Val Ala Gly Ala Ile Ser Asn Gly Ala Ser Ala Thr
 50 55 60
 ttg tgg aaa aag ggg cat cca aat aaa cct gaa ggt att gca gta att 240
 Leu Trp Lys Lys Gly His Pro Asn Lys Pro Glu Gly Ile Ala Val Ile
 65 70 75 80
 gaa gtt gat gat cca ctt gcc gct atg cag aca ctt gct cgt tat tat 288
 Glu Val Asp Asp Pro Leu Ala Ala Met Gln Thr Leu Ala Arg Tyr Tyr
 85 90 95
 ttg cgt aaa gtt aat cca act gta gtg gga att act ggt tca aat ggt 336
 Leu Arg Lys Val Asn Pro Thr Val Val Gly Ile Thr Gly Ser Asn Gly
 100 105 110
 aag acc act act aag gat atg atc gct gca gtt tta tca aag cgt ttc 384
 Lys Thr Thr Thr Lys Asp Met Ile Ala Ala Val Leu Ser Lys Arg Phe
 115 120 125
 aac gta cat aag act caa gct aat ttt aat aat gaa atc ggc gtg cca 432
 Asn Val His Lys Thr Gln Ala Asn Phe Asn Asn Glu Ile Gly Val Pro
 130 135 140
 atg acc gtt ctt gaa atg aag cca aat act gaa att ttg gtt ctt gaa 480
 Met Thr Val Leu Glu Met Lys Pro Asn Thr Glu Ile Leu Val Leu Glu
 145 150 155 160
 atg gga atg gat aga cca gga caa tta cat cac tta agt gaa ttg act 528
 Met Gly Met Asp Arg Pro Gly Gln Leu His His Leu Ser Glu Leu Thr
 165 170 175
 cgt cct gat gta gct gta att acc atg att ggt gaa gct cat att gag 576
 Arg Pro Asp Val Ala Val Ile Thr Met Ile Gly Glu Ala His Ile Glu

180	185	190	
ttc ttc ggt agt cgt gat aag att gct gac gct aag atg gag atc act	624		
Phe Phe Gly Ser Arg Asp Lys Ile Ala Asp Ala Lys Met Glu Ile Thr			
195	200	205	
gat ttt ctc cgt gaa gat gga gaa ttt att tat aat ggt gat gaa cca	672		
Asp Phe Leu Arg Glu Asp Gly Glu Phe Ile Tyr Asn Gly Asp Glu Pro			
210	215	220	
tta ctt caa gaa aga gct aag aag ctt gat caa gct aaa gca act ttt	720		
Leu Leu Gln Glu Arg Ala Lys Lys Leu Asp Gln Ala Lys Ala Thr Phe			
225	230	235	240
ggt ttt gaa gat gat gac acg gtt cat gct act ggt ttt aag agt tac	768		
Gly Phe Glu Asp Asp Asp Thr Val His Ala Thr Gly Phe Lys Ser Tyr			
	245	250	255
atg cat cat gcg act ttt aca att aat gat tca gag cag aaa ttc tct	816		
Met His His Ala Thr Phe Thr Ile Asn Asp Ser Glu Gln Lys Phe Ser			
	260	265	270
att cca atg atc ggt aag cat aat gtt tct aat gct atg gct gct att	864		
Ile Pro Met Ile Gly Lys His Asn Val Ser Asn Ala Met Ala Ala Ile			
	275	280	285
agt gtt gga cgt cat ttt ggt gaa agt gat gag gaa att gcg tca tcg	912		
Ser Val Gly Arg His Phe Gly Glu Ser Asp Glu Ile Ala Ser Ser			
	290	295	300
ttg tct aac ttt aag cca acc gct aat cgt atg gaa tgg gaa aaa ggc	960		
Leu Ser Asn Phe Lys Pro Thr Ala Asn Arg Met Glu Trp Glu Lys Gly			
305	310	315	320
gat gtt ggc gaa gca att atg agt gat atc tat aac tca aac cca act	1008		
Asp Val Gly Glu Ala Ile Met Ser Asp Ile Tyr Asn Ser Asn Pro Thr			
	325	330	335
gcg gta aga gct gtt att act agc ttt ggc caa gtt gag gta aaa gat	1056		
Ala Val Arg Ala Val Ile Thr Ser Phe Gly Gln Val Glu Val Lys Asp			
	340	345	350
ggc ggt cgt aga att gct gtt ttg ggt gat atg ctt gaa tta ggt gag	1104		
Gly Gly Arg Arg Ile Ala Val Leu Gly Asp Met Leu Glu Leu Gly Glu			
	355	360	365
aat tct ccg aag ctt cat gcc gaa tta agc gat act ttg gat cca caa	1152		
Asn Ser Pro Lys Leu His Ala Glu Leu Ser Asp Thr Leu Asp Pro Gln			
	370	375	380
att att aat gaa gta tat tta tac ggc cct gaa atg aaa aat ctg tat	1200		
Ile Ile Asn Glu Val Tyr Leu Tyr Gly Pro Glu Met Lys Asn Leu Tyr			
385	390	395	400
gat gca tta caa ggc aag tat gag tca gag cat ttg cat tac tat act	1248		
Asp Ala Leu Gln Gly Lys Tyr Glu Ser Glu His Leu His Tyr Tyr Thr			
	405	410	415

```

aaa gat caa atg gat cgt atg att gat gat ctt aaa aat gat att aag 1296
Lys Asp Gln Met Asp Arg Met Ile Asp Asp Leu Lys Asn Asp Ile Lys
      420                      425                      430

tcg gac gac att gtt gtg ttg aaa ggt tca cac ggg atg cac cta gaa 1344
Ser Asp Asp Ile Val Val Leu Lys Gly Ser His Gly Met His Leu Glu
      435                      440                      445

aat gtc tta gcc cga cta aga 1365
Asn Val Leu Ala Arg Leu Arg
      450                      455

```

```

<210> 116
<211> 455
<212> PRT
<213> Lactobacillus acidophilus

```

```

<400> 116
Met Lys Met Gln Met Ala Glu Ile Ala Lys Ala Leu Asp Lys Thr Cys
 1      5      10      15
Glu Gly Asp Asp Lys Thr Val Ile Thr Ser Val Ala Phe Asp Ser Arg
 20      25      30
Lys Ile Thr Asn Gly Gly Leu Phe Val Pro Leu Glu Gly Glu Arg Asp
 35      40      45
Gly His Asp Phe Val Ala Gly Ala Ile Ser Asn Gly Ala Ser Ala Thr
 50      55      60
Leu Trp Lys Lys Gly His Pro Asn Lys Pro Glu Gly Ile Ala Val Ile
 65      70      75      80
Glu Val Asp Asp Pro Leu Ala Ala Met Gln Thr Leu Ala Arg Tyr Tyr
 85      90      95
Leu Arg Lys Val Asn Pro Thr Val Val Gly Ile Thr Gly Ser Asn Gly
100      105      110
Lys Thr Thr Thr Lys Asp Met Ile Ala Ala Val Leu Ser Lys Arg Phe
115      120      125
Asn Val His Lys Thr Gln Ala Asn Phe Asn Asn Glu Ile Gly Val Pro
130      135      140
Met Thr Val Leu Glu Met Lys Pro Asn Thr Glu Ile Leu Val Leu Glu
145      150      155      160
Met Gly Met Asp Arg Pro Gly Gln Leu His His Leu Ser Glu Leu Thr
165      170      175
Arg Pro Asp Val Ala Val Ile Thr Met Ile Gly Glu Ala His Ile Glu
180      185      190
Phe Phe Gly Ser Arg Asp Lys Ile Ala Asp Ala Lys Met Glu Ile Thr
195      200      205
Asp Phe Leu Arg Glu Asp Gly Glu Phe Ile Tyr Asn Gly Asp Glu Pro
210      215      220
Leu Leu Gln Glu Arg Ala Lys Lys Leu Asp Gln Ala Lys Ala Thr Phe
225      230      235      240
Gly Phe Glu Asp Asp Asp Thr Val His Ala Thr Gly Phe Lys Ser Tyr
245      250      255
Met His His Ala Thr Phe Thr Ile Asn Asp Ser Glu Gln Lys Phe Ser
260      265      270
Ile Pro Met Ile Gly Lys His Asn Val Ser Asn Ala Met Ala Ala Ile
275      280      285
Ser Val Gly Arg His Phe Gly Glu Ser Asp Glu Glu Ile Ala Ser Ser

```

```

      290              295              300
Leu Ser Asn Phe Lys Pro Thr Ala Asn Arg Met Glu Trp Glu Lys Gly
305              310              315              320
Asp Val Gly Glu Ala Ile Met Ser Asp Ile Tyr Asn Ser Asn Pro Thr
      325              330              335
Ala Val Arg Ala Val Ile Thr Ser Phe Gly Gln Val Glu Val Lys Asp
      340              345              350
Gly Gly Arg Arg Ile Ala Val Leu Gly Asp Met Leu Glu Leu Gly Glu
      355              360              365
Asn Ser Pro Lys Leu His Ala Glu Leu Ser Asp Thr Leu Asp Pro Gln
      370              375              380
Ile Ile Asn Glu Val Tyr Leu Tyr Gly Pro Glu Met Lys Asn Leu Tyr
385              390              395              400
Asp Ala Leu Gln Gly Lys Tyr Glu Ser Glu His Leu His Tyr Tyr Thr
      405              410              415
Lys Asp Gln Met Asp Arg Met Ile Asp Asp Leu Lys Asn Asp Ile Lys
      420              425              430
Ser Asp Asp Ile Val Val Leu Lys Gly Ser His Gly Met His Leu Glu
      435              440              445
Asn Val Leu Ala Arg Leu Arg
      450              455

```

<210> 117
 <211> 1296
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1603 - d-alanyl-d-alanine carboxypeptidase

<220>
 <221> CDS
 <222> (1)...(1296)

```

<400> 117
atg gtt ttt agt aaa aaa ata aaa cgg aca tta att agt ctt gtt gct   48
Met Val Phe Ser Lys Lys Ile Lys Arg Thr Leu Ile Ser Leu Val Ala
  1              5              10              15

tta gtt tct tta gtt tct tgt ggt gca gta ttt aca aca ccg gtt agt   96
Leu Val Ser Leu Val Ser Cys Gly Ala Val Phe Thr Thr Pro Val Ser
      20              25              30

gca gat aca tca agt agt tat cgc aat aat gaa gtg aat tta gat gtt   144
Ala Asp Thr Ser Ser Ser Tyr Arg Asn Asn Glu Val Asn Leu Asp Val
      35              40              45

aaa tct gca att gca att gat agt aat tcg ggg caa att ttg tat gct   192
Lys Ser Ala Ile Ala Ile Asp Ser Asn Ser Gly Gln Ile Leu Tyr Ala
      50              55              60

aaa aat gct gat aag act tta cca att gct tca atg aca aag tta att   240
Lys Asn Ala Asp Lys Thr Leu Pro Ile Ala Ser Met Thr Lys Leu Ile

```

65	70	75	80	
aca gtt tat tta act tta aat gca att aaa aat aaa aaa tta tct tgg	288			
Thr Val Tyr Leu Thr Leu Asn Ala Ile Lys Asn Lys Lys Leu Ser Trp				
85 90 95				
aat caa aag gtg aag cca act gct tca att gta aaa gta gct aat aat	336			
Asn Gln Lys Val Lys Pro Thr Ala Ser Ile Val Lys Val Ala Asn Asn				
100 105 110				
gcg gaa tat tca aat gta cgc ctt aag atg ggg cat tct tat act att	384			
Ala Glu Tyr Ser Asn Val Pro Leu Lys Met Gly His Ser Tyr Thr Ile				
115 120 125				
cgt cag ctt tat caa gca act tta att gaa tca gct aat ggg gcc gca	432			
Arg Gln Leu Tyr Gln Ala Thr Leu Ile Glu Ser Ala Asn Gly Ala Ala				
130 135 140				
atg ctt ttg ggc caa act att gct ggt tca caa aag aaa ttt att gat	480			
Met Leu Leu Gly Gln Thr Ile Ala Gly Ser Gln Lys Lys Phe Ile Asp				
145 150 155 160				
caa atg cgt gcc caa gtt aaa aaa tgg ggg att gaa gat gcc gag att	528			
Gln Met Arg Ala Gln Val Lys Lys Trp Gly Ile Glu Asp Ala Glu Ile				
165 170 175				
tat acg gca tgt ggt tta cct aat ggt aat gta ggt aaa gat gcc tat	576			
Tyr Thr Ala Cys Gly Leu Pro Asn Gly Asn Val Gly Lys Asp Ala Tyr				
180 185 190				
cct ggt gta aat aag aat gct gaa aat act atg tca gct aag gat atg	624			
Pro Gly Val Asn Lys Asn Ala Glu Asn Thr Met Ser Ala Lys Asp Met				
195 200 205				
gcc att gtt gga caa cat tta ctt aaa gaa tac cca gaa att tta gat	672			
Ala Ile Val Gly Gln His Leu Leu Lys Glu Tyr Pro Glu Ile Leu Asp				
210 215 220				
act act aaa tta gct cat tta gat ttt aaa gac ggt aat aaa act act	720			
Thr Thr Lys Leu Ala His Leu Asp Phe Lys Asp Gly Asn Lys Thr Thr				
225 230 235 240				
aaa atg gcc aac ttt aac tgg atg ctt aaa gga ctt tct caa tat gat	768			
Lys Met Ala Asn Phe Asn Trp Met Leu Lys Gly Leu Ser Gln Tyr Asp				
245 250 255				
caa gca tat cca gtt gat gga tta aag act ggt acc act gat gca gca	816			
Gln Ala Tyr Pro Val Asp Gly Leu Lys Thr Gly Thr Thr Asp Ala Ala				
260 265 270				
ggt gca tgt ttt att ggt aca gtt gaa cat aat ggt gct cgt ttg att	864			
Gly Ala Cys Phe Ile Gly Thr Val Glu His Asn Gly Ala Arg Leu Ile				
275 280 285				
act gtt gtc atg ggt gca cgt cac caa gat ggt acg gat cct tca cgt	912			
Thr Val Val Met Gly Ala Arg His Gln Asp Gly Thr Asp Pro Ser Arg				
290 295 300				

ttt att caa act aag aaa tta atg agt ttt att ttc aac aaa tac cgt 960
 Phe Ile Gln Thr Lys Lys Leu Met Ser Phe Ile Phe Asn Lys Tyr Arg
 305 310 315 320
 cca gtt aca atg act gct gga agt caa ata aat ggt gca aaa agt att 1008
 Pro Val Thr Met Thr Ala Gly Ser Gln Ile Asn Gly Ala Lys Ser Ile
 325 330 335
 aaa gtt act gat ggt aaa gac gct aca act aat att ggt tta aag aat 1056
 Lys Val Thr Asp Gly Lys Asp Ala Thr Thr Asn Ile Gly Leu Lys Asn
 340 345 350
 aag aca act att tgg gat cca gca gat ggt aaa aca ttg act gct agt 1104
 Lys Thr Thr Ile Trp Asp Pro Ala Asp Gly Lys Thr Leu Thr Ala Ser
 355 360 365
 tta aac aaa aaa aca ata gat gcg cct ctt gaa aag aat cag aca gtt 1152
 Leu Asn Lys Lys Thr Ile Asp Ala Pro Leu Glu Lys Asn Gln Thr Val
 370 375 380
 ggt aat tat caa tta aaa tca ggt agt gaa aaa att gtt tca ttg gat 1200
 Gly Asn Tyr Gln Leu Lys Ser Gly Ser Glu Lys Ile Val Ser Leu Asp
 385 390 395 400
 aat cct aat gga atg aat gta aaa gct aaa gct tta tca gct aat gga 1248
 Asn Pro Asn Gly Met Asn Val Lys Ala Lys Ala Leu Ser Ala Asn Gly
 405 410 415
 aaa gtt aat ttc ttt gtt aga att tgg cgt tgg ctt ttc ggg ggc aga 1296
 Lys Val Asn Phe Phe Val Arg Ile Trp Arg Trp Leu Phe Gly Gly Arg
 420 425 430

<210> 118

<211> 432

<212> PRT

<213> Lactobacillus acidophilus

<400> 118

Met Val Phe Ser Lys Lys Ile Lys Arg Thr Leu Ile Ser Leu Val Ala
 1 5 10 15
 Leu Val Ser Leu Val Ser Cys Gly Ala Val Phe Thr Thr Pro Val Ser
 20 25 30
 Ala Asp Thr Ser Ser Ser Tyr Arg Asn Asn Glu Val Asn Leu Asp Val
 35 40 45
 Lys Ser Ala Ile Ala Ile Asp Ser Asn Ser Gly Gln Ile Leu Tyr Ala
 50 55 60
 Lys Asn Ala Asp Lys Thr Leu Pro Ile Ala Ser Met Thr Lys Leu Ile
 65 70 75 80
 Thr Val Tyr Leu Thr Leu Asn Ala Ile Lys Asn Lys Lys Leu Ser Trp
 85 90 95
 Asn Gln Lys Val Lys Pro Thr Ala Ser Ile Val Lys Val Ala Asn Asn
 100 105 110
 Ala Glu Tyr Ser Asn Val Pro Leu Lys Met Gly His Ser Tyr Thr Ile
 115 120 125

```

Arg Gln Leu Tyr Gln Ala Thr Leu Ile Glu Ser Ala Asn Gly Ala Ala
 130                135                140
Met Leu Leu Gly Gln Thr Ile Ala Gly Ser Gln Lys Lys Phe Ile Asp
145                150                155                160
Gln Met Arg Ala Gln Val Lys Lys Trp Gly Ile Glu Asp Ala Glu Ile
                165                170                175
Tyr Thr Ala Cys Gly Leu Pro Asn Gly Asn Val Gly Lys Asp Ala Tyr
                180                185                190
Pro Gly Val Asn Lys Asn Ala Glu Asn Thr Met Ser Ala Lys Asp Met
                195                200                205
Ala Ile Val Gly Gln His Leu Leu Lys Glu Tyr Pro Glu Ile Leu Asp
                210                215                220
Thr Thr Lys Leu Ala His Leu Asp Phe Lys Asp Gly Asn Lys Thr Thr
225                230                235                240
Lys Met Ala Asn Phe Asn Trp Met Leu Lys Gly Leu Ser Gln Tyr Asp
                245                250                255
Gln Ala Tyr Pro Val Asp Gly Leu Lys Thr Gly Thr Thr Asp Ala Ala
                260                265                270
Gly Ala Cys Phe Ile Gly Thr Val Glu His Asn Gly Ala Arg Leu Ile
                275                280                285
Thr Val Val Met Gly Ala Arg His Gln Asp Gly Thr Asp Pro Ser Arg
290                295                300
Phe Ile Gln Thr Lys Lys Leu Met Ser Phe Ile Phe Asn Lys Tyr Arg
305                310                315                320
Pro Val Thr Met Thr Ala Gly Ser Gln Ile Asn Gly Ala Lys Ser Ile
                325                330                335
Lys Val Thr Asp Gly Lys Asp Ala Thr Thr Asn Ile Gly Leu Lys Asn
                340                345                350
Lys Thr Thr Ile Trp Asp Pro Ala Asp Gly Lys Thr Leu Thr Ala Ser
                355                360                365
Leu Asn Lys Lys Thr Ile Asp Ala Pro Leu Glu Lys Asn Gln Thr Val
                370                375                380
Gly Asn Tyr Gln Leu Lys Ser Gly Ser Glu Lys Ile Val Ser Leu Asp
385                390                395                400
Asn Pro Asn Gly Met Asn Val Lys Ala Lys Ala Leu Ser Ala Asn Gly
                405                410                415
Lys Val Asn Phe Phe Val Arg Ile Trp Arg Trp Leu Phe Gly Gly Arg
                420                425                430

```

<210> 119

<211> 1323

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 234 - udp-n-acetylglucosamine
1-carboxyvinyltransferase

<220>

<221> CDS

<222> (1)...(1323)

<400> 119

ttg aaa gta gaa aag gat ttg ttt tcg cca atg aag cag atg att att	48
Met Lys Val Glu Lys Asp Leu Phe Ser Pro Met Lys Gln Met Ile Ile	
1 5 10 15	
cat ggt gga aag ccc ttg cag ggt gat gtt tgg atc ggt gga gct aaa	96
His Gly Gly Lys Pro Leu Gln Gly Asp Val Trp Ile Gly Gly Ala Lys	
20 25 30	
aat tca aca gtt gca tta atc cca gca tca att ttg tcg aga aca cca	144
Asn Ser Thr Val Ala Leu Ile Pro Ala Ser Ile Leu Ser Arg Thr Pro	
35 40 45	
gta gtc ttg gaa ggc gtc cca aga att gct gat gtg atc aac ttg atg	192
Val Val Leu Glu Gly Val Pro Arg Ile Ala Asp Val Ile Asn Leu Met	
50 55 60	
gac tta tta gat gaa atg gat gta cgt tgt gag ttt aaa gaa aca act	240
Asp Leu Leu Asp Glu Met Asp Val Arg Cys Glu Phe Lys Glu Thr Thr	
65 70 75 80	
tta cgc att gat cca aca gat att aag atg agt cca ttg cca gct ggt	288
Leu Arg Ile Asp Pro Thr Asp Ile Lys Met Ser Pro Leu Pro Ala Gly	
85 90 95	
aag att aag agt tta cgt gca tca tat tac ttt atg ggt gca ctt ctt	336
Lys Ile Lys Ser Leu Arg Ala Ser Tyr Tyr Phe Met Gly Ala Leu Leu	
100 105 110	
ggg cga ttt ggc aaa gca gtt gtg ggc ttc cct ggt ggt gac gat atc	384
Gly Arg Phe Gly Lys Ala Val Val Gly Phe Pro Gly Gly Asp Asp Ile	
115 120 125	
gga cca cgt cct ata gac caa cat att aaa ggc ttt gaa gcc tta ggc	432
Gly Pro Arg Pro Ile Asp Gln His Ile Lys Gly Phe Glu Ala Leu Gly	
130 135 140	
gcc agc gtt aaa aat gaa aat gat caa att ata att act gct cca gaa	480
Ala Ser Val Lys Asn Glu Asn Asp Gln Ile Ile Ile Thr Ala Pro Glu	
145 150 155 160	
gat ggc ttg cat ggt gcg aag att cat ctt aag atg cca tct gtt ggg	528
Asp Gly Leu His Gly Ala Lys Ile His Leu Lys Met Pro Ser Val Gly	
165 170 175	
gca aca atg aat att att atg gct agt gta act gca caa ggc caa act	576
Ala Thr Met Asn Ile Ile Met Ala Ser Val Thr Ala Gln Gly Gln Thr	
180 185 190	
att att gaa aat gcc gcg aaa gaa ccg gaa att atc gat tta gca acc	624
Ile Ile Glu Asn Ala Ala Lys Glu Pro Glu Ile Ile Asp Leu Ala Thr	
195 200 205	
ttc tta aat aac atg ggg gca gtt att cgt ggt gcc ggt act gat gtg	672
Phe Leu Asn Asn Met Gly Ala Val Ile Arg Gly Ala Gly Thr Asp Val	
210 215 220	
att cgt att gaa ggt gtg gaa atg ctt aaa gcg caa att ccg cat aca	720

Ile Arg Ile Glu Gly Val Glu Met Leu Lys Ala Gln Ile Pro His Thr	
225 230 235 240	
att att cca gat aga att gaa gct ggt act tat gta tct ctt gct gcg	768
Ile Ile Pro Asp Arg Ile Glu Ala Gly Thr Tyr Val Ser Leu Ala Ala	
245 250 255	
tgc att ggt aat ggt att cgt att cat aat att att gag gaa cac ctt	816
Cys Ile Gly Asn Gly Ile Arg Ile His Asn Ile Ile Glu Glu His Leu	
260 265 270	
gat tca tac ctt gct aag gtg gaa gag atg ggc gtt gta att gat gcc	864
Asp Ser Tyr Leu Ala Lys Val Glu Glu Met Gly Val Val Ile Asp Ala	
275 280 285	
gat gaa gat tct ctt tat gtg tat cct gct ggt gat ttg aag atg gtg	912
Asp Glu Asp Ser Leu Tyr Val Tyr Pro Ala Gly Asp Leu Lys Met Val	
290 295 300	
caa gta aag act gat gtt tat cca ggt ttt gcc aca gat tta caa cag	960
Gln Val Lys Thr Asp Val Tyr Pro Gly Phe Ala Thr Asp Leu Gln Gln	
305 310 315 320	
ccg att act cca ctg ctt ctt act gct aag tct ggt gaa ggt gtt gta	1008
Pro Ile Thr Pro Leu Leu Leu Thr Ala Lys Ser Gly Glu Gly Val Val	
325 330 335	
atc gat aat att tat ccg caa cga att ggt cat att gct caa tta caa	1056
Ile Asp Asn Ile Tyr Pro Gln Arg Ile Gly His Ile Ala Gln Leu Gln	
340 345 350	
aag atg ggt gcc aat att aaa gtt gca gat aac atc atc ttg gct cac	1104
Lys Met Gly Ala Asn Ile Lys Val Ala Asp Asn Ile Ile Leu Ala His	
355 360 365	
cca act gaa caa ctt cac ggt gca gaa gta att gca ggt gag att cgt	1152
Pro Thr Glu Gln Leu His Gly Ala Glu Val Ile Ala Gly Glu Ile Arg	
370 375 380	
gca ggt gca tgt ttg atg att gct gga ttg atg gca cac ggt acg acg	1200
Ala Gly Ala Cys Leu Met Ile Ala Gly Leu Met Ala His Gly Thr Thr	
385 390 395 400	
gtt atc gat aaa gcc ggt aat att tta cgt ggt tat gat cga att caa	1248
Val Ile Asp Lys Ala Gly Asn Ile Leu Arg Gly Tyr Asp Arg Ile Gln	
405 410 415	
gaa aag tta cgt caa ctt ggt gct gat gta acg att aaa gat aac cct	1296
Glu Lys Leu Arg Gln Leu Gly Ala Asp Val Thr Ile Lys Asp Asn Pro	
420 425 430	
gat gta cca ggc att tta gat aat ata	1323
Asp Val Pro Gly Ile Leu Asp Asn Ile	
435 440	

<210> 120

<211> 441

<212> PRT

<213> Lactobacillus acidophilus

<400> 120

```

Met Lys Val Glu Lys Asp Leu Phe Ser Pro Met Lys Gln Met Ile Ile
 1          5          10          15
His Gly Gly Lys Pro Leu Gln Gly Asp Val Trp Ile Gly Gly Ala Lys
 20          25          30
Asn Ser Thr Val Ala Leu Ile Pro Ala Ser Ile Leu Ser Arg Thr Pro
 35          40          45
Val Val Leu Glu Gly Val Pro Arg Ile Ala Asp Val Ile Asn Leu Met
 50          55          60
Asp Leu Leu Asp Glu Met Asp Val Arg Cys Glu Phe Lys Glu Thr Thr
 65          70          75          80
Leu Arg Ile Asp Pro Thr Asp Ile Lys Met Ser Pro Leu Pro Ala Gly
 85          90          95
Lys Ile Lys Ser Leu Arg Ala Ser Tyr Tyr Phe Met Gly Ala Leu Leu
 100         105         110
Gly Arg Phe Gly Lys Ala Val Val Gly Phe Pro Gly Gly Asp Asp Ile
 115         120         125
Gly Pro Arg Pro Ile Asp Gln His Ile Lys Gly Phe Glu Ala Leu Gly
 130         135         140
Ala Ser Val Lys Asn Glu Asn Asp Gln Ile Ile Thr Ala Pro Glu
 145         150         155         160
Asp Gly Leu His Gly Ala Lys Ile His Leu Lys Met Pro Ser Val Gly
 165         170         175
Ala Thr Met Asn Ile Ile Met Ala Ser Val Thr Ala Gln Gly Gln Thr
 180         185         190
Ile Ile Glu Asn Ala Ala Lys Glu Pro Glu Ile Ile Asp Leu Ala Thr
 195         200         205
Phe Leu Asn Asn Met Gly Ala Val Ile Arg Gly Ala Gly Thr Asp Val
 210         215         220
Ile Arg Ile Glu Gly Val Glu Met Leu Lys Ala Gln Ile Pro His Thr
 225         230         235         240
Ile Ile Pro Asp Arg Ile Glu Ala Gly Thr Tyr Val Ser Leu Ala Ala
 245         250         255
Cys Ile Gly Asn Gly Ile Arg Ile His Asn Ile Ile Glu Glu His Leu
 260         265         270
Asp Ser Tyr Leu Ala Lys Val Glu Glu Met Gly Val Val Ile Asp Ala
 275         280         285
Asp Glu Asp Ser Leu Tyr Val Tyr Pro Ala Gly Asp Leu Lys Met Val
 290         295         300
Gln Val Lys Thr Asp Val Tyr Pro Gly Phe Ala Thr Asp Leu Gln Gln
 305         310         315         320
Pro Ile Thr Pro Leu Leu Leu Thr Ala Lys Ser Gly Glu Gly Val Val
 325         330         335
Ile Asp Asn Ile Tyr Pro Gln Arg Ile Gly His Ile Ala Gln Leu Gln
 340         345         350
Lys Met Gly Ala Asn Ile Lys Val Ala Asp Asn Ile Ile Leu Ala His
 355         360         365
Pro Thr Glu Gln Leu His Gly Ala Glu Val Ile Ala Gly Glu Ile Arg
 370         375         380
Ala Gly Ala Cys Leu Met Ile Ala Gly Leu Met Ala His Gly Thr Thr
 385         390         395         400
Val Ile Asp Lys Ala Gly Asn Ile Leu Arg Gly Tyr Asp Arg Ile Gln
 405         410         415

```

Glu Lys Leu Arg Gln Leu Gly Ala Asp Val Thr Ile Lys Asp Asn Pro
 420 425 430
 Asp Val Pro Gly Ile Leu Asp Asn Ile
 435 440

<210> 121
 <211> 1377
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 219 - udp-n-acetylglucosamine
 pyrophosphorylase

<220>
 <221> CDS
 <222> (1)...(1377)

<400> 121
 atg gaa aaa tac gta gtt gtt ctt gct gca ggc aag ggt aca cga atg 48
 Met Glu Lys Tyr Val Val Val Leu Ala Ala Gly Lys Gly Thr Arg Met
 1 5 10 15
 aag tct aaa ttg tat aag gtt ttg cat aaa gtt tgc ggt aag act atg 96
 Lys Ser Lys Leu Tyr Lys Val Leu His Lys Val Cys Gly Lys Thr Met
 20 25 30
 gtt gaa cat gtc gta gat gct gca agt ggt gtt gag cct act gaa att 144
 Val Glu His Val Val Asp Ala Ala Ser Gly Val Glu Pro Thr Glu Ile
 35 40 45
 gtt act gtt gta ggt act ggt gct ggc gat gtg gaa aaa gtt ttg gct 192
 Val Thr Val Val Gly Thr Gly Ala Gly Asp Val Glu Lys Val Leu Ala
 50 55 60
 gac aag tca aaa ttc gtt ttc caa gaa aag caa ctc ggt acc ggt gat 240
 Asp Lys Ser Lys Phe Val Phe Gln Glu Lys Gln Leu Gly Thr Gly Asp
 65 70 75 80
 gcc gtg atg act gct aaa gaa gtc tta ggt gac aaa gat ggt gca aca 288
 Ala Val Met Thr Ala Lys Glu Val Leu Gly Asp Lys Asp Gly Ala Thr
 85 90 95
 tta gta gtt act ggt gat act cca tta ttt act act gat act ttc aat 336
 Leu Val Val Thr Gly Asp Thr Pro Leu Phe Thr Thr Asp Thr Phe Asn
 100 105 110
 gaa ttg ttt aag tat cat aca gaa aaa ggc aat gca gct act gtt tta 384
 Glu Leu Phe Lys Tyr His Thr Glu Lys Gly Asn Ala Ala Thr Val Leu
 115 120 125
 act gct gaa gct cca aat cca ttt ggt tat ggt cga att att cgt gat 432
 Thr Ala Glu Ala Pro Asn Pro Phe Gly Tyr Gly Arg Ile Ile Arg Asp

130	135	140	
gag caa ggc aat gtt tta aga att gtt gaa caa aaa gac ggt aat cca			480
Glu Gln Gly Asn Val Leu Arg Ile Val Glu Gln Lys Asp Gly Asn Pro			
145	150	155	160
gaa gaa tta aag gtt aag gaa att aac act ggt gta ttt tgc ttt gat			528
Glu Glu Leu Lys Val Lys Glu Ile Asn Thr Gly Val Phe Cys Phe Asp			
165	170		175
aat aaa aag tta ttt gaa gca tta aaa cat gtt gat aat aat aac gct			576
Asn Lys Lys Leu Phe Glu Ala Leu Lys His Val Asp Asn Asn Asn Ala			
180	185		190
caa ggt gag tac tac ttg act gat gtt ctt gaa att ttg cgt aat agt			624
Gln Gly Glu Tyr Tyr Leu Thr Asp Val Leu Glu Ile Leu Arg Asn Ser			
195	200		205
ggg gaa aat gtc ggt gca tat aag atg cct gat ttt agt gaa agc tta			672
Gly Glu Asn Val Gly Ala Tyr Lys Met Pro Asp Phe Ser Glu Ser Leu			
210	215		220
ggg gtt aat gat cgt atc gct tta gcc caa gct act aag att atg caa			720
Gly Val Asn Asp Arg Ile Ala Leu Ala Gln Ala Thr Lys Ile Met Gln			
225	230	235	240
aga aga att aat gaa gaa cat atg cgt aat ggt gtt tca ttc att gat			768
Arg Arg Ile Asn Glu Glu His Met Arg Asn Gly Val Ser Phe Ile Asp			
245	250		255
cca gat act gcc tat att gat gct gac gta aaa att ggt aat gat aca			816
Pro Asp Thr Ala Tyr Ile Asp Ala Asp Val Lys Ile Gly Asn Asp Thr			
260	265		270
gta att gaa ggt aat gtt gtt att aag ggt aac act gaa att ggc agt			864
Val Ile Glu Gly Asn Val Val Ile Lys Gly Asn Thr Glu Ile Gly Ser			
275	280		285
gaa tgt tac att aca agc ggc tca aga att att gat tca aag atc ggt			912
Glu Cys Tyr Ile Thr Ser Gly Ser Arg Ile Ile Asp Ser Lys Ile Gly			
290	295	300	
aac aat gtt act gta act tct tca acc att gaa aaa tca gaa atg gaa			960
Asn Asn Val Thr Val Thr Ser Ser Thr Ile Glu Lys Ser Glu Met Glu			
305	310	315	320
gat aat act gat atc ggt cct aat tca cac ctt cgt cca aag gct ctt			1008
Asp Asn Thr Asp Ile Gly Pro Asn Ser His Leu Arg Pro Lys Ala Leu			
325	330		335
att aag aag gga gca cat att ggt aac ttc gtt gaa gtt aag aag gct			1056
Ile Lys Lys Gly Ala His Ile Gly Asn Phe Val Glu Val Lys Lys Ala			
340	345		350
gaa att ggt gaa aat act aag gtt gga cac tta act tat gtt ggg gat			1104
Glu Ile Gly Glu Asn Thr Lys Val Gly His Leu Thr Tyr Val Gly Asp			
355	360	365	

```

gca act ttg ggt aag gat att aat atc ggt tgt ggt act att ttc tct 1152
Ala Thr Leu Gly Lys Asp Ile Asn Ile Gly Cys Gly Thr Ile Phe Ser
370 375 380

aac tat gat ggt gtt aag aag ttc cat act aat gtt ggt gat cat gca 1200
Asn Tyr Asp Gly Val Lys Lys Phe His Thr Asn Val Gly Asp His Ala
385 390 395 400

ttt atc ggt gct ggt tca act ttg att gcc cca att aat gta gct gat 1248
Phe Ile Gly Ala Gly Ser Thr Leu Ile Ala Pro Ile Asn Val Ala Asp
405 410 415

cat gca ttt atc gca gct gac tct act att act aag gat gta gac aaa 1296
His Ala Phe Ile Ala Ala Asp Ser Thr Ile Thr Lys Asp Val Asp Lys
420 425 430

tac gac atg gca att gct cgt gga cgt caa gtt aat aag cct gat tac 1344
Tyr Asp Met Ala Ile Ala Arg Gly Arg Gln Val Asn Lys Pro Asp Tyr
435 440 445

tgg cat aaa tta cca ctt tca aaa aat gaa gat 1377
Trp His Lys Leu Pro Leu Ser Lys Asn Glu Asp
450 455

```

<210> 122

<211> 459

<212> PRT

<213> Lactobacillus acidophilus

<400> 122

```

Met Glu Lys Tyr Val Val Val Leu Ala Ala Gly Lys Gly Thr Arg Met
1 5 10 15
Lys Ser Lys Leu Tyr Lys Val Leu His Lys Val Cys Gly Lys Thr Met
20 25 30
Val Glu His Val Val Asp Ala Ala Ser Gly Val Glu Pro Thr Glu Ile
35 40 45
Val Thr Val Val Gly Thr Gly Ala Gly Asp Val Glu Lys Val Leu Ala
50 55 60
Asp Lys Ser Lys Phe Val Phe Gln Glu Lys Gln Leu Gly Thr Gly Asp
65 70 75 80
Ala Val Met Thr Ala Lys Glu Val Leu Gly Asp Lys Asp Gly Ala Thr
85 90 95
Leu Val Val Thr Gly Asp Thr Pro Leu Phe Thr Thr Asp Thr Phe Asn
100 105 110
Glu Leu Phe Lys Tyr His Thr Glu Lys Gly Asn Ala Ala Thr Val Leu
115 120 125
Thr Ala Glu Ala Pro Asn Pro Phe Gly Tyr Gly Arg Ile Ile Arg Asp
130 135 140
Glu Gln Gly Asn Val Leu Arg Ile Val Glu Gln Lys Asp Gly Asn Pro
145 150 155 160
Glu Glu Leu Lys Val Lys Glu Ile Asn Thr Gly Val Phe Cys Phe Asp
165 170 175
Asn Lys Lys Leu Phe Glu Ala Leu Lys His Val Asp Asn Asn Asn Ala
180 185 190
Gln Gly Glu Tyr Tyr Leu Thr Asp Val Leu Glu Ile Leu Arg Asn Ser

```

```

      195      200      205
Gly Glu Asn Val Gly Ala Tyr Lys Met Pro Asp Phe Ser Glu Ser Leu
  210      215      220
Gly Val Asn Asp Arg Ile Ala Leu Ala Gln Ala Thr Lys Ile Met Gln
  225      230      235      240
Arg Arg Ile Asn Glu His Met Arg Asn Gly Val Ser Phe Ile Asp
      245      250      255
Pro Asp Thr Ala Tyr Ile Asp Ala Asp Val Lys Ile Gly Asn Asp Thr
      260      265      270
Val Ile Glu Gly Asn Val Val Ile Lys Gly Asn Thr Glu Ile Gly Ser
      275      280      285
Glu Cys Tyr Ile Thr Ser Gly Ser Arg Ile Ile Asp Ser Lys Ile Gly
      290      295      300
Asn Asn Val Thr Val Thr Ser Ser Thr Ile Glu Lys Ser Glu Met Glu
  305      310      315      320
Asp Asn Thr Asp Ile Gly Pro Asn Ser His Leu Arg Pro Lys Ala Leu
      325      330      335
Ile Lys Lys Gly Ala His Ile Gly Asn Phe Val Glu Val Lys Lys Ala
      340      345      350
Glu Ile Gly Glu Asn Thr Lys Val Gly His Leu Thr Tyr Val Gly Asp
      355      360      365
Ala Thr Leu Gly Lys Asp Ile Asn Ile Gly Cys Gly Thr Ile Phe Ser
  370      375      380
Asn Tyr Asp Gly Val Lys Lys Phe His Thr Asn Val Gly Asp His Ala
  385      390      395      400
Phe Ile Gly Ala Gly Ser Thr Leu Ile Ala Pro Ile Asn Val Ala Asp
      405      410      415
His Ala Phe Ile Ala Ala Asp Ser Thr Ile Thr Lys Asp Val Asp Lys
      420      425      430
Tyr Asp Met Ala Ile Ala Arg Gly Arg Gln Val Asn Lys Pro Asp Tyr
      435      440      445
Trp His Lys Leu Pro Leu Ser Lys Asn Glu Asp
      450      455

```

<210> 123

<211> 732

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1266 - undecaprenyl pyrophosphate synthetase

<220>

<221> CDS

<222> (1)...(732)

<400> 123

```

atg agt aaa aaa gac aat gaa tta aat cat tta gcc att atc atg gat 48
Met Ser Lys Lys Asp Asn Glu Leu Asn His Leu Ala Ile Ile Met Asp
  1          5          10          15

```

```

ggg aat ggt cgt tgg gct aaa aag aga cat aaa cca aga ttt gtt ggt 96
Gly Asn Gly Arg Trp Ala Lys Lys Arg His Lys Pro Arg Phe Val Gly

```

20	25	30	
cac cgt gaa ggt atg gat aac gtt gaa cga att act tta gct gct aac			144
His Arg Glu Gly Met Asp Asn Val Glu Arg Ile Thr Leu Ala Ala Asn			
35	40	45	
caa cta gga att aaa gtc ttg act cta tat gca ttt tca act gaa aat			192
Gln Leu Gly Ile Lys Val Leu Thr Leu Tyr Ala Phe Ser Thr Glu Asn			
50	55	60	
tgg gct cgt cct aaa gag gag gtt gca tat tta atg aat ctt ccc gta			240
Trp Ala Arg Pro Lys Glu Val Ala Tyr Leu Met Asn Leu Pro Val			
65	70	75	80
cgt ttt ttt gat aaa tat atg cca act tta atg gaa aat aat gtt aaa			288
Arg Phe Phe Asp Lys Tyr Met Pro Thr Leu Met Glu Asn Asn Val Lys			
85	90	95	
gtt aac att atg ggg tat tta gat gaa tta ccg gaa aaa acg tat aaa			336
Val Asn Ile Met Gly Tyr Leu Asp Glu Leu Pro Glu Lys Thr Tyr Lys			
100	105	110	
att gtt caa cgt gct atg tct gaa acg gta aat aat act ggt tta att			384
Ile Val Gln Arg Ala Met Ser Glu Thr Val Asn Asn Thr Gly Leu Ile			
115	120	125	
ctt aat ttt gct ttt aat tat ggt tct aga cga gaa ata act tct gct			432
Leu Asn Phe Ala Phe Asn Tyr Gly Ser Arg Arg Glu Ile Thr Ser Ala			
130	135	140	
gta aaa gaa ttg ggt gga atg att gaa tct gga tct tta aag agt gaa			480
Val Lys Glu Leu Gly Gly Met Ile Glu Ser Gly Ser Leu Lys Ser Glu			
145	150	155	160
gag atc aca gaa agt atg att tca gat cat ttg atg act ggg aat ttt			528
Glu Ile Thr Glu Ser Met Ile Ser Asp His Leu Met Thr Gly Asn Phe			
165	170	175	
gga aaa tat cga gat cct gac tta tta att aga act tct ggt gaa caa			576
Gly Lys Tyr Arg Asp Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu Gln			
180	185	190	
aga att tct aat ttc ttg ctt tgg caa tta gca tat tca gaa ctt gct			624
Arg Ile Ser Asn Phe Leu Leu Trp Gln Leu Ala Tyr Ser Glu Leu Ala			
195	200	205	
ttt agc gaa aaa aat tgg cca gat ttt gat aaa gat gat ttg aaa gaa			672
Phe Ser Glu Lys Asn Trp Pro Asp Phe Asp Lys Asp Asp Leu Lys Glu			
210	215	220	
ttt gta gat gaa tat aag cac cgt aat cgg cgc ttc ggt aaa gta gac			720
Phe Val Asp Glu Tyr Lys His Arg Asn Arg Arg Phe Gly Lys Val Asp			
225	230	235	240
gaa tcg gat agt			732
Glu Ser Asp Ser			

<210> 124
 <211> 244
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 124
 Met Ser Lys Lys Asp Asn Glu Leu Asn His Leu Ala Ile Ile Met Asp
 1 5 10 15
 Gly Asn Gly Arg Trp Ala Lys Lys Arg His Lys Pro Arg Phe Val Gly
 20 25 30
 His Arg Glu Gly Met Asp Asn Val Glu Arg Ile Thr Leu Ala Ala Asn
 35 40 45
 Gln Leu Gly Ile Lys Val Leu Thr Leu Tyr Ala Phe Ser Thr Glu Asn
 50 55 60
 Trp Ala Arg Pro Lys Glu Glu Val Ala Tyr Leu Met Asn Leu Pro Val
 65 70 75 80
 Arg Phe Phe Asp Lys Tyr Met Pro Thr Leu Met Glu Asn Asn Val Lys
 85 90 95
 Val Asn Ile Met Gly Tyr Leu Asp Glu Leu Pro Glu Lys Thr Tyr Lys
 100 105 110
 Ile Val Gln Arg Ala Met Ser Glu Thr Val Asn Asn Thr Gly Leu Ile
 115 120 125
 Leu Asn Phe Ala Phe Asn Tyr Gly Ser Arg Arg Glu Ile Thr Ser Ala
 130 135 140
 Val Lys Glu Leu Gly Gly Met Ile Glu Ser Gly Ser Leu Lys Ser Glu
 145 150 155 160
 Glu Ile Thr Glu Ser Met Ile Ser Asp His Leu Met Thr Gly Asn Phe
 165 170 175
 Gly Lys Tyr Arg Asp Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu Gln
 180 185 190
 Arg Ile Ser Asn Phe Leu Leu Trp Gln Leu Ala Tyr Ser Glu Leu Ala
 195 200 205
 Phe Ser Glu Lys Asn Trp Pro Asp Phe Asp Lys Asp Asp Leu Lys Glu
 210 215 220
 Phe Val Asp Glu Tyr Lys His Arg Asn Arg Arg Phe Gly Lys Val Asp
 225 230 235 240
 Glu Ser Asp Ser

<210> 125
 <211> 1167
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 668 - undecaprenyl-phosphate
 N-acetyl-glucosaminyltransferase

<220>
 <221> CDS
 <222> (1)...(1167)

<400> 125

```

atg ttt aaa att att gtt gaa tta ttc tta tta gta att att tca gct 48
Met Phe Lys Ile Ile Val Glu Leu Phe Leu Leu Val Ile Ile Ser Ala
1 5 10 15

gca att acg cca ttt att agg cgt tta gcc ttt gtg tta gga gcg gtt 96
Ala Ile Thr Pro Phe Ile Arg Arg Leu Ala Phe Val Leu Gly Ala Val
20 25 30

gat aat cct aat gct cgt cgt gtt aat aag aaa cca atg cca act att 144
Asp Asn Pro Asn Ala Arg Arg Val Asn Lys Lys Pro Met Pro Thr Ile
35 40 45

ggg gga tta ggt att ttt gtt acg ttt aac atc ggt gca ttt gta tta 192
Gly Gly Leu Gly Ile Phe Val Thr Phe Asn Ile Gly Ala Phe Val Leu
50 55 60

ctg aga gaa caa ttt cct act cat gaa att ttt tcg ata tta tta gca 240
Leu Arg Glu Gln Phe Pro Thr His Glu Ile Phe Ser Ile Leu Leu Ala
65 70 75 80

tca agt gtc gtt gta tta acg gga tta att gat gat att ctt gaa ctg 288
Ser Ser Val Val Val Leu Thr Gly Leu Ile Asp Asp Ile Leu Glu Leu
85 90 95

aaa cct agg caa aaa atg ttt ggt att ttt att gct tca tta att att 336
Lys Pro Arg Gln Lys Met Phe Gly Ile Phe Ile Ala Ser Leu Ile Ile
100 105 110

tac ttc tta gca gga att aga atg aat gta tta aaa tta cca ttt att 384
Tyr Phe Leu Ala Gly Ile Arg Met Asn Val Leu Lys Leu Pro Phe Ile
115 120 125

acc aat gag att aac tta ggt tgg tgg agt ttt cca att act att ttt 432
Thr Asn Glu Ile Asn Leu Gly Trp Trp Ser Phe Pro Ile Thr Ile Phe
130 135 140

tgg ata tta gct ttg act aat gca gtt aat tta att gat ggc cta gat 480
Trp Ile Leu Ala Leu Thr Asn Ala Val Asn Leu Ile Asp Gly Leu Asp
145 150 155 160

ggg tta gct gat ggt gta tct atg ata tct tta acg act atg ggg atc 528
Gly Leu Ala Asp Gly Val Ser Met Ile Ser Leu Thr Thr Met Gly Ile
165 170 175

gtg gga tat ttc ttt tta cat acg cat caa ttg tat gtg cca att gcc 576
Val Gly Tyr Phe Phe Leu His Thr His Gln Leu Tyr Val Pro Ile Ala
180 185 190

tgt ttt atg tta gca gca tgt tta tta ggt ttt ttg cca tat aat ttc 624
Cys Phe Met Leu Ala Ala Cys Leu Leu Gly Phe Leu Pro Tyr Asn Phe
195 200 205

cat cct gcc aag att ttc ttg ggt gac aca ggt gca ctt tat att ggg 672
His Pro Ala Lys Ile Phe Leu Gly Asp Thr Gly Ala Leu Tyr Ile Gly
210 215 220

```

```

ttt atg att gcg gtt ttg tct tta aaa gga ctg aaa aac gta act ttc 720
Phe Met Ile Ala Val Leu Ser Leu Lys Gly Leu Lys Asn Val Thr Phe
225                230                235                240

att tca ttg tta gtg cca ata att att tta ggg gtg cca ata act gat 768
Ile Ser Leu Leu Val Pro Ile Ile Ile Leu Gly Val Pro Ile Thr Asp
                245                250                255

aca gtt tat gca atg att cgt agg aaa ttg aac aaa aaa ccg att tca 816
Thr Val Tyr Ala Met Ile Arg Arg Lys Leu Asn Lys Lys Pro Ile Ser
                260                265                270

gaa gct gat aaa cat cac tta cat cac caa tta atg cga atg gga cta 864
Glu Ala Asp Lys His His Leu His His Gln Leu Met Arg Met Gly Leu
                275                280                285

act cat aga caa aca gtt tta aca atc tat gca ctc tca tta gtt ttt 912
Thr His Arg Gln Thr Val Leu Thr Ile Tyr Ala Leu Ser Leu Val Phe
                290                295                300

tca ttc att tca ctt tta ttt tta cta tca cca gct tgg gga act tgg 960
Ser Phe Ile Ser Leu Leu Phe Leu Leu Ser Pro Ala Trp Gly Thr Trp
305                310                315                320

ctt ttg att ctt ggt tta ctg gtt gca ctt gaa tat ttc gtg gaa tcg 1008
Leu Leu Ile Leu Gly Leu Leu Val Ala Leu Glu Tyr Phe Val Glu Ser
                325                330                335

att ggt ctt tta ggt gag aaa tat cat cct tta atg cat atc att caa 1056
Ile Gly Leu Leu Gly Glu Lys Tyr His Pro Leu Met His Ile Ile Gln
                340                345                350

aaa gtt att aat caa aag agt aaa att gat cca aca gtc gag gtt tgg 1104
Lys Val Ile Asn Gln Lys Ser Lys Ile Asp Pro Thr Val Glu Val Trp
                355                360                365

cat tta ggt gat gaa aag cca gat caa ttg aaa gca gaa aag gat aga 1152
His Leu Gly Asp Glu Lys Pro Asp Gln Leu Lys Ala Glu Lys Asp Arg
                370                375                380

aaa aat tat aaa aag
Lys Asn Tyr Lys Lys
385

```

<210> 126

<211> 389

<212> PRT

<213> Lactobacillus acidophilus

<400> 126

```

Met Phe Lys Ile Ile Val Glu Leu Phe Leu Leu Val Ile Ile Ser Ala
 1                5                10                15
Ala Ile Thr Pro Phe Ile Arg Arg Leu Ala Phe Val Leu Gly Ala Val
                20                25                30
Asp Asn Pro Asn Ala Arg Arg Val Asn Lys Lys Pro Met Pro Thr Ile

```

```

      35      40      45
Gly Gly Leu Gly Ile Phe Val Thr Phe Asn Ile Gly Ala Phe Val Leu
  50      55      60
Leu Arg Glu Gln Phe Pro Thr His Glu Ile Phe Ser Ile Leu Leu Ala
  65      70      75      80
Ser Ser Val Val Val Leu Thr Gly Leu Ile Asp Asp Ile Leu Glu Leu
      85      90      95
Lys Pro Arg Gln Lys Met Phe Gly Ile Phe Ile Ala Ser Leu Ile Ile
      100      105      110
Tyr Phe Leu Ala Gly Ile Arg Met Asn Val Leu Lys Leu Pro Phe Ile
      115      120      125
Thr Asn Glu Ile Asn Leu Gly Trp Trp Ser Phe Pro Ile Thr Ile Phe
      130      135      140
Trp Ile Leu Ala Leu Thr Asn Ala Val Asn Leu Ile Asp Gly Leu Asp
      145      150      155      160
Gly Leu Ala Asp Gly Val Ser Met Ile Ser Leu Thr Thr Met Gly Ile
      165      170      175
Val Gly Tyr Phe Phe Leu His Thr His Gln Leu Tyr Val Pro Ile Ala
      180      185      190
Cys Phe Met Leu Ala Ala Cys Leu Leu Gly Phe Leu Pro Tyr Asn Phe
      195      200      205
His Pro Ala Lys Ile Phe Leu Gly Asp Thr Gly Ala Leu Tyr Ile Gly
      210      215      220
Phe Met Ile Ala Val Leu Ser Leu Lys Gly Leu Lys Asn Val Thr Phe
      225      230      235      240
Ile Ser Leu Leu Val Pro Ile Ile Ile Leu Gly Val Pro Ile Thr Asp
      245      250      255
Thr Val Tyr Ala Met Ile Arg Arg Lys Leu Asn Lys Lys Pro Ile Ser
      260      265      270
Glu Ala Asp Lys His His Leu His His Gln Leu Met Arg Met Gly Leu
      275      280      285
Thr His Arg Gln Thr Val Leu Thr Ile Tyr Ala Leu Ser Leu Val Phe
      290      295      300
Ser Phe Ile Ser Leu Leu Phe Leu Leu Ser Pro Ala Trp Gly Thr Trp
      305      310      315      320
Leu Leu Ile Leu Gly Leu Leu Val Ala Leu Glu Tyr Phe Val Glu Ser
      325      330      335
Ile Gly Leu Leu Gly Glu Lys Tyr His Pro Leu Met His Ile Ile Gln
      340      345      350
Lys Val Ile Asn Gln Lys Ser Lys Ile Asp Pro Thr Val Glu Val Trp
      355      360      365
His Leu Gly Asp Glu Lys Pro Asp Gln Leu Lys Ala Glu Lys Asp Arg
      370      375      380
Lys Asn Tyr Lys Lys
      385

```

<210> 127

<211> 939

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1922 - penicillin binding protein

<220>

<221> CDS

<222> (1)...(939)

<400> 127

gtg cga cgg gct att aat aga tta ggt gtt aaa ggc tct gta ttg gta	48
Met Arg Arg Ala Ile Asn Arg Leu Gly Val Lys Gly Ser Val Leu Val	
1 5 10 15	
aca agt aat atg aag cct gtg cta aac tat gca aca aat aat agt act	96
Thr Ser Asn Met Lys Pro Val Leu Asn Tyr Ala Thr Asn Asn Ser Thr	
20 25 30	
gac act agc tat tta ata aat tct gtt caa aaa tca atg acc gct gca	144
Asp Thr Ser Tyr Leu Ile Asn Ser Val Gln Lys Ser Met Thr Ala Ala	
35 40 45	
atg gta atg cgt gag gtg caa aaa ggt aag ctt agc tta gat tat aag	192
Met Val Met Arg Glu Val Gln Lys Gly Lys Leu Ser Leu Asp Tyr Lys	
50 55 60	
ctt tct aag tat tat cct aac gta gac gga gct gat tca gtc aaa att	240
Leu Ser Lys Tyr Tyr Pro Asn Val Asp Gly Ala Asp Ser Val Lys Ile	
65 70 75 80	
agt aat ttg ctt gat atg act tcg ggt ctt gat tta cag caa ggt caa	288
Ser Asn Leu Leu Asp Met Thr Ser Gly Leu Asp Leu Gln Gln Gly Gln	
85 90 95	
gaa tta ggt aca aaa gaa ttt att tct gat gaa aag aac att gaa cat	336
Glu Leu Gly Thr Lys Glu Phe Ile Ser Asp Glu Lys Asn Ile Glu His	
100 105 110	
gat cag aaa tac acg ata ttt gat gca caa aat ctt ggt aaa tgg cac	384
Asp Gln Lys Tyr Thr Ile Phe Asp Ala Gln Asn Leu Gly Lys Trp His	
115 120 125	
tat act tca gtt aac tac att tat ctc tgc ggt atc tta tct aag ctt	432
Tyr Thr Ser Val Asn Tyr Ile Tyr Leu Cys Gly Ile Leu Ser Lys Leu	
130 135 140	
gag cac aag act tat gag caa tta ttt cat gag act tat atc aag cca	480
Glu His Lys Thr Tyr Glu Gln Leu Phe His Glu Thr Tyr Ile Lys Pro	
145 150 155 160	
ctt ggc tta aag caa acg gaa ttc ctt tgg tca gat atg tct aaa ctg	528
Leu Gly Leu Lys Gln Thr Glu Phe Leu Trp Ser Asp Met Ser Lys Leu	
165 170 175	
cgt gcc gtt aac tgg gta cca gga tat gag atg aag gaa ggt cag tac	576
Arg Ala Val Asn Trp Val Pro Gly Tyr Glu Met Lys Glu Gly Gln Tyr	
180 185 190	
gtt aaa gta aaa cat gat gct gca gtg aaa gat gca cat aat gag tta	624
Val Lys Val Lys His Asp Ala Ala Val Lys Asp Ala His Asn Glu Leu	
195 200 205	

```

ggt gct gga tca gtt gta atg tct aat ggt gat ttg gct aaa aca att 672
Gly Ala Gly Ser Val Val Met Ser Asn Gly Asp Leu Ala Lys Thr Ile
210 215 220

gaa tat att ttg cat ggt aac atg cta acc aaa caa agt aag cag atc 720
Glu Tyr Ile Leu His Gly Asn Met Leu Thr Lys Gln Ser Lys Gln Ile
225 230 235 240

ctc ttt aag ggg aag gct cct aca ttc tat aat ggt gga ttg tat aac 768
Leu Phe Lys Gly Lys Ala Pro Thr Phe Tyr Asn Gly Gly Leu Tyr Asn
245 250 255

ctt aag aat tac aaa tct gct aat ggt gca ggt gaa ggg tat tat act 816
Leu Lys Asn Tyr Lys Ser Ala Asn Gly Ala Gly Glu Gly Tyr Tyr Thr
260 265 270

ttt atg cgt act act aag gat ggg aag aat atg att att att cag gat 864
Phe Met Arg Thr Thr Lys Asp Gly Lys Asn Met Ile Ile Ile Gln Asp
275 280 285

aat cac acc gtt cct ggt gag ttt ggt aag gtt aag aag aaa gtg aac 912
Asn His Thr Val Pro Gly Glu Phe Gly Lys Val Lys Lys Val Asn
290 295 300

cgc atc atg tca atg atg atg aac ttt 939
Arg Ile Met Ser Met Met Met Asn Phe
305 310

```

<210> 128

<211> 313

<212> PRT

<213> Lactobacillus acidophilus

<400> 128

```

Met Arg Arg Ala Ile Asn Arg Leu Gly Val Lys Gly Ser Val Leu Val
1 5 10 15
Thr Ser Asn Met Lys Pro Val Leu Asn Tyr Ala Thr Asn Asn Ser Thr
20 25 30
Asp Thr Ser Tyr Leu Ile Asn Ser Val Gln Lys Ser Met Thr Ala Ala
35 40 45
Met Val Met Arg Glu Val Gln Lys Gly Lys Leu Ser Leu Asp Tyr Lys
50 55 60
Leu Ser Lys Tyr Tyr Pro Asn Val Asp Gly Ala Asp Ser Val Lys Ile
65 70 75 80
Ser Asn Leu Leu Asp Met Thr Ser Gly Leu Asp Leu Gln Gln Gly Gln
85 90 95
Glu Leu Gly Thr Lys Glu Phe Ile Ser Asp Glu Lys Asn Ile Glu His
100 105 110
Asp Gln Lys Tyr Thr Ile Phe Asp Ala Gln Asn Leu Gly Lys Trp His
115 120 125
Tyr Thr Ser Val Asn Tyr Ile Tyr Leu Cys Gly Ile Leu Ser Lys Leu
130 135 140
Glu His Lys Thr Tyr Glu Gln Leu Phe His Glu Thr Tyr Ile Lys Pro
145 150 155 160
Leu Gly Leu Lys Gln Thr Glu Phe Leu Trp Ser Asp Met Ser Lys Leu

```

```

          165          170          175
Arg Ala Val Asn Trp Val Pro Gly Tyr Glu Met Lys Glu Gly Gln Tyr
          180          185          190
Val Lys Val Lys His Asp Ala Ala Val Lys Asp Ala His Asn Glu Leu
          195          200          205
Gly Ala Gly Ser Val Val Met Ser Asn Gly Asp Leu Ala Lys Thr Ile
          210          215          220
Glu Tyr Ile Leu His Gly Asn Met Leu Thr Lys Gln Ser Lys Gln Ile
          225          230          235
Leu Phe Lys Gly Lys Ala Pro Thr Phe Tyr Asn Gly Gly Leu Tyr Asn
          245          250          255
Leu Lys Asn Tyr Lys Ser Ala Asn Gly Ala Gly Glu Gly Tyr Tyr Thr
          260          265          270
Phe Met Arg Thr Thr Lys Asp Gly Lys Asn Met Ile Ile Ile Gln Asp
          275          280          285
Asn His Thr Val Pro Gly Glu Phe Gly Lys Val Lys Lys Lys Val Asn
          290          295          300
Arg Ile Met Ser Met Met Met Asn Phe
          305          310

```

<210> 129

<211> 1122

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 59 - penicillin binding protein (pbpX)

<220>

<221> CDS

<222> (1)...(1122)

<400> 129

```

ttg aag aaa tta ctt atc aaa ctt gca gct gct agt ctt tta tca gca 48
Met Lys Lys Leu Leu Ile Lys Leu Ala Ala Ser Leu Leu Ser Ala
  1          5          10          15

```

```

aca gta cca aca atg att gct cca acc gca acg gtt cat gca agt tca 96
Thr Val Pro Thr Met Ile Ala Pro Thr Ala Thr Val His Ala Ser Ser
          20          25          30

```

```

tat tcc aga act gag atg cgt aat ttt gta cgt aat gtt ttt gca caa 144
Tyr Ser Arg Thr Glu Met Arg Asn Phe Val Arg Asn Val Phe Ala Gln
          35          40          45

```

```

aat aat agt cgc ggt agc gcg gta att att aag gat ggt caa ccg caa 192
Asn Asn Ser Arg Gly Ser Ala Val Ile Ile Lys Asp Gly Gln Pro Gln
          50          55          60

```

```

caa att agt tac ggt tgg gcc tgg tat ggt aaa aag atc ggc aat ggt 240
Gln Ile Ser Tyr Gly Trp Ala Trp Tyr Gly Lys Lys Ile Gly Asn Gly
          65          70          75          80

```

aat gaa cgc gta gtt tat cct aca ggt tct tta caa aaa gtt att act	288
Asn Glu Arg Val Val Tyr Pro Thr Gly Ser Leu Gln Lys Val Ile Thr	
85 90 95	
gcc gca att att att caa tta atg aat gaa aat ttg cat act aac caa	336
Ala Ala Ile Ile Ile Gln Leu Met Asn Glu Asn Leu His Thr Asn Gln	
100 105 110	
cgc ttt tca caa tat aca aaa att tcg cgt tgg tat cct aat cta aaa	384
Arg Phe Ser Gln Tyr Thr Lys Ile Ser Arg Trp Tyr Pro Asn Leu Lys	
115 120 125	
aat gcc gat aat att acc tta ggt caa ctg atg aca cac act tca ggt	432
Asn Ala Asp Asn Ile Thr Leu Gly Gln Leu Met Thr His Thr Ser Gly	
130 135 140	
atc aat gca gtt aac act gaa att gat cgt aat att aat tat tca gaa	480
Ile Asn Ala Val Asn Thr Glu Ile Asp Arg Asn Ile Asn Tyr Ser Glu	
145 150 155 160	
gac gat gca atc aac tgg gca att gat aat gtg aac aac act agc aca	528
Asp Asp Ala Ile Asn Trp Ala Ile Asp Asn Val Asn Asn Thr Ser Thr	
165 170 175	
ggc acc cca gga aca tac ttt tac aat aat acg aac tac att ttg ctt	576
Gly Thr Pro Gly Thr Tyr Phe Tyr Asn Asn Thr Asn Tyr Ile Leu Leu	
180 185 190	
gca gga att atc aaa aaa att agt ggc caa tcc tat gaa gag aat ttt	624
Ala Gly Ile Ile Lys Lys Ile Ser Gly Gln Ser Tyr Glu Glu Asn Phe	
195 200 205	
aac aat cga att gtt aac aaa ctt ggt tta gcc aat aca ttc ctt tat	672
Asn Asn Arg Ile Val Asn Lys Leu Gly Leu Ala Asn Thr Phe Leu Tyr	
210 215 220	
caa aac atc cct agc tgg aag aca gat cca att tct tat ata tgg aac	720
Gln Asn Ile Pro Ser Trp Lys Thr Asp Pro Ile Ser Tyr Ile Trp Asn	
225 230 235 240	
aat ggc aaa aac tat caa gaa cct gaa tat gtt tca aga tca tta gcc	768
Asn Gly Lys Asn Tyr Gln Glu Pro Glu Tyr Val Ser Arg Ser Leu Ala	
245 250 255	
tct caa cta ccg ggt gcg ggg aac atg ttc acc aca cca att gat tat	816
Ser Gln Leu Pro Gly Ala Gly Asn Met Phe Thr Thr Pro Ile Asp Tyr	
260 265 270	
tac aaa att cag ctt ggt tta act aat gga agt att tta agt cga gag	864
Tyr Lys Ile Gln Leu Gly Leu Thr Asn Gly Ser Ile Leu Ser Arg Glu	
275 280 285	
gac ttt agg tat ctt act cat tta aaa aat aga gta aat gat tac tct	912
Asp Phe Arg Tyr Leu Thr His Leu Lys Asn Arg Val Asn Asp Tyr Ser	
290 295 300	
ggg ggt cta tat ctt gat aat aat gac act att aaa tct gct tat gga	960

Gly Gly Leu Tyr Leu Asp Asn Asn Asp Thr Ile Lys Ser Ala Tyr Gly
 305 310 315 320

aat tta aca aat act cac ttt ggt gca tgg att caa atg acg gct gat 1008
 Asn Leu Thr Asn Thr His Phe Gly Ala Trp Ile Gln Met Thr Ala Asp
 325 330 335

aac cgc aat ggg tta atc atg ttt tta aac caa aca tca ggc gat gaa 1056
 Asn Arg Asn Gly Leu Ile Met Phe Leu Asn Gln Thr Ser Gly Asp Glu
 340 345 350

aat gcc caa aag caa atg gga tat caa att tta aat cat att aag cca 1104
 Asn Ala Gln Lys Gln Met Gly Tyr Gln Ile Leu Asn His Ile Lys Pro
 355 360 365

tat aca ttc ctt agt aga 1122
 Tyr Thr Phe Leu Ser Arg
 370

<210> 130

<211> 374

<212> PRT

<213> Lactobacillus acidophilus

<400> 130

Met Lys Lys Leu Leu Ile Lys Leu Ala Ala Ala Ser Leu Leu Ser Ala
 1 5 10 15

Thr Val Pro Thr Met Ile Ala Pro Thr Ala Thr Val His Ala Ser Ser
 20 25 30

Tyr Ser Arg Thr Glu Met Arg Asn Phe Val Arg Asn Val Phe Ala Gln
 35 40 45

Asn Asn Ser Arg Gly Ser Ala Val Ile Ile Lys Asp Gly Gln Pro Gln
 50 55 60

Gln Ile Ser Tyr Gly Trp Ala Trp Tyr Gly Lys Lys Ile Gly Asn Gly
 65 70 75 80

Asn Glu Arg Val Val Tyr Pro Thr Gly Ser Leu Gln Lys Val Ile Thr
 85 90 95

Ala Ala Ile Ile Ile Gln Leu Met Asn Glu Asn Leu His Thr Asn Gln
 100 105 110

Arg Phe Ser Gln Tyr Thr Lys Ile Ser Arg Trp Tyr Pro Asn Leu Lys
 115 120 125

Asn Ala Asp Asn Ile Thr Leu Gly Gln Leu Met Thr His Thr Ser Gly
 130 135 140

Ile Asn Ala Val Asn Thr Glu Ile Asp Arg Asn Ile Asn Tyr Ser Glu
 145 150 155 160

Asp Asp Ala Ile Asn Trp Ala Ile Asp Asn Val Asn Asn Thr Ser Thr
 165 170 175

Gly Thr Pro Gly Thr Tyr Phe Tyr Asn Asn Thr Asn Tyr Ile Leu Leu
 180 185 190

Ala Gly Ile Ile Lys Lys Ile Ser Gly Gln Ser Tyr Glu Glu Asn Phe
 195 200 205

Asn Asn Arg Ile Val Asn Lys Leu Gly Leu Ala Asn Thr Phe Leu Tyr
 210 215 220

Gln Asn Ile Pro Ser Trp Lys Thr Asp Pro Ile Ser Tyr Ile Trp Asn
 225 230 235 240

Asn Gly Lys Asn Tyr Gln Glu Pro Glu Tyr Val Ser Arg Ser Leu Ala

```

                245                250                255
Ser Gln Leu Pro Gly Ala Gly Asn Met Phe Thr Thr Pro Ile Asp Tyr
                260                265                270
Tyr Lys Ile Gln Leu Gly Leu Thr Asn Gly Ser Ile Leu Ser Arg Glu
                275                280                285
Asp Phe Arg Tyr Leu Thr His Leu Lys Asn Arg Val Asn Asp Tyr Ser
                290                295                300
Gly Gly Leu Tyr Leu Asp Asn Asn Asp Thr Ile Lys Ser Ala Tyr Gly
305                310                315                320
Asn Leu Thr Asn Thr His Phe Gly Ala Trp Ile Gln Met Thr Ala Asp
                325                330                335
Asn Arg Asn Gly Leu Ile Met Phe Leu Asn Gln Thr Ser Gly Asp Glu
                340                345                350
Asn Ala Gln Lys Gln Met Gly Tyr Gln Ile Leu Asn His Ile Lys Pro
                355                360                365
Tyr Thr Phe Leu Ser Arg
                370

```

```

<210> 131
<211> 2106
<212> DNA
<213> Lactobacillus acidophilus

<220>
<221> misc_feature
<222> (0)...(0)
<223> ORF 1509 - penicillin binding protein

```

```

<220>
<221> CDS
<222> (1)...(2106)

```

```

<400> 131
gtg gac tat ttt aga aaa aac agt ggg act ggt tca aat aaa cag tcc 48
Met Asp Tyr Phe Arg Lys Asn Ser Gly Thr Gly Ser Asn Lys Gln Ser
 1                5                10                15

tca aca cca ata aga atg cga atc att ctg ggt gtg atc ctc gta ctt 96
Ser Thr Pro Ile Arg Met Arg Ile Ile Leu Gly Val Ile Leu Val Leu
                20                25                30

ttt gcg atg ctg ata ggg cag ctt gca tat ttg caa ctg gtt tat ggt 144
Phe Ala Met Leu Ile Gly Gln Leu Ala Tyr Leu Gln Leu Val Tyr Gly
                35                40                45

tct cgc ttt aaa gcc gag gta cag cag tct gat tcc aca gtt gta tca 192
Ser Arg Phe Lys Ala Glu Val Gln Gln Ser Asp Ser Thr Val Val Ser
                50                55                60

aat caa gtg cct cgt ggt gta atg tat gac gcc aag gga cga gta tta 240
Asn Gln Val Pro Arg Gly Val Met Tyr Asp Ala Lys Gly Arg Val Leu
                65                70                75                80

gta ggt aat aaa gca act aat gcg att act tat act aaa agt gca tcg 288
Val Gly Asn Lys Ala Thr Asn Ala Ile Thr Tyr Thr Lys Ser Ala Ser

```

85										90					95					
act	acg	acg	gcg	caa	att	tac	caa	att	tcg	aac	gct	ttg	agt	aat	tat	336				
Thr	Thr	Thr	Ala	Gln	Ile	Tyr	Gln	Ile	Ser	Asn	Ala	Leu	Ser	Asn	Tyr					
100										105					110					
atc	aag	att	act	gat	gaa	aag	ccg	aca	aag	caa	atg	acg	gct	gat	tac	384				
Ile	Lys	Ile	Thr	Asp	Glu	Lys	Pro	Thr	Lys	Gln	Met	Thr	Ala	Asp	Tyr					
115										120					125					
tac	tta	gca	gat	gaa	aag	aat	aat	acc	aaa	ata	gaa	tca	tta	ttg	cct	432				
Tyr	Leu	Ala	Asp	Glu	Lys	Asn	Asn	Thr	Lys	Ile	Glu	Ser	Leu	Leu	Pro					
130										135					140					
aaa	tca	gct	aag	gtt	gat	gct	ggc	ggc	aat	aag	aag	act	aat	tct	gaa	480				
Lys	Ser	Ala	Lys	Val	Asp	Ala	Gly	Gly	Asn	Lys	Lys	Thr	Asn	Ser	Glu					
145										150					155					160
gtt	tat	caa	gct	gaa	tta	gcg	tat	gtt	gaa	aaa	atg	aat	cct	aag	ctg	528				
Val	Tyr	Gln	Ala	Glu	Leu	Ala	Tyr	Val	Glu	Lys	Met	Asn	Pro	Lys	Leu					
165										170					175					
act	gaa	aaa	cag	aaa	aca	gca	gct	ttg	atc	ttc	aat	aag	att	tca	gga	576				
Thr	Glu	Lys	Gln	Lys	Thr	Ala	Ala	Leu	Ile	Phe	Asn	Lys	Ile	Ser	Gly					
180										185					190					
gcc	tac	act	tta	tca	act	att	tat	att	aaa	aat	aaa	ggg	tta	acg	gat	624				
Ala	Tyr	Thr	Leu	Ser	Thr	Ile	Tyr	Ile	Lys	Asn	Lys	Gly	Leu	Thr	Asp					
195										200					205					
aga	gaa	att	gct	caa	gta	ggg	gaa	cac	ttg	tca	gaa	ctt	cca	ggg	gta	672				
Arg	Glu	Ile	Ala	Gln	Val	Gly	Glu	His	Leu	Ser	Glu	Leu	Pro	Gly	Val					
210										215					220					
ggg	atc	gga	act	gac	tgg	caa	aga	tca	tat	cca	aat	ggg	tca	tca	att	720				
Gly	Ile	Gly	Thr	Asp	Trp	Gln	Arg	Ser	Tyr	Pro	Asn	Gly	Ser	Ser	Ile					
225										230					235					240
caa	agt	att	atc	ggg	tca	gtt	tca	act	gaa	aaa	tct	ggg	ttg	cct	agc	768				
Gln	Ser	Ile	Ile	Gly	Ser	Val	Ser	Thr	Glu	Lys	Ser	Gly	Leu	Pro	Ser					
245										250					255					
gat	aac	tta	cag	tac	tat	tta	aga	aat	ggg	tac	tct	aga	aat	gat	cgt	816				
Asp	Asn	Leu	Gln	Tyr	Tyr	Leu	Arg	Asn	Gly	Tyr	Ser	Arg	Asn	Asp	Arg					
260										265					270					
gtt	ggg	acg	tca	tat	cta	gaa	gaa	gaa	tat	gaa	ccg	ctt	tta	aaa	ggg	864				
Val	Gly	Thr	Ser	Tyr	Leu	Glu	Glu	Glu	Tyr	Glu	Pro	Leu	Leu	Lys	Gly					
275										280					285					
acg	aag	tca	act	agt	cag	gta	act	act	aaa	tca	aat	ggg	aat	att	caa	912				
Thr	Lys	Ser	Thr	Ser	Gln	Val	Thr	Thr	Lys	Ser	Asn	Gly	Asn	Ile	Gln					
290										295					300					
caa	acc	aag	act	gtt	tat	aac	ggg	caa	gct	ggg	gca	agt	ttg	atg	tta	960				
Gln	Thr	Lys	Thr	Val	Tyr	Asn	Gly	Gln	Ala	Gly	Ala	Ser	Leu	Met	Leu					
305										310					315					320

act att gat gcc aag tat caa aaa caa gtt caa gct gct tta aag cgt	1008
Thr Ile Asp Ala Lys Tyr Gln Lys Gln Val Gln Ala Ala Leu Lys Arg	
325 330 335	
gtt tat agt tct gct gaa gcg gca ggt gct gca cga tat tcc aat ggt	1056
Val Tyr Ser Ser Ala Glu Ala Ala Gly Ala Ala Arg Tyr Ser Asn Gly	
340 345 350	
gcg tat gct gta gca atg aat cct caa act ggt gcg ctt ctc gct gtt	1104
Ala Tyr Ala Val Ala Met Asn Pro Gln Thr Gly Ala Leu Leu Ala Val	
355 360 365	
gcc ggt att aat aga aat act aat act ggt aaa act acg gat aat gcg	1152
Ala Gly Ile Asn Arg Asn Thr Asn Thr Gly Lys Thr Thr Asp Asn Ala	
370 375 380	
tta ggc gta att aac caa tca ttt gtt atg ggg tcc gtt gtt aaa gga	1200
Leu Gly Val Ile Asn Gln Ser Phe Val Met Gly Ser Val Val Lys Gly	
385 390 395 400	
gcg act gta tcg ggt ggt tta att aat aaa gta att aca cca aca aat	1248
Ala Thr Val Ser Gly Gly Leu Ile Asn Lys Val Ile Thr Pro Thr Asn	
405 410 415	
aat act tta cct gat acg cca att tac ttg cca ggt tct cca gtt aag	1296
Asn Thr Leu Pro Asp Thr Pro Ile Tyr Leu Pro Gly Ser Pro Val Lys	
420 425 430	
aaa tca gtt tac cca gta ggt act ttc agt tct ctt gat gca gaa acc	1344
Lys Ser Val Tyr Pro Val Gly Thr Phe Ser Ser Leu Asp Ala Glu Thr	
435 440 445	
gct ttg gaa gtt tcc agt aac att tac atg atg cac tta gct atg aat	1392
Ala Leu Glu Val Ser Ser Asn Ile Tyr Met Met His Leu Ala Met Asn	
450 455 460	
tggttt ggt gct aag tat gtg cct aag act tat att cat atg ccc aat	1440
Trp Val Gly Ala Lys Tyr Val Pro Lys Thr Tyr Ile His Met Pro Asn	
465 470 475 480	
aat tca ttt gac att tta cgt cgt aac ttt gca atg ttt ggg tta gga	1488
Asn Ser Phe Asp Ile Leu Arg Arg Asn Phe Ala Met Phe Gly Leu Gly	
485 490 495	
caa aag act ggt gtt gac tta cca ggt gaa gtt tca ggt att cag ggt	1536
Gln Lys Thr Gly Val Asp Leu Pro Gly Glu Val Ser Gly Ile Gln Gly	
500 505 510	
aag tca ttt aac tct aaa ggt aat att tta tca ggt tct gta ctt gac	1584
Lys Ser Phe Asn Ser Lys Gly Asn Ile Leu Ser Gly Ser Val Leu Asp	
515 520 525	
ttg gcc tat ggt aac tat gat gca tat acg cca att caa ctt gcg caa	1632
Leu Ala Tyr Gly Asn Tyr Asp Ala Tyr Thr Pro Ile Gln Leu Ala Gln	
530 535 540	

tat gta tca act att gct aat ggc ggc tac aga atg cag cca tat att 1680
 Tyr Val Ser Thr Ile Ala Asn Gly Gly Tyr Arg Met Gln Pro Tyr Ile
 545 550 555 560
 gtg caa tct gta ggt aag aca agc aaa gat ggt aaa aag atc tat att 1728
 Val Gln Ser Val Gly Lys Thr Ser Lys Asp Gly Lys Lys Ile Tyr Ile
 565 570 575
 aat tac aat aaa aag cca aat gtt caa caa tcc att cca tgg act cca 1776
 Asn Tyr Asn Lys Lys Pro Asn Val Gln Gln Ser Ile Pro Trp Thr Pro
 580 585 590
 gat gag ctt aac gtt gta aga caa ggg ttt tac cgt gta gtt cac ggt 1824
 Asp Glu Leu Asn Val Val Arg Gln Gly Phe Tyr Arg Val Val His Gly
 595 600 605
 act aac ggt tgg ggt act gct cac cca ctg aag aat gtt aaa cct tca 1872
 Thr Asn Gly Trp Gly Thr Ala His Pro Leu Lys Asn Val Lys Pro Ser
 610 615 620
 att tca ggt aag acc ggt act gct caa act ttc tat tac gat gca gaa 1920
 Ile Ser Gly Lys Thr Gly Thr Ala Gln Thr Phe Tyr Tyr Asp Ala Glu
 625 630 635 640
 cat cct aat aga aag cac aac att gaa tta atc aat gca act ttc atc 1968
 His Pro Asn Arg Lys His Asn Ile Glu Leu Ile Asn Ala Thr Phe Ile
 645 650 655
 ggt tat gct cca tct aat aat cca aaa tta gca atc gca gtt gta ttc 2016
 Gly Tyr Ala Pro Ser Asn Asn Pro Lys Leu Ala Ile Ala Val Val Phe
 660 665 670
 cca gga ctt gat cct gat ggt gaa ggt aca tat act tta cag gtt gct 2064
 Pro Gly Leu Asp Pro Asp Gly Glu Gly Thr Tyr Thr Leu Gln Val Ala
 675 680 685
 aaa gca atg gtt caa gat tat ttc aag ctt cat tcc aca aaa 2106
 Lys Ala Met Val Gln Asp Tyr Phe Lys Leu His Ser Thr Lys
 690 695 700

<210> 132

<211> 702

<212> PRT

<213> Lactobacillus acidophilus

<400> 132

Met Asp Tyr Phe Arg Lys Asn Ser Gly Thr Gly Ser Asn Lys Gln Ser
 1 5 10 15
 Ser Thr Pro Ile Arg Met Arg Ile Ile Leu Gly Val Ile Leu Val Leu
 20 25 30
 Phe Ala Met Leu Ile Gly Gln Leu Ala Tyr Leu Gln Leu Val Tyr Gly
 35 40 45
 Ser Arg Phe Lys Ala Glu Val Gln Gln Ser Asp Ser Thr Val Val Ser
 50 55 60
 Asn Gln Val Pro Arg Gly Val Met Tyr Asp Ala Lys Gly Arg Val Leu

65					70					75				80
Val	Gly	Asn	Lys	Ala	Thr	Asn	Ala	Ile	Thr	Tyr	Thr	Lys	Ser	Ala
				85						90				95
Thr	Thr	Thr	Ala	Gln	Ile	Tyr	Gln	Ile	Ser	Asn	Ala	Leu	Ser	Asn
			100					105						110
Ile	Lys	Ile	Thr	Asp	Glu	Lys	Pro	Thr	Lys	Gln	Met	Thr	Ala	Asp
			115					120						125
Tyr	Leu	Ala	Asp	Glu	Lys	Asn	Asn	Thr	Lys	Ile	Glu	Ser	Leu	Leu
			130				135					140		Pro
Lys	Ser	Ala	Lys	Val	Asp	Ala	Gly	Gly	Asn	Lys	Lys	Thr	Asn	Ser
			145			150					155			Glu
Val	Tyr	Gln	Ala	Glu	Leu	Ala	Tyr	Val	Glu	Lys	Met	Asn	Pro	Lys
			165						170					175
Thr	Glu	Lys	Gln	Lys	Thr	Ala	Ala	Leu	Ile	Phe	Asn	Lys	Ile	Ser
			180					185						190
Ala	Tyr	Thr	Leu	Ser	Thr	Ile	Tyr	Ile	Lys	Asn	Lys	Gly	Leu	Thr
			195				200					205		Asp
Arg	Glu	Ile	Ala	Gln	Val	Gly	Glu	His	Leu	Ser	Glu	Leu	Pro	Gly
			210				215					220		Val
Gly	Ile	Gly	Thr	Asp	Trp	Gln	Arg	Ser	Tyr	Pro	Asn	Gly	Ser	Ser
			225			230				235				240
Gln	Ser	Ile	Ile	Gly	Ser	Val	Ser	Thr	Glu	Lys	Ser	Gly	Leu	Pro
			245						250					255
Asp	Asn	Leu	Gln	Tyr	Tyr	Leu	Arg	Asn	Gly	Tyr	Ser	Arg	Asn	Asp
			260					265					270	Arg
Val	Gly	Thr	Ser	Tyr	Leu	Glu	Glu	Glu	Tyr	Glu	Pro	Leu	Leu	Lys
			275				280					285		Gly
Thr	Lys	Ser	Thr	Ser	Gln	Val	Thr	Thr	Lys	Ser	Asn	Gly	Asn	Ile
			290				295					300		Gln
Gln	Thr	Lys	Thr	Val	Tyr	Asn	Gly	Gln	Ala	Gly	Ala	Ser	Leu	Met
			305			310				315				320
Thr	Ile	Asp	Ala	Lys	Tyr	Gln	Lys	Gln	Val	Gln	Ala	Ala	Leu	Lys
			325						330					335
Val	Tyr	Ser	Ser	Ala	Glu	Ala	Ala	Gly	Ala	Ala	Arg	Tyr	Ser	Asn
			340					345					350	Gly
Ala	Tyr	Ala	Val	Ala	Met	Asn	Pro	Gln	Thr	Gly	Ala	Leu	Leu	Ala
			355				360					365		Val
Ala	Gly	Ile	Asn	Arg	Asn	Thr	Asn	Thr	Gly	Lys	Thr	Thr	Asp	Asn
			370			375					380			Ala
Leu	Gly	Val	Ile	Asn	Gln	Ser	Phe	Val	Met	Gly	Ser	Val	Val	Lys
			385			390				395				400
Ala	Thr	Val	Ser	Gly	Gly	Leu	Ile	Asn	Lys	Val	Ile	Thr	Pro	Thr
			405						410					415
Asn	Thr	Leu	Pro	Asp	Thr	Pro	Ile	Tyr	Leu	Pro	Gly	Ser	Pro	Val
			420					425					430	Lys
Lys	Ser	Val	Tyr	Pro	Val	Gly	Thr	Phe	Ser	Ser	Leu	Asp	Ala	Glu
			435				440					445		Thr
Ala	Leu	Glu	Val	Ser	Ser	Asn	Ile	Tyr	Met	Met	His	Leu	Ala	Met
			450			455					460			Asn
Trp	Val	Gly	Ala	Lys	Tyr	Val	Pro	Lys	Thr	Tyr	Ile	His	Met	Pro
			465			470				475				480
Asn	Ser	Phe	Asp	Ile	Leu	Arg	Arg	Asn	Phe	Ala	Met	Phe	Gly	Leu
			485						490					Gly
Gln	Lys	Thr	Gly	Val	Asp	Leu	Pro	Gly	Glu	Val	Ser	Gly	Ile	Gln
			500					505					510	Gly
Lys	Ser	Phe	Asn	Ser	Lys	Gly	Asn	Ile	Leu	Ser	Gly	Ser	Val	Leu
			515				520					525		Asp

Leu Ala Tyr Gly Asn Tyr Asp Ala Tyr Thr Pro Ile Gln Leu Ala Gln
 530 535 540
 Tyr Val Ser Thr Ile Ala Asn Gly Gly Tyr Arg Met Gln Pro Tyr Ile
 545 550 555 560
 Val Gln Ser Val Gly Lys Thr Ser Lys Asp Gly Lys Lys Ile Tyr Ile
 565 570 575
 Asn Tyr Asn Lys Lys Pro Asn Val Gln Gln Ser Ile Pro Trp Thr Pro
 580 585 590
 Asp Glu Leu Asn Val Val Arg Gln Gly Phe Tyr Arg Val Val His Gly
 595 600 605
 Thr Asn Gly Trp Gly Thr Ala His Pro Leu Lys Asn Val Lys Pro Ser
 610 615 620
 Ile Ser Gly Lys Thr Gly Thr Ala Gln Thr Phe Tyr Tyr Asp Ala Glu
 625 630 635 640
 His Pro Asn Arg Lys His Asn Ile Glu Leu Ile Asn Ala Thr Phe Ile
 645 650 655
 Gly Tyr Ala Pro Ser Asn Asn Pro Lys Leu Ala Ile Ala Val Val Phe
 660 665 670
 Pro Gly Leu Asp Pro Asp Gly Glu Gly Thr Tyr Thr Leu Gln Val Ala
 675 680 685
 Lys Ala Met Val Gln Asp Tyr Phe Lys Leu His Ser Thr Lys
 690 695 700

<210> 133

<211> 2112

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1593 - penicillin binding protein

<220>

<221> CDS

<222> (1)...(2112)

<400> 133

atg tgt ttt agc aac tat gat aca att ttc ttg ttt cta aaa agg agc	48
Met Cys Phe Ser Asn Tyr Asp Thr Ile Phe Leu Phe Leu Lys Arg Ser	
1 5 10 15	
atg tat tta atg aat aat gac caa cca aga aga agt agt ttt aaa gat	96
Met Tyr Leu Met Asn Asn Asp Gln Pro Arg Arg Ser Ser Phe Lys Asp	
20 25 30	
gct tgg cat cga ttt gat aac cgc ttc ttt atc gga cgc tgg att att	144
Ala Trp His Arg Phe Asp Asn Arg Phe Phe Ile Gly Arg Trp Ile Ile	
35 40 45	
tta atc ctg ctt att ctt atg ctt tta act tgt aca tat tat aca atc	192
Leu Ile Leu Leu Ile Leu Met Leu Leu Thr Cys Thr Tyr Tyr Thr Ile	
50 55 60	
aaa gtt aaa act tcg aat atc tcg aat tta aaa gca tca tta tca aca	240

Lys Val Lys Thr Ser Asn Ile Ser Asn Leu Lys Ala Ser Leu Ser Thr	
65 70 75 80	
aca aca acc att tat gat tac aag ggt aaa aaa gct ggt tct ttg tat	288
Thr Thr Thr Ile Tyr Asp Tyr Lys Gly Lys Lys Ala Gly Ser Leu Tyr	
85 90 95	
tca caa aag gga tcg ttt gtt gaa tat gac aaa att tcg cca aat att	336
Ser Gln Lys Gly Ser Phe Val Glu Tyr Asp Lys Ile Ser Pro Asn Ile	
100 105 110	
caa aat gcc gtg att tcg aca gaa gat cgt act ttc tgg aaa aac ccc	384
Gln Asn Ala Val Ile Ser Thr Glu Asp Arg Thr Phe Trp Lys Asn Pro	
115 120 125	
ggc ttt agc gtt aaa gga atg gcc cgt gct gcc att agt tta att att	432
Gly Phe Ser Val Lys Gly Met Ala Arg Ala Ala Ile Ser Leu Ile Ile	
130 135 140	
cat cat ggt caa gtt acc ggt ggt gga tcg acg tta aca cag cag tta	480
His His Gly Gln Val Thr Gly Gly Gly Ser Thr Leu Thr Gln Gln Leu	
145 150 155 160	
gct aag aat tcg ctt ctt acg cag cag caa act ttt tcg cgg aaa tta	528
Ala Lys Asn Ser Leu Leu Thr Gln Gln Gln Thr Phe Ser Arg Lys Leu	
165 170 175	
gag gaa cta ttt ttt gca att gaa atc aat cat gtt tac tct aaa aaa	576
Glu Glu Leu Phe Phe Ala Ile Glu Ile Asn His Val Tyr Ser Lys Lys	
180 185 190	
gat att ttg aca atg tat ttg aac aat gcc tac ttc gga aat ggg gta	624
Asp Ile Leu Thr Met Tyr Leu Asn Asn Ala Tyr Phe Gly Asn Gly Val	
195 200 205	
tgg ggt gtt caa gac gct agt cgt aga tat ttt ggt aaa gat gct agt	672
Trp Gly Val Gln Asp Ala Ser Arg Arg Tyr Phe Gly Lys Asp Ala Ser	
210 215 220	
gaa gta act gtc agt gaa gcc gca aca ctt gct gca att ttg cgt aat	720
Glu Val Thr Val Ser Glu Ala Ala Thr Leu Ala Ala Ile Leu Arg Asn	
225 230 235 240	
cca agt tat tat aat cca gtt gac cat atg gct aat gca tta tca cgt	768
Pro Ser Tyr Tyr Asn Pro Val Asp His Met Ala Asn Ala Leu Ser Arg	
245 250 255	
cga aac cta gtt tta agt tta atg gct gat aat ggc aaa ata act gct	816
Arg Asn Leu Val Leu Ser Leu Met Ala Asp Asn Gly Lys Ile Thr Ala	
260 265 270	
gct caa gct aaa gct tat tct aaa gaa gga tta act tta aga aac act	864
Ala Gln Ala Lys Ala Tyr Ser Lys Glu Gly Leu Thr Leu Arg Asn Thr	
275 280 285	
ttt aaa aac aaa gat ggc tat cgc tat cct tac ttc ttt gat gct gta	912
Phe Lys Asn Lys Asp Gly Tyr Arg Tyr Pro Tyr Phe Phe Asp Ala Val	

290	295	300	
gtt gat gag gca att aac aaa tat ggt tta act gaa gaa cag gta atg			960
Val Asp Glu Ala Ile Asn Lys Tyr Gly Leu Thr Glu Glu Gln Val Met			
305	310	315	320
aat aag gga tta aag att tac act act ctt aat caa aat tac caa gga			1008
Asn Lys Gly Leu Lys Ile Tyr Thr Thr Leu Asn Gln Asn Tyr Gln Gly			
	325	330	335
caa tta caa aat acc ttt gag caa agt tgg ctg ttt cca caa gcg gga			1056
Gln Leu Gln Thr Phe Glu Gln Ser Trp Leu Phe Pro Gln Ala Gly			
	340	345	350
agc gat ggt gtt gaa tgt caa ggt gct agt gtg gca atg gat cca ggt			1104
Ser Asp Gly Val Glu Cys Gln Gly Ala Ser Val Ala Met Asp Pro Gly			
	355	360	365
act gga gcg gtt cgt gca gta att ggt gga cgt ggt caa cat gtc ttt			1152
Thr Gly Ala Val Arg Ala Val Ile Gly Gly Arg Gly Gln His Val Phe			
	370	375	380
cgt ggt tat aac cgt gca aca caa atg aaa cgt cag ccg ggt tct tca			1200
Arg Gly Tyr Asn Arg Ala Thr Gln Met Lys Arg Gln Pro Gly Ser Ser			
	385	390	400
att aag ccg ata gca gta tat gcg cca gct ctt caa aat ggc tat cat			1248
Ile Lys Pro Ile Ala Val Tyr Ala Pro Ala Leu Gln Asn Gly Tyr His			
	405	410	415
tat gat tca gag cta tca aat aaa ttg caa aaa ttt ggt aag aat ggg			1296
Tyr Asp Ser Glu Leu Ser Asn Lys Leu Gln Lys Phe Gly Lys Asn Gly			
	420	425	430
tac gaa cca cat aac gtt gac aac ggc tat tct gat aaa atc cca atg			1344
Tyr Glu Pro His Asn Val Asp Asn Gly Tyr Ser Asp Lys Ile Pro Met			
	435	440	445
tac caa gcc ttg gct caa agt aaa aat gtg cca gca gtt tgg tta tta			1392
Tyr Gln Ala Leu Ala Gln Ser Lys Asn Val Pro Ala Val Trp Leu Leu			
	450	455	460
gat aaa att ggt gta aat aaa ggg gtt caa tct gtt gaa aac ttt ggt			1440
Asp Lys Ile Gly Val Asn Lys Gly Val Gln Ser Val Glu Asn Phe Gly			
	465	470	480
att aaa gta ccg aaa agt gat cgt aac ctt gct ttg gcc tta ggt ggt			1488
Ile Lys Val Pro Lys Ser Asp Arg Asn Leu Ala Leu Ala Leu Gly Gly			
	485	490	495
ctt tca agt ggt gta tca cca ttg caa atg gct cga gct tat tct gct			1536
Leu Ser Ser Gly Val Ser Pro Leu Gln Met Ala Arg Ala Tyr Ser Ala			
	500	505	510
ttt gcc aat aag ggt aac tta cca aat aac tca tac ttt att act aag			1584
Phe Ala Asn Lys Gly Asn Leu Pro Asn Asn Ser Tyr Phe Ile Thr Lys			
	515	520	525

```

att aca gat gca agt ggt aat gtt ttg gca gaa aac aat aat cta ggt 1632
Ile Thr Asp Ala Ser Gly Asn Val Leu Ala Glu Asn Asn Asn Leu Gly
530 535 540

acc cat aga gtt att tca gag aat aca gca aaa gaa atg act acg atg 1680
Thr His Arg Val Ile Ser Glu Asn Thr Ala Lys Glu Met Thr Thr Met
545 550 555 560

atg ctt ggg gtg ttt act aat ggt aca ggt cag tct gct caa cct aat 1728
Met Leu Gly Val Phe Thr Asn Gly Thr Gly Gln Ser Ala Gln Pro Asn
565 570 575

ggg tat aaa gta gct ggt aaa act gga tca acg gaa gta cct aat tca 1776
Gly Tyr Lys Val Ala Gly Lys Thr Gly Ser Thr Glu Val Pro Asn Ser
580 585 590

tat ggt ttc ggt acc aaa gat caa tgg att gtc ggg tat aca cca gat 1824
Tyr Gly Phe Gly Thr Lys Asp Gln Trp Ile Val Gly Tyr Thr Pro Asp
595 600 605

att gtt tta gct act tgg gtc ggc ttt gat cgt act aac cgg caa cat 1872
Ile Val Leu Ala Thr Trp Val Gly Phe Asp Arg Thr Asn Arg Gln His
610 615 620

tat atg caa ggt atc tct gaa aca gga att act agg ttg tat aaa gca 1920
Tyr Met Gln Gly Ile Ser Glu Thr Gly Ile Thr Arg Leu Tyr Lys Ala
625 630 635 640

gaa atg gaa gga atc ttg cca tat act gca caa acg caa ttt act gaa 1968
Glu Met Glu Gly Ile Leu Pro Tyr Thr Ala Gln Thr Gln Phe Thr Glu
645 650 655

aaa gca cct agc caa att ata aag aat aat ggt tca aat tct gat tgg 2016
Lys Ala Pro Ser Gln Ile Ile Lys Asn Asn Gly Ser Asn Ser Asp Trp
660 665 670

act ggt gga tta gga caa aaa att caa gat ggt ata ggt tct gcg gga 2064
Thr Gly Gly Leu Gly Gln Lys Ile Gln Asp Gly Ile Gly Ser Ala Gly
675 680 685

cag aca att aat gaa tgg tat aat agt ctg aaa ggg cta tta ggc cga 2112
Gln Thr Ile Asn Glu Trp Tyr Asn Ser Leu Lys Gly Leu Leu Gly Arg
690 695 700

```

<210> 134

<211> 704

<212> PRT

<213> Lactobacillus acidophilus

<400> 134

```

Met Cys Phe Ser Asn Tyr Asp Thr Ile Phe Leu Phe Leu Lys Arg Ser
1 5 10 15
Met Tyr Leu Met Asn Asn Asp Gln Pro Arg Arg Ser Ser Phe Lys Asp
20 25 30

```

Ala Trp His Arg Phe Asp Asn Arg Phe Phe Ile Gly Arg Trp Ile Ile
 35 40 45
 Leu Ile Leu Leu Ile Leu Met Leu Leu Thr Cys Thr Tyr Tyr Thr Ile
 50 55 60
 Lys Val Lys Thr Ser Asn Ile Ser Asn Leu Lys Ala Ser Leu Ser Thr
 65 70 75 80
 Thr Thr Thr Ile Tyr Asp Tyr Lys Gly Lys Lys Ala Gly Ser Leu Tyr
 85 90 95
 Ser Gln Lys Gly Ser Phe Val Glu Tyr Asp Lys Ile Ser Pro Asn Ile
 100 105 110
 Gln Asn Ala Val Ile Ser Thr Glu Asp Arg Thr Phe Trp Lys Asn Pro
 115 120 125
 Gly Phe Ser Val Lys Gly Met Ala Arg Ala Ala Ile Ser Leu Ile Ile
 130 135 140
 His His Gly Gln Val Thr Gly Gly Gly Ser Thr Leu Thr Gln Gln Leu
 145 150 155 160
 Ala Lys Asn Ser Leu Thr Gln Gln Gln Thr Phe Ser Arg Lys Leu
 165 170 175
 Glu Glu Leu Phe Phe Ala Ile Glu Ile Asn His Val Tyr Ser Lys Lys
 180 185 190
 Asp Ile Leu Thr Met Tyr Leu Asn Asn Ala Tyr Phe Gly Asn Gly Val
 195 200 205
 Trp Gly Val Gln Asp Ala Ser Arg Arg Tyr Phe Gly Lys Asp Ala Ser
 210 215 220
 Glu Val Thr Val Ser Glu Ala Ala Thr Leu Ala Ala Ile Leu Arg Asn
 225 230 235 240
 Pro Ser Tyr Tyr Asn Pro Val Asp His Met Ala Asn Ala Leu Ser Arg
 245 250 255
 Arg Asn Leu Val Leu Ser Leu Met Ala Asp Asn Gly Lys Ile Thr Ala
 260 265 270
 Ala Gln Ala Lys Ala Tyr Ser Lys Glu Gly Leu Thr Leu Arg Asn Thr
 275 280 285
 Phe Lys Asn Lys Asp Gly Tyr Arg Tyr Pro Tyr Phe Phe Asp Ala Val
 290 295 300
 Val Asp Glu Ala Ile Asn Lys Tyr Gly Leu Thr Glu Glu Gln Val Met
 305 310 315 320
 Asn Lys Gly Leu Lys Ile Tyr Thr Thr Leu Asn Gln Asn Tyr Gln Gly
 325 330 335
 Gln Leu Gln Asn Thr Phe Glu Gln Ser Trp Leu Phe Pro Gln Ala Gly
 340 345 350
 Ser Asp Gly Val Glu Cys Gln Gly Ala Ser Val Ala Met Asp Pro Gly
 355 360 365
 Thr Gly Ala Val Arg Ala Val Ile Gly Gly Arg Gly Gln His Val Phe
 370 375 380
 Arg Gly Tyr Asn Arg Ala Thr Gln Met Lys Arg Gln Pro Gly Ser Ser
 385 390 395 400
 Ile Lys Pro Ile Ala Val Tyr Ala Pro Ala Leu Gln Asn Gly Tyr His
 405 410 415
 Tyr Asp Ser Glu Leu Ser Asn Lys Leu Gln Lys Phe Gly Lys Asn Gly
 420 425 430
 Tyr Glu Pro His Asn Val Asp Asn Gly Tyr Ser Asp Lys Ile Pro Met
 435 440 445
 Tyr Gln Ala Leu Ala Gln Ser Lys Asn Val Pro Ala Val Trp Leu Leu
 450 455 460
 Asp Lys Ile Gly Val Asn Lys Gly Val Gln Ser Val Glu Asn Phe Gly
 465 470 475 480
 Ile Lys Val Pro Lys Ser Asp Arg Asn Leu Ala Leu Ala Leu Gly Gly

```

      485      490      495
Leu Ser Ser Gly Val Ser Pro Leu Gln Met Ala Arg Ala Tyr Ser Ala
      500      505      510
Phe Ala Asn Lys Gly Asn Leu Pro Asn Asn Ser Tyr Phe Ile Thr Lys
      515      520      525
Ile Thr Asp Ala Ser Gly Asn Val Leu Ala Glu Asn Asn Leu Gly
      530      535      540
Thr His Arg Val Ile Ser Glu Asn Thr Ala Lys Glu Met Thr Thr Met
      545      550      555      560
Met Leu Gly Val Phe Thr Asn Gly Thr Gly Gln Ser Ala Gln Pro Asn
      565      570      575
Gly Tyr Lys Val Ala Gly Lys Thr Gly Ser Thr Glu Val Pro Asn Ser
      580      585      590
Tyr Gly Phe Gly Thr Lys Asp Gln Trp Ile Val Gly Tyr Thr Pro Asp
      595      600      605
Ile Val Leu Ala Thr Trp Val Gly Phe Asp Arg Thr Asn Arg Gln His
      610      615      620
Tyr Met Gln Gly Ile Ser Glu Thr Gly Ile Thr Arg Leu Tyr Lys Ala
      625      630      635      640
Glu Met Glu Gly Ile Leu Pro Tyr Thr Ala Gln Thr Gln Phe Thr Glu
      645      650      655
Lys Ala Pro Ser Gln Ile Ile Lys Asn Asn Gly Ser Asn Ser Asp Trp
      660      665      670
Thr Gly Gly Leu Gly Gln Lys Ile Gln Asp Gly Ile Gly Ser Ala Gly
      675      680      685
Gln Thr Ile Asn Glu Trp Tyr Asn Ser Leu Lys Gly Leu Leu Gly Arg
      690      695      700

```

<210> 135

<211> 1029

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1605 - penicillin binding protein

<220>

<221> CDS

<222> (1)...(1029)

<400> 135

```

atg cat tta aaa aaa tct atc ctg tcc atc ttt tta aca cta tgc att 48
Met His Leu Lys Lys Ser Ile Leu Ser Ile Phe Leu Thr Leu Cys Ile
1      5      10      15

```

```

ttt ttg ttg ttt att tta ata tca gtg aac aga gtg gat gtt ggc gat 96
Phe Leu Leu Phe Ile Leu Ile Ser Val Asn Arg Val Asp Val Gly Asp
20      25      30

```

```

ata gct tta tca aaa caa ctt cat gat tat atg caa tta cat cat att 144
Ile Ala Leu Ser Lys Gln Leu His Asp Tyr Met Gln Leu His His Ile
35      40      45

```

aat ggt gta atg ttg gtc aat gat aaa aaa ggt aaa cca att ata att	192
Asn Gly Val Met Leu Val Asn Asp Lys Lys Gly Lys Pro Ile Ile Ile	
50 55 60	
gaa aat aga gag act tct aat aaa ggc caa ata gta gat gaa aat caa	240
Glu Asn Arg Glu Thr Ser Asn Lys Gly Gln Ile Val Asp Glu Asn Gln	
65 70 75 80	
tta ttt ccg att gct tct ctt caa aag att atg aca ggg act gca att	288
Leu Phe Pro Ile Ala Ser Leu Gln Lys Ile Met Thr Gly Thr Ala Ile	
85 90 95	
tat caa tta cat caa aaa aag cag ata aat tgg aat act tct ttg gct	336
Tyr Gln Leu His Gln Lys Lys Gln Ile Asn Trp Asn Thr Ser Leu Ala	
100 105 110	
aaa tat ttt cct caa atc ccg ggt agt aaa gat ata aca att cgt gaa	384
Lys Tyr Phe Pro Gln Ile Pro Gly Ser Lys Asp Ile Thr Ile Arg Glu	
115 120 125	
ttg atg aat cat acg agt gga tta att aat aat gat cgt cca aca tcc	432
Leu Met Asn His Thr Ser Gly Leu Ile Asn Asn Asp Arg Pro Thr Ser	
130 135 140	
cca tta aga aat gaa aaa caa cag att aat tat atg ctt aaa cat ata	480
Pro Leu Arg Asn Glu Lys Gln Gln Ile Asn Tyr Met Leu Lys His Ile	
145 150 155 160	
aaa tat gat cat att cat act tgg gac tat caa gat ata gat tat gaa	528
Lys Tyr Asp His Ile His Thr Trp Asp Tyr Gln Asp Ile Asp Tyr Glu	
165 170 175	
tta tta gca gca att att agt aaa caa act aac aca acc tat aat act	576
Leu Leu Ala Ala Ile Ile Ser Lys Gln Thr Asn Thr Thr Tyr Asn Thr	
180 185 190	
tat att aaa aat aat ttt gtc aag tct gct aat ctc cat aaa att aaa	624
Tyr Ile Lys Asn Asn Phe Val Lys Ser Ala Asn Leu His Lys Ile Lys	
195 200 205	
gat ttt tca gaa gtt gat caa aga gaa gtt cct caa cct atg aat aaa	672
Asp Phe Ser Glu Val Asp Gln Arg Glu Val Pro Gln Pro Met Asn Lys	
210 215 220	
aag atc agt tgg cat gaa gtt aca gta aca aca tca tct gat ttt gga	720
Lys Ile Ser Trp His Glu Val Thr Val Thr Thr Ser Ser Asp Phe Gly	
225 230 235 240	
gct gga aac ttg ttt att tca cct aac gat tat tgg aaa ttt gta aat	768
Ala Gly Asn Leu Phe Ile Ser Pro Asn Asp Tyr Trp Lys Phe Val Asn	
245 250 255	
aat ggt gtt tta aat aat cat caa atg ata aat gaa tat tat cat cag	816
Asn Gly Val Leu Asn Asn His Gln Met Ile Asn Glu Tyr Tyr His Gln	
260 265 270	
gca caa cat caa gaa gtt gct tat ttt ggt ggt gtt tat ttt aaa ggc	864

Ala Gln His Gln Glu Val Ala Tyr Phe Gly Gly Val Tyr Phe Lys Gly
 275 280 285

gat att att cgt gca gaa ggg agt att cct gga tat aat tcc tgc ttt 912
 Asp Ile Ile Arg Ala Glu Gly Ser Ile Pro Gly Tyr Asn Ser Cys Phe
 290 295 300

gta gct aac tat aga act aag aaa atg att atg ctt ttt tct aat aat 960
 Val Ala Asn Tyr Arg Thr Lys Lys Met Ile Met Leu Phe Ser Asn Asn
 305 310 315 320

att aat tat ttt act ttg aaa atg gca tct gat cat att ttg cat aaa 1008
 Ile Asn Tyr Phe Thr Leu Lys Met Ala Ser Asp His Ile Leu His Lys
 325 330 335

tac ata gag aaa cac att att 1029
 Tyr Ile Glu Lys His Ile Ile
 340

<210> 136

<211> 343

<212> PRT

<213> Lactobacillus acidophilus

<400> 136

Met His Leu Lys Lys Ser Ile Leu Ser Ile Phe Leu Thr Leu Cys Ile
 1 5 10 15
 Phe Leu Leu Phe Ile Leu Ile Ser Val Asn Arg Val Asp Val Gly Asp
 20 25 30
 Ile Ala Leu Ser Lys Gln Leu His Asp Tyr Met Gln Leu His His Ile
 35 40 45
 Asn Gly Val Met Leu Val Asn Asp Lys Lys Gly Lys Pro Ile Ile Ile
 50 55 60
 Glu Asn Arg Glu Thr Ser Asn Lys Gly Gln Ile Val Asp Glu Asn Gln
 65 70 75 80
 Leu Phe Pro Ile Ala Ser Leu Gln Lys Ile Met Thr Gly Thr Ala Ile
 85 90 95
 Tyr Gln Leu His Gln Lys Lys Gln Ile Asn Trp Asn Thr Ser Leu Ala
 100 105 110
 Lys Tyr Phe Pro Gln Ile Pro Gly Ser Lys Asp Ile Thr Ile Arg Glu
 115 120 125
 Leu Met Asn His Thr Ser Gly Leu Ile Asn Asn Asp Arg Pro Thr Ser
 130 135 140
 Pro Leu Arg Asn Glu Lys Gln Gln Ile Asn Tyr Met Leu Lys His Ile
 145 150 155 160
 Lys Tyr Asp His Ile His Thr Trp Asp Tyr Gln Asp Ile Asp Tyr Glu
 165 170 175
 Leu Leu Ala Ala Ile Ile Ser Lys Gln Thr Asn Thr Thr Tyr Asn Thr
 180 185 190
 Tyr Ile Lys Asn Asn Phe Val Lys Ser Ala Asn Leu His Lys Ile Lys
 195 200 205
 Asp Phe Ser Glu Val Asp Gln Arg Glu Val Pro Gln Pro Met Asn Lys
 210 215 220
 Lys Ile Ser Trp His Glu Val Thr Val Thr Thr Ser Ser Asp Phe Gly
 225 230 235 240
 Ala Gly Asn Leu Phe Ile Ser Pro Asn Asp Tyr Trp Lys Phe Val Asn

```

                245                250                255
Asn Gly Val Leu Asn Asn His Gln Met Ile Asn Glu Tyr Tyr His Gln
                260                265                270
Ala Gln His Gln Glu Val Ala Tyr Phe Gly Gly Val Tyr Phe Lys Gly
                275                280                285
Asp Ile Ile Arg Ala Glu Gly Ser Ile Pro Gly Tyr Asn Ser Cys Phe
                290                295                300
Val Ala Asn Tyr Arg Thr Lys Lys Met Ile Met Leu Phe Ser Asn Asn
305                310                315                320
Ile Asn Tyr Phe Thr Leu Lys Met Ala Ser Asp His Ile Leu His Lys
                325                330                335
Tyr Ile Glu Lys His Ile Ile
                340

```

<210> 137

<211> 2328

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1159 - penicillin binding protein 1A (pbp1)

<220>

<221> CDS

<222> (1)...(2328)

<400> 137

```

atg gca gat aat aca aat aat atg aaa cgt gaa tca cga cga aac tat      48
Met Ala Asp Asn Thr Asn Asn Met Lys Arg Glu Ser Arg Arg Asn Tyr
 1                5                10                15

cac gga cga agg tcg agt ggt ggc cat tta tgg ata aaa ata ata aaa      96
His Gly Arg Arg Ser Ser Gly Gly His Leu Trp Ile Lys Ile Ile Lys
                20                25                30

tgg cta ttt ctt gct gca cta tta gtg gta gtt tct ggt att ggg ctt     144
Trp Leu Phe Leu Ala Ala Leu Leu Val Val Val Ser Gly Ile Gly Leu
                35                40                45

ttt gct ttc tat gca aag gat gct cct aat att agt caa agc caa ctt     192
Phe Ala Phe Tyr Ala Lys Asp Ala Pro Asn Ile Ser Gln Ser Gln Leu
                50                55                60

caa agt ggt ggt act tct agc ctt tat acc aat gat ggt aaa ttt tta     240
Gln Ser Gly Gly Thr Ser Ser Leu Tyr Thr Asn Asp Gly Lys Phe Leu
                65                70                75                80

tta tca ctt gga tct gaa aaa aga atc tac gtt aag aat aaa gat att     288
Leu Ser Leu Gly Ser Glu Lys Arg Ile Tyr Val Lys Asn Lys Asp Ile
                85                90                95

cct cga cag tta aaa gac gca att gtt tct gtt gaa gat aaa aga ttc     336
Pro Arg Gln Leu Lys Asp Ala Ile Val Ser Val Glu Asp Lys Arg Phe

```

100	105	110	
tac aaa gat aga ctt gga gta gat	cca att aga att gtg gga tca atg		384
Tyr Lys Asp Arg Leu Gly Val Asp	Pro Ile Arg Ile Val Gly Ser Met		
115	120	125	
ctt act aat gct aag agt aat agt	att gct gca ggt gga tca act att		432
Leu Thr Asn Ala Lys Ser Asn Ser	Ile Ala Ala Gly Gly Ser Thr Ile		
130	135	140	
act caa caa ttg gtt aag tta acc gta ttt	tca act gcg gct tca caa		480
Thr Gln Gln Leu Val Lys Leu Thr Val Phe	Ser Thr Ala Ala Ser Gln		
145	150	155	160
cgt act tta aaa aga aaa gcc caa gaa gct	tgg tta gca atg aaa gtg		528
Arg Thr Leu Lys Arg Lys Ala Gln Glu Ala	Trp Leu Ala Met Lys Val		
165	170	175	
caa cat gaa ttt agt aaa gac caa att tta	gaa ttc tat gtt aat aaa		576
Gln His Glu Phe Ser Lys Asp Gln Ile Leu	Glu Phe Tyr Val Asn Lys		
180	185	190	
gtc ttt atg aat tat ggt aat tac ggt atg	gga aca gcc gct aat tat		624
Val Phe Met Asn Tyr Gly Asn Tyr Gly Met	Gly Thr Ala Ala Asn Tyr		
195	200	205	
tat tac aat aaa tct cta aag gat ctc gat	tta gca caa act gct tta		672
Tyr Tyr Asn Lys Ser Leu Lys Asp Leu Asp	Leu Ala Gln Thr Ala Leu		
210	215	220	
att gca ggg atg cct aat gct cct gta atg	tat gat cca tat tta tac		720
Ile Ala Gly Met Pro Asn Ala Pro Val Met	Tyr Asp Pro Tyr Leu Tyr		
225	230	235	240
cct caa aaa gct cgc tat cgt aga aat atc	gtt tta aag aca atg ctt		768
Pro Gln Lys Ala Arg Tyr Arg Arg Asn Ile	Val Leu Lys Thr Met Leu		
245	250	255	
gaa aat gat aag att acg aag gct caa tat	aat caa gca att aat gaa		816
Glu Asn Asp Lys Ile Thr Lys Ala Gln Tyr	Asn Gln Ala Ile Asn Glu		
260	265	270	
cct att acc aaa gga tta cgc cct aga cac	act aat aat gaa tct aag		864
Pro Ile Thr Lys Gly Leu Arg Pro Arg His	Thr Asn Asn Glu Ser Lys		
275	280	285	
att aga caa atc gat gat cca tat att aag	gag gta att tct gaa gtt		912
Ile Arg Gln Ile Asp Asp Pro Tyr Ile Lys	Glu Val Ile Ser Glu Val		
290	295	300	
aaa agt aaa ggt ttt gat cca tat aat gat	aat ttg aag att aca ata		960
Lys Ser Lys Gly Phe Asp Pro Tyr Asn Asp	Asn Leu Lys Ile Thr Ile		
305	310	315	320
aat att gat caa aaa gct caa aac aag tta	tat caa tta gcg aac aat		1008
Asn Ile Asp Gln Lys Ala Gln Asn Lys Leu	Tyr Gln Leu Ala Asn Asn		
325	330	335	

ggt gaa gta cca ttt act aat gac aaa atg cag att ggt gca act gta	1056
Gly Glu Val Pro Phe Thr Asn Asp Lys Met Gln Ile Gly Ala Thr Val	
340 345 350	
ggt gat cct aat aat ggt cat gta gta gca att tta ggt ggt cga cat	1104
Val Asp Pro Asn Asn Gly His Val Val Ala Ile Leu Gly Gly Arg His	
355 360 365	
tta cct tct gtt caa tta ggt ctt gat cgt gca gtt caa act ggt cgt	1152
Leu Pro Ser Val Gln Leu Gly Leu Asp Arg Ala Val Gln Thr Gly Arg	
370 375 380	
tct acc gga tcg tca att aaa cct gtt ctt gat tat gca cca gcg att	1200
Ser Thr Gly Ser Ser Ile Lys Pro Val Leu Asp Tyr Ala Pro Ala Ile	
385 390 395 400	
caa tat ttg aat tgg tca aca gct aaa atg tta gat gat agt aaa tat	1248
Gln Tyr Leu Asn Trp Ser Thr Ala Lys Met Leu Asp Asp Ser Lys Tyr	
405 410 415	
ggt tat cca gga acc aat att caa tta tat gat tgg gat aac aaa tat	1296
Val Tyr Pro Gly Thr Asn Ile Gln Leu Tyr Asp Trp Asp Asn Lys Tyr	
420 425 430	
gat ggc atg atg aca atg cgt aaa gca ttg gaa caa tca cgt aac gtt	1344
Asp Gly Met Met Thr Met Arg Lys Ala Leu Glu Gln Ser Arg Asn Val	
435 440 445	
cca gca gtt aaa acc ctt gct gat gta gga gta aaa cgt gct tcc gca	1392
Pro Ala Val Lys Thr Leu Ala Asp Val Gly Val Lys Arg Ala Ser Ala	
450 455 460	
ttt gct aga cgt atg ggt gta gat gtt cct gca aat tca ggc tta tca	1440
Phe Ala Arg Arg Met Gly Val Asp Val Pro Ala Asn Ser Gly Leu Ser	
465 470 475 480	
gtg gca att ggt gct aat gca tca agt tta caa atg gct ggt gca tac	1488
Val Ala Ile Gly Ala Asn Ala Ser Ser Leu Gln Met Ala Gly Ala Tyr	
485 490 495	
agt gca ttt gct acc atg ggt gtt tat cat aaa cca caa ttt gta tct	1536
Ser Ala Phe Ala Thr Met Gly Val Tyr His Lys Pro Gln Phe Val Ser	
500 505 510	
aaa att gaa act cca gat ggt tta act aga aat tat gat tca aat ggt	1584
Lys Ile Glu Thr Pro Asp Gly Leu Thr Arg Asn Tyr Asp Ser Asn Gly	
515 520 525	
gtg cgt gta atg aag aaa tct acc gca tat atg att act gat atg tta	1632
Val Arg Val Met Lys Lys Ser Thr Ala Tyr Met Ile Thr Asp Met Leu	
530 535 540	
aaa gga gtt att aaa aga ggt tct ggt aca aac gct aaa ata gct gac	1680
Lys Gly Val Ile Lys Arg Gly Ser Gly Thr Asn Ala Lys Ile Ala Asp	
545 550 555 560	

ctt tat caa gct ggt aaa aca ggt act gtt aaa tac tcc gat gaa gat	1728
Leu Tyr Gln Ala Gly Lys Thr Gly Thr Val Lys Tyr Ser Asp Glu Asp	
565 570 575	
tta gcc aag tat cca ggc tat aat tca act cct aag gat tca tgg ttt	1776
Leu Ala Lys Tyr Pro Gly Tyr Asn Ser Thr Pro Lys Asp Ser Trp Phe	
580 585 590	
gta ggt tat act aga tcg tat gtt atg ggt gtg tgg aca gga tat gat	1824
Val Gly Tyr Thr Arg Ser Tyr Val Met Gly Val Trp Thr Gly Tyr Asp	
595 600 605	
aat cta aaa gat ggt act atc tct gga att ggt cag caa tct gct caa	1872
Asn Leu Lys Asp Gly Thr Ile Ser Gly Ile Gly Gln Gln Ser Ala Gln	
610 615 620	
tta att tat aag agt atg atg acc tac tta atg aga aat aag cct aat	1920
Leu Ile Tyr Lys Ser Met Met Thr Tyr Leu Met Arg Asn Lys Pro Asn	
625 630 635 640	
ttg gat tgc aaa caa cct aat tca gta gtt aga gca aga att gtt aat	1968
Leu Asp Cys Lys Gln Pro Asn Ser Val Val Arg Ala Arg Ile Val Asn	
645 650 655	
aat tct aat cct cca gaa gtt gct act agt ggc gga act tgg caa ttg	2016
Asn Ser Asn Pro Pro Glu Val Ala Thr Ser Gly Gly Thr Trp Gln Leu	
660 665 670	
ttt gtt cgt ggg cat gct cct gca ggt atc gga aat agt gct gca agt	2064
Phe Val Arg Gly His Ala Pro Ala Gly Ile Gly Asn Ser Ala Ala Ser	
675 680 685	
tat gat gaa gaa gat gaa gaa aca gat act act agt aac aat act gat	2112
Tyr Asp Glu Glu Asp Glu Glu Thr Asp Thr Thr Ser Asn Asn Thr Asp	
690 695 700	
aac act acc tca tcc agt tct tca gta acc gta gag agt cgt gtt tct	2160
Asn Thr Thr Ser Ser Ser Ser Ser Val Thr Val Glu Ser Arg Val Ser	
705 710 715 720	
tct aga aga gaa aat ggt act act act caa tca agt agc agt caa aga	2208
Ser Arg Arg Glu Asn Gly Thr Thr Thr Gln Ser Ser Ser Ser Gln Arg	
725 730 735	
gtc tct tct tca agt gaa agt cga gag caa tct tca tcg cgt gaa caa	2256
Val Ser Ser Ser Ser Glu Ser Arg Glu Gln Ser Ser Ser Arg Glu Gln	
740 745 750	
agt agc agt gaa cag caa tct aga ccc gat aat aca gaa cga gat cag	2304
Ser Ser Ser Glu Gln Gln Ser Arg Pro Asp Asn Thr Glu Arg Asp Gln	
755 760 765	
gaa aat act gat aga aat aat gat	2328
Glu Asn Thr Asp Arg Asn Asn Asp	
770 775	

<210> 138

<211> 776

<212> PRT

<213> Lactobacillus acidophilus

<400> 138

```

Met Ala Asp Asn Thr Asn Asn Met Lys Arg Glu Ser Arg Arg Asn Tyr
 1          5          10          15
His Gly Arg Arg Ser Ser Gly Gly His Leu Trp Ile Lys Ile Ile Lys
          20          25          30
Trp Leu Phe Leu Ala Ala Leu Leu Val Val Val Ser Gly Ile Gly Leu
          35          40          45
Phe Ala Phe Tyr Ala Lys Asp Ala Pro Asn Ile Ser Gln Ser Gln Leu
          50          55          60
Gln Ser Gly Gly Thr Ser Ser Leu Tyr Thr Asn Asp Gly Lys Phe Leu
          65          70          75          80
Leu Ser Leu Gly Ser Glu Lys Arg Ile Tyr Val Lys Asn Lys Asp Ile
          85          90          95
Pro Arg Gln Leu Lys Asp Ala Ile Val Ser Val Glu Asp Lys Arg Phe
          100          105          110
Tyr Lys Asp Arg Leu Gly Val Asp Pro Ile Arg Ile Val Gly Ser Met
          115          120          125
Leu Thr Asn Ala Lys Ser Asn Ser Ile Ala Ala Gly Gly Ser Thr Ile
          130          135          140
Thr Gln Gln Leu Val Lys Leu Thr Val Phe Ser Thr Ala Ala Ser Gln
          145          150          155          160
Arg Thr Leu Lys Arg Lys Ala Gln Glu Ala Trp Leu Ala Met Lys Val
          165          170          175
Gln His Glu Phe Ser Lys Asp Gln Ile Leu Glu Phe Tyr Val Asn Lys
          180          185          190
Val Phe Met Asn Tyr Gly Asn Tyr Gly Met Gly Thr Ala Ala Asn Tyr
          195          200          205
Tyr Tyr Asn Lys Ser Leu Lys Asp Leu Asp Leu Ala Gln Thr Ala Leu
          210          215          220
Ile Ala Gly Met Pro Asn Ala Pro Val Met Tyr Asp Pro Tyr Leu Tyr
          225          230          235          240
Pro Gln Lys Ala Arg Tyr Arg Arg Asn Ile Val Leu Lys Thr Met Leu
          245          250          255
Glu Asn Asp Lys Ile Thr Lys Ala Gln Tyr Asn Gln Ala Ile Asn Glu
          260          265          270
Pro Ile Thr Lys Gly Leu Arg Pro Arg His Thr Asn Asn Glu Ser Lys
          275          280          285
Ile Arg Gln Ile Asp Asp Pro Tyr Ile Lys Glu Val Ile Ser Glu Val
          290          295          300
Lys Ser Lys Gly Phe Asp Pro Tyr Asn Asp Asn Leu Lys Ile Thr Ile
          305          310          315          320
Asn Ile Asp Gln Lys Ala Gln Asn Lys Leu Tyr Gln Leu Ala Asn Asn
          325          330          335
Gly Glu Val Pro Phe Thr Asn Asp Lys Met Gln Ile Gly Ala Thr Val
          340          345          350
Val Asp Pro Asn Asn Gly His Val Val Ala Ile Leu Gly Gly Arg His
          355          360          365
Leu Pro Ser Val Gln Leu Gly Leu Asp Arg Ala Val Gln Thr Gly Arg
          370          375          380
Ser Thr Gly Ser Ser Ile Lys Pro Val Leu Asp Tyr Ala Pro Ala Ile
          385          390          395          400
Gln Tyr Leu Asn Trp Ser Thr Ala Lys Met Leu Asp Asp Ser Lys Tyr

```

<210> 139
<211> 654
<212> DNA
<213> *Lactobacillus acidophilus*

```
<220>
<221> misc_feature
<222> (0)...(0)
```

<223> ORF 1158 - penicillin binding protein related
factor A

<220>

<221> CDS

<222> (1)...(654)

<400> 139

atg cta aca gga gtg agg tta atg gtc aaa tat cca agc ggt agt tta	48
Met Leu Thr Gly Val Arg Leu Met Val Lys Tyr Pro Ser Gly Ser Leu	
1 5 10 15	
gcc gca ttt aga aaa cca gtg aca aca caa aaa aag atg cgc act ggt	96
Ala Ala Phe Arg Lys Pro Val Thr Thr Gln Lys Lys Met Arg Thr Gly	
20 25 30	
aaa cgt tca tat aca cat aaa aaa ggc gtt aac ttt tct gat cgt ggt	144
Lys Arg Ser Tyr Thr His Lys Lys Gly Val Asn Phe Ser Asp Arg Gly	
35 40 45	
atg aca ctt gaa caa cag att aat gaa tct aat aaa tat tat tta act	192
Met Thr Leu Glu Gln Gln Ile Asn Glu Ser Asn Lys Tyr Tyr Leu Thr	
50 55 60	
gaa gaa att gca gta gtt cat aaa aaa cca acg cca att caa atc gta	240
Glu Glu Ile Ala Val Val His Lys Lys Pro Thr Pro Ile Gln Ile Val	
65 70 75 80	
aag gtt gat tac cct aag cga tct aaa gca gtt att cgt gaa gct tat	288
Lys Val Asp Tyr Pro Lys Arg Ser Lys Ala Val Ile Arg Glu Ala Tyr	
85 90 95	
ttc aga caa gct tct aca act gat tat aat ggc gtt tat aag gga tat	336
Phe Arg Gln Ala Ser Thr Thr Asp Tyr Asn Gly Val Tyr Lys Gly Tyr	
100 105 110	
tat ctt gac ttt gaa gca aaa gaa aca aag aat aag aca aac ttc ccg	384
Tyr Leu Asp Phe Glu Ala Lys Glu Thr Lys Asn Lys Thr Asn Phe Pro	
115 120 125	
tta aaa aat ttt cat gaa cat caa att ttt cat tta gct gaa tgc tta	432
Leu Lys Asn Phe His Glu His Gln Ile Phe His Leu Ala Glu Cys Leu	
130 135 140	
aag caa cag ggg att tgt ttt acg att att aga ttt gct agc ttg gag	480
Lys Gln Gln Gly Ile Cys Phe Thr Ile Ile Arg Phe Ala Ser Leu Glu	
145 150 155 160	
cga tat ttt gtt aca cca gct agt ttt gta att aat gct tgg aga aaa	528
Arg Tyr Phe Val Thr Pro Ala Ser Phe Val Ile Asn Ala Trp Arg Lys	
165 170 175	
gca gaa aaa agt tct atg act tta aaa gag att gaa agc cat tct tat	576
Ala Glu Lys Ser Ser Met Thr Leu Lys Glu Ile Glu Ser His Ser Tyr	
180 185 190	

gag atc aaa agc ggt ttt cga cct acc cta cct tat ctt aag gca gtg 624
 Glu Ile Lys Ser Gly Phe Arg Pro Thr Leu Pro Tyr Leu Lys Ala Val
 195 200 205

gat aat ttt att gca gat agg aaa aga gaa 654
 Asp Asn Phe Ile Ala Asp Arg Lys Arg Glu
 210 215

<210> 140

<211> 218

<212> PRT

<213> Lactobacillus acidophilus

<400> 140

Met Leu Thr Gly Val Arg Leu Met Val Lys Tyr Pro Ser Gly Ser Leu
 1 5 10 15
 Ala Ala Phe Arg Lys Pro Val Thr Thr Gln Lys Lys Met Arg Thr Gly
 20 25 30
 Lys Arg Ser Tyr Thr His Lys Lys Gly Val Asn Phe Ser Asp Arg Gly
 35 40 45
 Met Thr Leu Glu Gln Gln Ile Asn Glu Ser Asn Lys Tyr Tyr Leu Thr
 50 55 60
 Glu Glu Ile Ala Val Val His Lys Lys Pro Thr Pro Ile Gln Ile Val
 65 70 75 80
 Lys Val Asp Tyr Pro Lys Arg Ser Lys Ala Val Ile Arg Glu Ala Tyr
 85 90 95
 Phe Arg Gln Ala Ser Thr Thr Asp Tyr Asn Gly Val Tyr Lys Gly Tyr
 100 105 110
 Tyr Leu Asp Phe Glu Ala Lys Glu Thr Lys Asn Lys Thr Asn Phe Pro
 115 120 125
 Leu Lys Asn Phe His Glu His Gln Ile Phe His Leu Ala Glu Cys Leu
 130 135 140
 Lys Gln Gln Gly Ile Cys Phe Thr Ile Ile Arg Phe Ala Ser Leu Glu
 145 150 155 160
 Arg Tyr Phe Val Thr Pro Ala Ser Phe Val Ile Asn Ala Trp Arg Lys
 165 170 175
 Ala Glu Lys Ser Ser Met Thr Leu Lys Glu Ile Glu Ser His Ser Tyr
 180 185 190
 Glu Ile Lys Ser Gly Phe Arg Pro Thr Leu Pro Tyr Leu Lys Ala Val
 195 200 205
 Asp Asn Phe Ile Ala Asp Arg Lys Arg Glu
 210 215

<210> 141

<211> 1092

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1006 - penicillin binding protein

<220>

<221> CDS

<222> (1)...(1092)

<400> 141

atg	aaa	gca	gca	gct	tca	ttg	aca	gta	att	gct	tca	ttg	cca	atg	gga	48
Met	Lys	Ala	Ala	Ala	Ser	Leu	Thr	Val	Ile	Ala	Ser	Leu	Pro	Met	Gly	
1				5					10					15		
gtt	ttg	gca	aat	acc	aaa	act	gta	cat	gct	gca	tat	gat	caa	agt	gaa	96
Val	Leu	Ala	Asn	Thr	Lys	Thr	Val	His	Ala	Ala	Tyr	Asp	Gln	Ser	Glu	
			20					25					30			
atg	cgt	agt	ttt	gtt	aga	aga	aca	ata	gct	aat	tat	tat	gcc	cgt	ggg	144
Met	Arg	Ser	Phe	Val	Arg	Arg	Thr	Ile	Ala	Asn	Tyr	Tyr	Ala	Arg	Gly	
		35					40					45				
act	acc	gtc	att	att	aaa	gat	ggg	cat	gct	caa	caa	att	agt	tat	ggg	192
Thr	Thr	Val	Ile	Ile	Lys	Asp	Gly	His	Ala	Gln	Gln	Ile	Ser	Tyr	Gly	
	50					55					60					
tat	ggc	tat	tac	ggg	aaa	agg	tta	ggg	gct	ggg	aat	agc	aag	gtt	gtt	240
Tyr	Gly	Tyr	Tyr	Gly	Lys	Arg	Leu	Gly	Ala	Gly	Asn	Ser	Lys	Val	Val	
65					70				75					80		
tat	cca	gta	tgt	tct	ttg	caa	aaa	gtg	att	aca	gga	gct	att	atc	acc	288
Tyr	Pro	Val	Cys	Ser	Leu	Gln	Lys	Val	Ile	Thr	Gly	Ala	Ile	Ile	Thr	
				85				90						95		
caa	ttg	att	tat	gca	gga	aag	ttt	aat	caa	gat	act	aag	att	tca	aca	336
Gln	Leu	Ile	Tyr	Ala	Gly	Lys	Phe	Asn	Gln	Asp	Thr	Lys	Ile	Ser	Thr	
			100					105					110			
tgg	tat	cct	aac	cta	aaa	ggg	gca	tcc	aat	att	act	gta	gga	aac	ttg	384
Trp	Tyr	Pro	Asn	Leu	Lys	Gly	Ala	Ser	Asn	Ile	Thr	Val	Gly	Asn	Leu	
		115				120						125				
atg	aca	cac	act	tct	gga	ttg	aaa	gca	gcc	gat	act	gaa	gtt	aat	cgt	432
Met	Thr	His	Thr	Ser	Gly	Leu	Lys	Ala	Ala	Asp	Thr	Glu	Val	Asn	Arg	
	130					135				140						
aga	cgt	atg	tat	tct	gaa	gag	gac	gct	att	aat	tgg	gtt	gtt	gat	cga	480
Arg	Arg	Met	Tyr	Ser	Glu	Glu	Asp	Ala	Ile	Asn	Trp	Val	Val	Asp	Arg	
145					150				155					160		
tta	aat	gaa	acc	tcc	caa	aat	aat	cca	ggg	aat	ttt	tca	tat	aat	aat	528
Leu	Asn	Glu	Thr	Ser	Gln	Asn	Asn	Pro	Gly	Asn	Phe	Ser	Tyr	Asn	Asn	
			165					170						175		
acc	aat	tat	att	ttg	tta	gcg	ggg	att	atc	cgt	aaa	gta	acg	ggg	caa	576
Thr	Asn	Tyr	Ile	Leu	Leu	Ala	Gly	Ile	Ile	Arg	Lys	Val	Thr	Gly	Gln	
			180				185					190				
tct	tat	aag	caa	aat	gtt	caa	gaa	aga	att	att	agt	cct	ctt	aat	ttg	624
Ser	Tyr	Lys	Gln	Asn	Val	Gln	Glu	Arg	Ile	Ile	Ser	Pro	Leu	Asn	Leu	
		195				200						205				
aag	cgg	aca	tat	ttc	tta	gaa	gat	att	cct	gcg	ggg	atg	act	gat	ggg	672

Lys Arg Thr Tyr Phe Leu Glu Asp Ile Pro Ala Gly Met Thr Asp Gly
 210 215 220
 att tcg tat acc tgg aat gct aag aat tat caa tgg gcg caa tat gta 720
 Ile Ser Tyr Thr Trp Asn Ala Lys Asn Tyr Gln Trp Ala Gln Tyr Val
 225 230 235 240
 aaa aaa caa caa gct tcc caa tta gta ggt gct ggc aat tta ttc tca 768
 Lys Lys Gln Gln Ala Ser Gln Leu Val Gly Ala Gly Asn Leu Phe Ser
 245 250 255
 aca cca atg gat tat tac cga att caa gtt ggc tta act aat ggt aaa 816
 Thr Pro Met Asp Tyr Tyr Arg Ile Gln Val Gly Leu Thr Asn Gly Lys
 260 265 270
 att tta aat caa gct gaa ttc aac tat atg act cat ttg agt tca aga 864
 Ile Leu Asn Gln Ala Glu Phe Asn Tyr Met Thr His Leu Ser Ser Arg
 275 280 285
 tcc agc aat ggg tat tcc ggt ggg tta tat atg aaa aat aat gat aat 912
 Ser Ser Asn Gly Tyr Ser Gly Gly Leu Tyr Met Lys Asn Asn Asp Asn
 290 295 300
 tta aaa tta gca tat ggt aac ttg tat aac acc cac ttt ggt aat tgg 960
 Leu Lys Leu Ala Tyr Gly Asn Leu Tyr Asn Thr His Phe Gly Asn Trp
 305 310 315 320
 att caa atg act tct gat aat agg aat ggt ttg att atg ttc tta aat 1008
 Ile Gln Met Thr Ser Asp Asn Arg Asn Gly Leu Ile Met Phe Leu Asn
 325 330 335
 cag act caa aat gat gaa gct aga aat aag act att ggt tat caa att 1056
 Gln Thr Gln Asn Asp Glu Ala Arg Asn Lys Thr Ile Gly Tyr Gln Ile
 340 345 350
 tta aat cat att caa cct aat aca ttt agt gca aaa 1092
 Leu Asn His Ile Gln Pro Asn Thr Phe Ser Ala Lys
 355 360

<210> 142

<211> 364

<212> PRT

<213> Lactobacillus acidophilus

<400> 142

Met Lys Ala Ala Ala Ser Leu Thr Val Ile Ala Ser Leu Pro Met Gly
 1 5 10 15
 Val Leu Ala Asn Thr Lys Thr Val His Ala Ala Tyr Asp Gln Ser Glu
 20 25 30
 Met Arg Ser Phe Val Arg Arg Thr Ile Ala Asn Tyr Tyr Ala Arg Gly
 35 40 45
 Thr Thr Val Ile Ile Lys Asp Gly His Ala Gln Gln Ile Ser Tyr Gly
 50 55 60
 Tyr Gly Tyr Tyr Gly Lys Arg Leu Gly Ala Gly Asn Ser Lys Val Val
 65 70 75 80
 Tyr Pro Val Cys Ser Leu Gln Lys Val Ile Thr Gly Ala Ile Ile Thr

					85					90					95				
Gln	Leu	Ile	Tyr	Ala	Gly	Lys	Phe	Asn	Gln	Asp	Thr	Lys	Ile	Ser	Thr				
			100					105					110						
Trp	Tyr	Pro	Asn	Leu	Lys	Gly	Ala	Ser	Asn	Ile	Thr	Val	Gly	Asn	Leu				
		115					120					125							
Met	Thr	His	Thr	Ser	Gly	Leu	Lys	Ala	Ala	Asp	Thr	Glu	Val	Asn	Arg				
	130					135					140								
Arg	Arg	Met	Tyr	Ser	Glu	Glu	Asp	Ala	Ile	Asn	Trp	Val	Val	Asp	Arg				
	145				150					155					160				
Leu	Asn	Glu	Thr	Ser	Gln	Asn	Asn	Pro	Gly	Asn	Phe	Ser	Tyr	Asn	Asn				
			165						170					175					
Thr	Asn	Tyr	Ile	Leu	Leu	Ala	Gly	Ile	Ile	Arg	Lys	Val	Thr	Gly	Gln				
		180						185					190						
Ser	Tyr	Lys	Gln	Asn	Val	Gln	Glu	Arg	Ile	Ile	Ser	Pro	Leu	Asn	Leu				
	195						200					205							
Lys	Arg	Thr	Tyr	Phe	Leu	Glu	Asp	Ile	Pro	Ala	Gly	Met	Thr	Asp	Gly				
	210				215						220								
Ile	Ser	Tyr	Thr	Trp	Asn	Ala	Lys	Asn	Tyr	Gln	Trp	Ala	Gln	Tyr	Val				
	225				230					235				240					
Lys	Lys	Gln	Gln	Ala	Ser	Gln	Leu	Val	Gly	Ala	Gly	Asn	Leu	Phe	Ser				
			245						250					255					
Thr	Pro	Met	Asp	Tyr	Tyr	Arg	Ile	Gln	Val	Gly	Leu	Thr	Asn	Gly	Lys				
			260					265					270						
Ile	Leu	Asn	Gln	Ala	Glu	Phe	Asn	Tyr	Met	Thr	His	Leu	Ser	Ser	Arg				
	275						280					285							
Ser	Ser	Asn	Gly	Tyr	Ser	Gly	Gly	Leu	Tyr	Met	Lys	Asn	Asn	Asp	Asn				
	290					295					300								
Leu	Lys	Leu	Ala	Tyr	Gly	Asn	Leu	Tyr	Asn	Thr	His	Phe	Gly	Asn	Trp				
	305				310				315					320					
Ile	Gln	Met	Thr	Ser	Asp	Asn	Arg	Asn	Gly	Leu	Ile	Met	Phe	Leu	Asn				
			325						330					335					
Gln	Thr	Gln	Asn	Asp	Glu	Ala	Arg	Asn	Lys	Thr	Ile	Gly	Tyr	Gln	Ile				
			340					345						350					
Leu	Asn	His	Ile	Gln	Pro	Asn	Thr	Phe	Ser	Ala	Lys								
		355					360												

<210> 143

<211> 1107

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 858 - penicillin binding protein (fmt)

<220>

<221> CDS

<222> (1)...(1107)

<400> 143

ttg	aaa	caa	act	aaa	aaa	ttc	tgg	tta	tta	tta	att	ttg	tta	gtg	tct	48
Met	Lys	Gln	Thr	Lys	Lys	Phe	Trp	Leu	Leu	Leu	Ile	Leu	Leu	Val	Ser	
1				5				10						15		

aca ttg ggg atg gca tta gaa caa acg caa aca gta aat gct aag gtc	96
Thr Leu Gly Met Ala Leu Glu Gln Thr Gln Thr Val Asn Ala Lys Val	
20 25 30	
tat tct aat agt caa tta cgt aaa tat gta aga aaa acc cta aga aag	144
Tyr Ser Asn Ser Gln Leu Arg Lys Tyr Val Arg Lys Thr Leu Arg Lys	
35 40 45	
cat cat ttg cgt gga agc gtg gta gta gtc aaa aat gga cat agt caa	192
His His Leu Arg Gly Ser Val Val Val Val Lys Asn Gly His Ser Gln	
50 55 60	
caa ata agt gag ggt tat ggc tat tat aga cgt aga atc aaa aat ggg	240
Gln Ile Ser Glu Gly Tyr Gly Tyr Tyr Arg Arg Arg Ile Lys Asn Gly	
65 70 75 80	
agt aaa aag tta gta tat cca acc ggt tct ttg caa aaa tcg ata act	288
Ser Lys Lys Leu Val Tyr Pro Thr Gly Ser Leu Gln Lys Ser Ile Thr	
85 90 95	
gct gcc att att gct caa tta atc tat caa aat aaa ttt tca caa aat	336
Ala Ala Ile Ile Ala Gln Leu Ile Tyr Gln Asn Lys Phe Ser Gln Asn	
100 105 110	
act aaa att tca aaa tgg tat gcc aat tta aga aat gct tct aaa att	384
Thr Lys Ile Ser Lys Trp Tyr Ala Asn Leu Arg Asn Ala Ser Lys Ile	
115 120 125	
agc gta ggg caa tta atg acg cat act tca ggg att ggt ttc agt ggg	432
Ser Val Gly Gln Leu Met Thr His Thr Ser Gly Ile Gly Phe Ser Gly	
130 135 140	
act gaa tct aat aat ggc gtt aat ttt tct gaa aat ggc gca gtt aat	480
Thr Glu Ser Asn Asn Gly Val Asn Phe Ser Glu Asn Gly Ala Val Asn	
145 150 155 160	
tgg gca gta gca aga gta aat gca caa gaa aat acc ggt atc aat agt	528
Trp Ala Val Ala Arg Val Asn Ala Gln Glu Asn Thr Gly Ile Asn Ser	
165 170 175	
ttt aac tat aat aat gcc aat tac att tta tta gct ggg att atc cgc	576
Phe Asn Tyr Asn Asn Ala Asn Tyr Ile Leu Leu Ala Gly Ile Ile Arg	
180 185 190	
aaa tct act ggt aaa tca tat gct act aat gta aaa gaa cgc ata att	624
Lys Ser Thr Gly Lys Ser Tyr Ala Thr Asn Val Lys Glu Arg Ile Ile	
195 200 205	
aag cca tta cat ttg aaa cat act tat att tat aac aat att cct cgt	672
Lys Pro Leu His Leu Lys His Thr Tyr Ile Tyr Asn Asn Ile Pro Arg	
210 215 220	
tct caa acg gat gct att tca tat ctt tac cgt tat ggc aaa aat tat	720
Ser Gln Thr Asp Ala Ile Ser Tyr Leu Tyr Arg Tyr Gly Lys Asn Tyr	
225 230 235 240	
gaa gca gct gca tat gca aat aaa aat gta gtt tct caa ttg cct ggt	768

Glu Ala Ala Ala Tyr Ala Asn Lys Asn Val Val Ser Gln Leu Pro Gly
 245 250 255
 gca ggg aat ctg ttt tct aca cca gct gat tat tta aaa att caa cgc 816
 Ala Gly Asn Leu Phe Ser Thr Pro Ala Asp Tyr Leu Lys Ile Gln Arg
 260 265 270
 agt tta tat aat ggg aaa att tta act gct aag caa ttc tcg tat tta 864
 Ser Leu Tyr Asn Gly Lys Ile Leu Thr Ala Lys Gln Phe Ser Tyr Leu
 275 280 285
 gct cat tta aaa tca aag gtt aat act tat tca ggt ggt ttt tac ttg 912
 Ala His Leu Lys Ser Lys Val Asn Thr Tyr Ser Gly Gly Phe Tyr Leu
 290 295 300
 aaa aaa agt ggt act ttg aaa ttg gca tat ggt aat ttt gga gat acc 960
 Lys Lys Ser Gly Thr Leu Lys Leu Ala Tyr Gly Asn Phe Gly Asp Thr
 305 310 315 320
 cat ttt gtt aat tgg atg caa ttg act aaa aat aat aaa aat gga att 1008
 His Phe Val Asn Trp Met Gln Leu Thr Lys Asn Asn Lys Asn Gly Ile
 325 330 335
 gtg atg ttt ctt aac caa act tat ggt act aag aat caa att aag agt 1056
 Val Met Phe Leu Asn Gln Thr Tyr Gly Thr Lys Asn Gln Ile Lys Ser
 340 345 350
 gtt ggt tat aat att ttg aaa cat att aaa tct aac acc ttt ata aaa 1104
 Val Gly Tyr Asn Ile Leu Lys His Ile Lys Ser Asn Thr Phe Ile Lys
 355 360 365
 gga 1107
 Gly

<210> 144

<211> 369

<212> PRT

<213> Lactobacillus acidophilus

<400> 144

Met Lys Gln Thr Lys Lys Phe Trp Leu Leu Leu Ile Leu Leu Val Ser
 1 5 10 15
 Thr Leu Gly Met Ala Leu Glu Gln Thr Gln Thr Val Asn Ala Lys Val
 20 25 30
 Tyr Ser Asn Ser Gln Leu Arg Lys Tyr Val Arg Lys Thr Leu Arg Lys
 35 40 45
 His His Leu Arg Gly Ser Val Val Val Val Lys Asn Gly His Ser Gln
 50 55 60
 Gln Ile Ser Glu Gly Tyr Gly Tyr Tyr Arg Arg Arg Ile Lys Asn Gly
 65 70 75 80
 Ser Lys Lys Leu Val Tyr Pro Thr Gly Ser Leu Gln Lys Ser Ile Thr
 85 90 95
 Ala Ala Ile Ile Ala Gln Leu Ile Tyr Gln Asn Lys Phe Ser Gln Asn
 100 105 110
 Thr Lys Ile Ser Lys Trp Tyr Ala Asn Leu Arg Asn Ala Ser Lys Ile

```

      115      120      125
Ser Val Gly Gln Leu Met Thr His Thr Ser Gly Ile Gly Phe Ser Gly
      130      135      140
Thr Glu Ser Asn Asn Gly Val Asn Phe Ser Glu Asn Gly Ala Val Asn
145      150      155      160
Trp Ala Val Ala Arg Val Asn Ala Gln Glu Asn Thr Gly Ile Asn Ser
      165      170      175
Phe Asn Tyr Asn Asn Ala Asn Tyr Ile Leu Leu Ala Gly Ile Ile Arg
      180      185      190
Lys Ser Thr Gly Lys Ser Tyr Ala Thr Asn Val Lys Glu Arg Ile Ile
      195      200      205
Lys Pro Leu His Leu Lys His Thr Tyr Ile Tyr Asn Asn Ile Pro Arg
      210      215      220
Ser Gln Thr Asp Ala Ile Ser Tyr Leu Tyr Arg Tyr Gly Lys Asn Tyr
225      230      235      240
Glu Ala Ala Ala Tyr Ala Asn Lys Asn Val Val Ser Gln Leu Pro Gly
      245      250      255
Ala Gly Asn Leu Phe Ser Thr Pro Ala Asp Tyr Leu Lys Ile Gln Arg
      260      265      270
Ser Leu Tyr Asn Gly Lys Ile Leu Thr Ala Lys Gln Phe Ser Tyr Leu
      275      280      285
Ala His Leu Lys Ser Lys Val Asn Thr Tyr Ser Gly Gly Phe Tyr Leu
      290      295      300
Lys Lys Ser Gly Thr Leu Lys Leu Ala Tyr Gly Asn Phe Gly Asp Thr
305      310      315      320
His Phe Val Asn Trp Met Gln Leu Thr Lys Asn Asn Lys Asn Gly Ile
      325      330      335
Val Met Phe Leu Asn Gln Thr Tyr Gly Thr Lys Asn Gln Ile Lys Ser
      340      345      350
Val Gly Tyr Asn Ile Leu Lys His Ile Lys Ser Asn Thr Phe Ile Lys
      355      360      365
Gly

```

<210> 145

<211> 2160

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 805 - penicillin binding protein (pbp-2B)

<220>

<221> CDS

<222> (1)...(2160)

<400> 145

```

atg aaa aaa aac agt aat tta aaa tta caa aaa tcc aaa gcc cac agc 48
Met Lys Lys Asn Ser Asn Leu Lys Leu Gln Lys Ser Lys Ala His Ser
1      5      10      15

```

```

tac cgc ttc aca gta ggg aga ttt ctc caa gta gct gtc gct ttg gtt 96
Tyr Arg Phe Thr Val Gly Arg Phe Leu Gln Val Ala Val Ala Leu Val

```

20	25	30	
ttt ctt gta ttt acg gct aga ttt tta tat ata ggt ata tct aaa acg Phe Leu Val Phe Thr Ala Arg Phe Leu Tyr Ile Gly Ile Ser Lys Thr 35 40 45			144
ggt aat gga caa aat ttg tcc gct aga aca caa cag ctt tat agg cga Val Asn Gly Gln Asn Leu Ser Ala Arg Thr Gln Gln Leu Tyr Arg Arg 50 55 60			192
aat caa gtt att aag gca acg cgt gga act att tat gat aga aat ggt Asn Gln Val Ile Lys Ala Thr Arg Gly Thr Ile Tyr Asp Arg Asn Gly 65 70 75 80			240
tta gcc att gct gaa gat tcg cat tta tat act att tat gca att ttg Leu Ala Ile Ala Glu Asp Ser His Leu Tyr Thr Ile Tyr Ala Ile Leu 85 90 95			288
gac aaa tcc tcg att aac tat aag aat aaa cca gaa tat gtt gtt aat Asp Lys Ser Ser Ile Asn Tyr Lys Asn Lys Pro Glu Tyr Val Val Asn 100 105 110			336
aaa aca gag aca gca gaa aaa cta gca aca gtg ttg cca tta tct gct Lys Thr Glu Thr Ala Glu Lys Leu Ala Thr Val Leu Pro Leu Ser Ala 115 120 125			384
gat aaa att tat caa tat tta aat ccc aag cat aaa gct ttc cag gtt Asp Lys Ile Tyr Gln Tyr Leu Asn Pro Lys His Lys Ala Phe Gln Val 130 135 140			432
caa ttt gga aca ggt ggt agt ggg tta aca att aaa caa aag aag aaa Gln Phe Gly Thr Gly Gly Ser Gly Leu Thr Ile Lys Gln Lys Lys Lys 145 150 155 160			480
att gaa gca atg aaa tta cca ggg att aag ttt ttg gct aca cca tct Ile Glu Ala Met Lys Leu Pro Gly Ile Lys Phe Leu Ala Thr Pro Ser 165 170 175			528
cgt cta tac cct aat ggt aat ttt gct tct cat att gtt ggc tta gct Arg Leu Tyr Pro Asn Gly Asn Phe Ala Ser His Ile Val Gly Leu Ala 180 185 190			576
caa cct gaa tat gat aaa aag acc aat gat gaa act ttg gtt ggg act Gln Pro Glu Tyr Asp Lys Lys Thr Asn Asp Glu Thr Leu Val Gly Thr 195 200 205			624
atg gga att gaa gct tat ttc aat aat aca ttg act ggt aca gat ggt Met Gly Ile Glu Ala Tyr Phe Asn Asn Thr Leu Thr Gly Thr Asp Gly 210 215 220			672
tat cga att tct tca gta gat gca tcg gaa tat cag atg cct aac ggt Tyr Arg Ile Ser Ser Val Asp Ala Ser Glu Tyr Gln Met Pro Asn Gly 225 230 235 240			720
aat caa gtt tat aaa ccg gtt aaa aat ggt aat aac ttg tac ttg aca Asn Gln Val Tyr Lys Pro Val Lys Asn Gly Asn Asn Leu Tyr Leu Thr 245 250 255			768

ctt gat tcc caa ctt caa agt tat ctt gaa tca cgc tta act gaa gtt	816
Leu Asp Ser Gln Leu Gln Ser Tyr Leu Glu Ser Arg Leu Thr Glu Val	
260 265 270	
caa aag gct tat gat cca act tca ata act gca gta gtt gag gat atg	864
Gln Lys Ala Tyr Asp Pro Thr Ser Ile Thr Ala Val Val Glu Asp Met	
275 280 285	
aag aca ggt aaa ata tta gct gct tca cag cgt cca acg ttt aat ccg	912
Lys Thr Gly Lys Ile Leu Ala Ala Ser Gln Arg Pro Thr Phe Asn Pro	
290 295 300	
cag act aaa aaa ggt ttg acc aaa tca tat aga aat att tta gtt caa	960
Gln Thr Lys Lys Gly Leu Thr Lys Ser Tyr Arg Asn Ile Leu Val Gln	
305 310 315 320	
gat aca tat gag cca ggt tct gtc ttt aaa ata cta tcg ttt gct gct	1008
Asp Thr Tyr Glu Pro Gly Ser Val Phe Lys Ile Leu Ser Phe Ala Ala	
325 330 335	
gta gta aat agt ggt aat tat aat ccg aat gag tat tat cgt tca ggt	1056
Val Val Asn Ser Gly Asn Tyr Asn Pro Asn Glu Tyr Tyr Arg Ser Gly	
340 345 350	
tca gta aac gtt ggg gga tct act att cac gat tgg ttg acc tct ggt	1104
Ser Val Asn Val Gly Gly Ser Thr Ile His Asp Trp Leu Thr Ser Gly	
355 360 365	
tgg gga act att cca ttt tca caa gcc ttt gaa cgt tca agt aat act	1152
Trp Gly Thr Ile Pro Phe Ser Gln Ala Phe Glu Arg Ser Ser Asn Thr	
370 375 380	
ggg ttt gtt aag tta gaa caa aaa atg ggt tcg aaa act tgg aag aaa	1200
Gly Phe Val Lys Leu Glu Gln Lys Met Gly Ser Lys Thr Trp Lys Lys	
385 390 395 400	
tat ttg aat aaa ttc cat att gga gaa aaa aca ggt atc act ctt cct	1248
Tyr Leu Asn Lys Phe His Ile Gly Glu Lys Thr Gly Ile Thr Leu Pro	
405 410 415	
gga gaa caa cca ggt ttc att tca ttt aaa acc cca gtc gat caa gcg	1296
Gly Glu Gln Pro Gly Phe Ile Ser Phe Lys Thr Pro Val Asp Gln Ala	
420 425 430	
gtt act gca ttt ggc caa ggc gta aat gtt aat gta atg cag atg atg	1344
Val Thr Ala Phe Gly Gln Gly Val Asn Val Asn Val Met Gln Met Met	
435 440 445	
caa gca tat agt tca tta gca aat aat ggt caa atg gta aag cca caa	1392
Gln Ala Tyr Ser Ser Leu Ala Asn Asn Gly Gln Met Val Lys Pro Gln	
450 455 460	
ttg gtt gat aaa gtt acc gat tca gat ggc aat atg att aaa gga tac	1440
Leu Val Asp Lys Val Thr Asp Ser Asp Gly Asn Met Ile Lys Gly Tyr	
465 470 475 480	

gaa att caa aaa gta ggg tca cct att tat agc agt aaa act cga aaa	1488
Glu Ile Gln Lys Val Gly Ser Pro Ile Tyr Ser Ser Lys Thr Arg Lys	
485 490 495	
ggt gtt tta gct aac atg aaa cga gtt ctt aac aaa cag tca ggt act	1536
Val Val Leu Ala Asn Met Lys Arg Val Leu Asn Lys Gln Ser Gly Thr	
500 505 510	
ggt aat gct tat aag atg ggg aat gca gat atc gct gtg aag acc ggt	1584
Gly Asn Ala Tyr Lys Met Gly Asn Ala Asp Ile Ala Val Lys Thr Gly	
515 520 525	
aca gca caa att gcc aat cca aaa ggt ggc gga tat ctc aaa ggt gat	1632
Thr Ala Gln Ile Ala Asn Pro Lys Gly Gly Gly Tyr Leu Lys Gly Asp	
530 535 540	
agc aat tat atc ttc tca gtg gtc ggc gtt tac cca gca agt aat cct	1680
Ser Asn Tyr Ile Phe Ser Val Val Gly Val Tyr Pro Ala Ser Asn Pro	
545 550 555 560	
aga tat tgt gtt tat ctg acg att aaa cag cct cat tta gta ggt ggt	1728
Arg Tyr Cys Val Tyr Leu Thr Ile Lys Gln Pro His Leu Val Gly Gly	
565 570 575	
gct act gct gaa aag atc tta gca tct att ttt aag cca atg atg agt	1776
Ala Thr Ala Glu Lys Ile Leu Ala Ser Ile Phe Lys Pro Met Met Ser	
580 585 590	
aga att att tct atg gcc aaa aat gat gat act tca act act gtt agt	1824
Arg Ile Ile Ser Met Ala Lys Asn Asp Asp Thr Ser Thr Thr Val Ser	
595 600 605	
gtg cca gac ttt aag aac tta act tat agc caa gct cta gct aag gca	1872
Val Pro Asp Phe Lys Asn Leu Thr Tyr Ser Gln Ala Leu Ala Lys Ala	
610 615 620	
aaa caa gtg gga ctc aat ttg gtt aaa gtt ggc gac ggt gac aga att	1920
Lys Gln Val Gly Leu Asn Leu Val Lys Val Gly Asp Gly Asp Arg Ile	
625 630 635 640	
acc gaa caa ggc ctt aaa aag ggc gaa aag ttg gaa tca ggg gat aaa	1968
Thr Glu Gln Gly Leu Lys Lys Gly Glu Lys Leu Glu Ser Gly Asp Lys	
645 650 655	
ata ttt gta tct acc tct gga aaa gtt gtt tgt cct aat atg aaa aat	2016
Ile Phe Val Ser Thr Ser Gly Lys Val Val Cys Pro Asn Met Lys Asn	
660 665 670	
tgg agt ata aat gat ttg cat caa ttt acc aat ttg aca gat gtt aaa	2064
Trp Ser Ile Asn Asp Leu His Gln Phe Thr Asn Leu Thr Asp Val Lys	
675 680 685	
ttt agt ata aag gga acc gga act gtt tct agt caa agt ata gct gca	2112
Phe Ser Ile Lys Gly Thr Gly Thr Val Ser Ser Gln Ser Ile Ala Ala	
690 695 700	
gga aca gaa tta aaa gcc gga aag aaa ata aaa gtt aat tta aag gag	2160

Gly Thr Glu Leu Lys Ala Gly Lys Lys Ile Lys Val Asn Leu Lys Glu
 705 710 715 720

<210> 146

<211> 720

<212> PRT

<213> Lactobacillus acidophilus

<400> 146

Met Lys Lys Asn Ser Asn Leu Lys Leu Gln Lys Ser Lys Ala His Ser
 1 5 10 15
 Tyr Arg Phe Thr Val Gly Arg Phe Leu Gln Val Ala Val Ala Leu Val
 20 25 30
 Phe Leu Val Phe Thr Ala Arg Phe Leu Tyr Ile Gly Ile Ser Lys Thr
 35 40 45
 Val Asn Gly Gln Asn Leu Ser Ala Arg Thr Gln Gln Leu Tyr Arg Arg
 50 55 60
 Asn Gln Val Ile Lys Ala Thr Arg Gly Thr Ile Tyr Asp Arg Asn Gly
 65 70 75 80
 Leu Ala Ile Ala Glu Asp Ser His Leu Tyr Thr Ile Tyr Ala Ile Leu
 85 90 95
 Asp Lys Ser Ser Ile Asn Tyr Lys Asn Lys Pro Glu Tyr Val Val Asn
 100 105 110
 Lys Thr Glu Thr Ala Glu Lys Leu Ala Thr Val Leu Pro Leu Ser Ala
 115 120 125
 Asp Lys Ile Tyr Gln Tyr Leu Asn Pro Lys His Lys Ala Phe Gln Val
 130 135 140
 Gln Phe Gly Thr Gly Gly Ser Gly Leu Thr Ile Lys Gln Lys Lys Lys
 145 150 155 160
 Ile Glu Ala Met Lys Leu Pro Gly Ile Lys Phe Leu Ala Thr Pro Ser
 165 170 175
 Arg Leu Tyr Pro Asn Gly Asn Phe Ala Ser His Ile Val Gly Leu Ala
 180 185 190
 Gln Pro Glu Tyr Asp Lys Lys Thr Asn Asp Glu Thr Leu Val Gly Thr
 195 200 205
 Met Gly Ile Glu Ala Tyr Phe Asn Asn Thr Leu Thr Gly Thr Asp Gly
 210 215 220
 Tyr Arg Ile Ser Ser Val Asp Ala Ser Glu Tyr Gln Met Pro Asn Gly
 225 230 235 240
 Asn Gln Val Tyr Lys Pro Val Lys Asn Gly Asn Asn Leu Tyr Leu Thr
 245 250 255
 Leu Asp Ser Gln Leu Gln Ser Tyr Leu Glu Ser Arg Leu Thr Glu Val
 260 265 270
 Gln Lys Ala Tyr Asp Pro Thr Ser Ile Thr Ala Val Val Glu Asp Met
 275 280 285
 Lys Thr Gly Lys Ile Leu Ala Ala Ser Gln Arg Pro Thr Phe Asn Pro
 290 295 300
 Gln Thr Lys Lys Gly Leu Thr Lys Ser Tyr Arg Asn Ile Leu Val Gln
 305 310 315 320
 Asp Thr Tyr Glu Pro Gly Ser Val Phe Lys Ile Leu Ser Phe Ala Ala
 325 330 335
 Val Val Asn Ser Gly Asn Tyr Asn Pro Asn Glu Tyr Tyr Arg Ser Gly
 340 345 350
 Ser Val Asn Val Gly Gly Ser Thr Ile His Asp Trp Leu Thr Ser Gly
 355 360 365

Trp Gly Thr Ile Pro Phe Ser Gln Ala Phe Glu Arg Ser Ser Asn Thr
 370 375 380
 Gly Phe Val Lys Leu Glu Gln Lys Met Gly Ser Lys Thr Trp Lys Lys
 385 390 395 400
 Tyr Leu Asn Lys Phe His Ile Gly Glu Lys Thr Gly Ile Thr Leu Pro
 405 410 415
 Gly Glu Gln Pro Gly Phe Ile Ser Phe Lys Thr Pro Val Asp Gln Ala
 420 425 430
 Val Thr Ala Phe Gly Gln Gly Val Asn Val Asn Val Met Gln Met Met
 435 440 445
 Gln Ala Tyr Ser Ser Leu Ala Asn Asn Gly Gln Met Val Lys Pro Gln
 450 455 460
 Leu Val Asp Lys Val Thr Asp Ser Asp Gly Asn Met Ile Lys Gly Tyr
 465 470 475 480
 Glu Ile Gln Lys Val Gly Ser Pro Ile Tyr Ser Ser Lys Thr Arg Lys
 485 490 495
 Val Val Leu Ala Asn Met Lys Arg Val Leu Asn Lys Gln Ser Gly Thr
 500 505 510
 Gly Asn Ala Tyr Lys Met Gly Asn Ala Asp Ile Ala Val Lys Thr Gly
 515 520 525
 Thr Ala Gln Ile Ala Asn Pro Lys Gly Gly Gly Tyr Leu Lys Gly Asp
 530 535 540
 Ser Asn Tyr Ile Phe Ser Val Val Gly Val Tyr Pro Ala Ser Asn Pro
 545 550 555 560
 Arg Tyr Cys Val Tyr Leu Thr Ile Lys Gln Pro His Leu Val Gly Gly
 565 570 575
 Ala Thr Ala Glu Lys Ile Leu Ala Ser Ile Phe Lys Pro Met Met Ser
 580 585 590
 Arg Ile Ile Ser Met Ala Lys Asn Asp Asp Thr Ser Thr Thr Val Ser
 595 600 605
 Val Pro Asp Phe Lys Asn Leu Thr Tyr Ser Gln Ala Leu Ala Lys Ala
 610 615 620
 Lys Gln Val Gly Leu Asn Leu Val Lys Val Gly Asp Gly Asp Arg Ile
 625 630 635 640
 Thr Glu Gln Gly Leu Lys Lys Gly Glu Lys Leu Glu Ser Gly Asp Lys
 645 650 655
 Ile Phe Val Ser Thr Ser Gly Lys Val Val Cys Pro Asn Met Lys Asn
 660 665 670
 Trp Ser Ile Asn Asp Leu His Gln Phe Thr Asn Leu Thr Asp Val Lys
 675 680 685
 Phe Ser Ile Lys Gly Thr Gly Thr Val Ser Ser Gln Ser Ile Ala Ala
 690 695 700
 Gly Thr Glu Leu Lys Ala Gly Lys Lys Ile Lys Val Asn Leu Lys Glu
 705 710 715 720

<210> 147

<211> 1512

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1926 - DltA D-alanine-D-alanyl carrier protein
ligase

<220>

<221> CDS

<222> (1)...(1512)

<400> 147

atg att caa gat gtt att aag aga att gac gag ata gct gaa aat gaa	48
Met Ile Gln Asp Val Ile Lys Arg Ile Asp Glu Ile Ala Glu Asn Glu	
1 5 10 15	
cca gat cgt gta gtt tac gat tat ctc ggt gaa acc aat aca tat ggt	96
Pro Asp Arg Val Val Tyr Asp Tyr Leu Gly Glu Thr Asn Thr Tyr Gly	
20 25 30	
gac ctt aag aag cgt tca aac gct tgg gca cac aag att gct agt atg	144
Asp Leu Lys Lys Arg Ser Asn Ala Trp Ala His Lys Ile Ala Ser Met	
35 40 45	
gat atc cca gaa cat gca cca atc atg atc tgg ggt ggt caa aca ttt	192
Asp Ile Pro Glu His Ala Pro Ile Met Ile Trp Gly Gly Gln Thr Phe	
50 55 60	
gaa atg att gct agt ttc tta ggt tgt gtt aaa tca ggc cac gca tat	240
Glu Met Ile Ala Ser Phe Leu Gly Cys Val Lys Ser Gly His Ala Tyr	
65 70 75 80	
att cca att gca agt tat tca aat gct gaa cgt tta aca atg att caa	288
Ile Pro Ile Ala Ser Tyr Ser Asn Ala Glu Arg Leu Thr Met Ile Gln	
85 90 95	
gat gtt tca aaa tca cct atg gtt ttg gaa att gat cca ttg cca gac	336
Asp Val Ser Lys Ser Pro Met Val Leu Glu Ile Asp Pro Leu Pro Asp	
100 105 110	
gtt aat tta gac ggc atc aag gta ctt aaa gct aat gaa gtt gaa gat	384
Val Asn Leu Asp Gly Ile Lys Val Leu Lys Ala Asn Glu Val Glu Asp	
115 120 125	
ggc gac ttt aca gtt gat gaa agt aat ttc gtt gaa ggc gac gaa aat	432
Gly Asp Phe Thr Val Asp Glu Ser Asn Phe Val Glu Gly Asp Glu Asn	
130 135 140	
tac tat att atc ttt act tca ggt act act ggt aag cca aag ggt gta	480
Tyr Tyr Ile Ile Phe Thr Ser Gly Thr Thr Gly Lys Pro Lys Gly Val	
145 150 155 160	
caa atc agt cat gat aat ttg ttg agt ttt gta aac tgg gaa tta tca	528
Gln Ile Ser His Asp Asn Leu Leu Ser Phe Val Asn Trp Glu Leu Ser	
165 170 175	
gat ttt aat ttg cca gaa cac cca agc ttt ttg gca caa gct cca tac	576
Asp Phe Asn Leu Pro Glu His Pro Ser Phe Leu Ala Gln Ala Pro Tyr	
180 185 190	
tca ttt gac ttg tca gtt atg agc ctt tat cct gca ctt gtt tca gca	624
Ser Phe Asp Leu Ser Val Met Ser Leu Tyr Pro Ala Leu Val Ser Ala	
195 200 205	

gga aag ctt gtt gtt tta cca cat gat gtt acg caa aac ttt ggt caa	672
Gly Lys Leu Val Val Leu Pro His Asp Val Thr Gln Asn Phe Gly Gln	
210 215 220	
ttg ttc caa act tta cca aaa atg caa ttt aat gtt tgg gta tca act	720
Leu Phe Gln Thr Leu Pro Lys Met Gln Phe Asn Val Trp Val Ser Thr	
225 230 235 240	
cca tca ttt gca caa atg tgt ttc tta gat aaa acc ttt gat gca gaa	768
Pro Ser Phe Ala Gln Met Cys Phe Leu Asp Lys Thr Phe Asp Ala Glu	
245 250 255	
cat cat cca gac tta act cac ttc tta ttc tgt ggt gaa gaa tta cca	816
His His Pro Asp Leu Thr His Phe Leu Phe Cys Gly Glu Glu Leu Pro	
260 265 270	
cat agt gaa gct gat atg ctt aag aag aag ttc cca gaa agt cat att	864
His Ser Glu Ala Asp Met Leu Lys Lys Lys Phe Pro Glu Ser His Ile	
275 280 285	
ttt aat act tac ggt cct act gaa act aca gtt gct gtg act caa gta	912
Phe Asn Thr Tyr Gly Pro Thr Glu Thr Thr Val Ala Val Thr Gln Val	
290 295 300	
gag atc act gat gaa ata ctt gaa aag tat gat cgt cta cca att ggt	960
Glu Ile Thr Asp Glu Ile Leu Glu Lys Tyr Asp Arg Leu Pro Ile Gly	
305 310 315 320	
aga gta aaa gaa gac act aag att act att gat act tca aag gga gat	1008
Arg Val Lys Glu Asp Thr Lys Ile Thr Ile Asp Thr Ser Lys Gly Asp	
325 330 335	
aag cct ggc gaa ggt gaa atc att atc agt ggt cct agc gtt tca aaa	1056
Lys Pro Gly Glu Gly Glu Ile Ile Ile Ser Gly Pro Ser Val Ser Lys	
340 345 350	
ggg tac atg aat aac cct gaa aag acc gaa gct gct ttc ttc caa aat	1104
Gly Tyr Met Asn Asn Pro Glu Lys Thr Glu Ala Ala Phe Phe Gln Asn	
355 360 365	
gag ggc gac aag tat cgc agc tac cgt agt gga gat gct gga ttc ttt	1152
Glu Gly Asp Lys Tyr Arg Ser Tyr Arg Ser Gly Asp Ala Gly Phe Phe	
370 375 380	
gat ggt gat atg cta ttt tat cgc ggt aga atc gac ttc caa atc aag	1200
Asp Gly Asp Met Leu Phe Tyr Arg Gly Arg Ile Asp Phe Gln Ile Lys	
385 390 395 400	
ttc aat ggt tac aga atc gaa ctt gaa gaa att aat ttc tac ttg tca	1248
Phe Asn Gly Tyr Arg Ile Glu Leu Glu Glu Ile Asn Phe Tyr Leu Ser	
405 410 415	
aag aat gaa ttt gta cgt tat ggt gtc gca gca cct aaa tac aat aaa	1296
Lys Asn Glu Phe Val Arg Tyr Gly Val Ala Ala Pro Lys Tyr Asn Lys	
420 425 430	

gat cat act gta aag caa att gtt gct gaa atc gaa ttg aag cat ggc 1344
Asp His Thr Val Lys Gln Ile Val Ala Glu Ile Glu Leu Lys His Gly
435 440 445

gtt cgt cgt aag tat tct gat gca caa ctt act aag ttg att cgt gaa 1392
Val Arg Arg Lys Tyr Ser Asp Ala Gln Leu Thr Lys Leu Ile Arg Glu
450 455 460

gac tta gct aag aac gtg atg cct tac atg att cca cag cgt tat gtt 1440
Asp Leu Ala Lys Asn Val Met Pro Tyr Met Ile Pro Gln Arg Tyr Val
465 470 475 480

tac caa gat aca tta cca att tct caa aac ggt aag gtg gat att aag 1488
Tyr Gln Asp Thr Leu Pro Ile Ser Gln Asn Gly Lys Val Asp Ile Lys
485 490 495

gca gtt att aag gag gtt aat aag 1512
Ala Val Ile Lys Glu Val Asn Lys
500

<210> 148

<211> 504

<212> PRT

<213> Lactobacillus acidophilus

<400> 148

Met Ile Gln Asp Val Ile Lys Arg Ile Asp Glu Ile Ala Glu Asn Glu
1 5 10 15
Pro Asp Arg Val Val Tyr Asp Tyr Leu Gly Glu Thr Asn Thr Tyr Gly
20 25 30
Asp Leu Lys Lys Arg Ser Asn Ala Trp Ala His Lys Ile Ala Ser Met
35 40 45
Asp Ile Pro Glu His Ala Pro Ile Met Ile Trp Gly Gly Gln Thr Phe
50 55 60
Glu Met Ile Ala Ser Phe Leu Gly Cys Val Lys Ser Gly His Ala Tyr
65 70 75 80
Ile Pro Ile Ala Ser Tyr Ser Asn Ala Glu Arg Leu Thr Met Ile Gln
85 90 95
Asp Val Ser Lys Ser Pro Met Val Leu Glu Ile Asp Pro Leu Pro Asp
100 105 110
Val Asn Leu Asp Gly Ile Lys Val Leu Lys Ala Asn Glu Val Glu Asp
115 120 125
Gly Asp Phe Thr Val Asp Glu Ser Asn Phe Val Glu Gly Asp Glu Asn
130 135 140
Tyr Tyr Ile Ile Phe Thr Ser Gly Thr Thr Gly Lys Pro Lys Gly Val
145 150 155 160
Gln Ile Ser His Asp Asn Leu Leu Ser Phe Val Asn Trp Glu Leu Ser
165 170 175
Asp Phe Asn Leu Pro Glu His Pro Ser Phe Leu Ala Gln Ala Pro Tyr
180 185 190
Ser Phe Asp Leu Ser Val Met Ser Leu Tyr Pro Ala Leu Val Ser Ala
195 200 205
Gly Lys Leu Val Val Leu Pro His Asp Val Thr Gln Asn Phe Gly Gln
210 215 220
Leu Phe Gln Thr Leu Pro Lys Met Gln Phe Asn Val Trp Val Ser Thr
225 230 235 240

Pro Ser Phe Ala Gln Met Cys Phe Leu Asp Lys Thr Phe Asp Ala Glu
 245 250 255
 His His Pro Asp Leu Thr His Phe Leu Phe Cys Gly Glu Glu Leu Pro
 260 265 270
 His Ser Glu Ala Asp Met Leu Lys Lys Lys Phe Pro Glu Ser His Ile
 275 280 285
 Phe Asn Thr Tyr Gly Pro Thr Glu Thr Thr Val Ala Val Thr Gln Val
 290 295 300
 Glu Ile Thr Asp Glu Ile Leu Glu Lys Tyr Asp Arg Leu Pro Ile Gly
 305 310 315 320
 Arg Val Lys Glu Asp Thr Lys Ile Thr Ile Asp Thr Ser Lys Gly Asp
 325 330 335
 Lys Pro Gly Glu Gly Glu Ile Ile Ile Ser Gly Pro Ser Val Ser Lys
 340 345 350
 Gly Tyr Met Asn Asn Pro Glu Lys Thr Glu Ala Ala Phe Phe Gln Asn
 355 360 365
 Glu Gly Asp Lys Tyr Arg Ser Tyr Arg Ser Gly Asp Ala Gly Phe Phe
 370 375 380
 Asp Gly Asp Met Leu Phe Tyr Arg Gly Arg Ile Asp Phe Gln Ile Lys
 385 390 395 400
 Phe Asn Gly Tyr Arg Ile Glu Leu Glu Glu Ile Asn Phe Tyr Leu Ser
 405 410 415
 Lys Asn Glu Phe Val Arg Tyr Gly Val Ala Ala Pro Lys Tyr Asn Lys
 420 425 430
 Asp His Thr Val Lys Gln Ile Val Ala Glu Ile Glu Leu Lys His Gly
 435 440 445
 Val Arg Arg Lys Tyr Ser Asp Ala Gln Leu Thr Lys Leu Ile Arg Glu
 450 455 460
 Asp Leu Ala Lys Asn Val Met Pro Tyr Met Ile Pro Gln Arg Tyr Val
 465 470 475 480
 Tyr Gln Asp Thr Leu Pro Ile Ser Gln Asn Gly Lys Val Asp Ile Lys
 485 490 495
 Ala Val Ile Lys Glu Val Asn Lys
 500

<210> 149

<211> 1236

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1925 - DltB basic membrane protein

<220>

<221> CDS

<222> (1)...(1236)

<400> 149

gtg aat ttt aat ttc att aac tta caa cct tac tca aat ccg caa tat 48
 Met Asn Phe Asn Phe Ile Asn Leu Gln Pro Tyr Ser Asn Pro Gln Tyr
 1 5 10 15

ttt gtt tac ttg atg atc gcg tta att cct att att att gga ctt tac 96

Phe Val Tyr	Leu Met Ile Ala Leu Ile Pro Ile Ile Ile Gly Leu Tyr	
	20 25 30	
tat ggt cat cgt ctc aag aca tat gaa gcg att ttc tca att gtt ttc	144	
Tyr Gly His Arg Leu Lys Thr Tyr Glu Ala Ile Phe Ser Ile Val Phe		
	35 40 45	
tta ttc ttg att ttt gac ggt agt cac tgg caa caa ggt gta aac ttg	192	
Leu Phe Leu Ile Phe Asp Gly Ser His Trp Gln Gln Gly Val Asn Leu		
	50 55 60	
cta atc tgg ctg gtt tat gaa ttt gct ttg acg ttt gct tat cag tat	240	
Leu Ile Trp Leu Val Tyr Glu Phe Ala Leu Thr Phe Ala Tyr Gln Tyr		
	65 70 75 80	
tat cgt cat cat ggt aaa aat aag act tgg gta ttt agc ttg gct gta	288	
Tyr Arg His His Gly Lys Asn Lys Thr Trp Val Phe Ser Leu Ala Val		
	85 90 95	
att tta gcg att att ccg ctg gct gca gtt aag tat ttg acc gca ttc	336	
Ile Leu Ala Ile Ile Pro Leu Ala Ala Val Lys Tyr Leu Thr Ala Phe		
	100 105 110	
cca ctt aat tca atc aac ttt gtt att gga ttt tta ggt att tct tac	384	
Pro Leu Asn Ser Ile Asn Phe Val Ile Gly Phe Leu Gly Ile Ser Tyr		
	115 120 125	
gta act ttc aaa aca gtg caa gtt att atg gaa atg cgt gac ggt gcg	432	
Val Thr Phe Lys Thr Val Gln Val Ile Met Glu Met Arg Asp Gly Ala		
	130 135 140	
att aag aag gtg gat cct gta acc tat gca aga ttc tta ctc ttc ttc	480	
Ile Lys Lys Val Asp Pro Val Thr Tyr Ala Arg Phe Leu Leu Phe Phe		
	145 150 155 160	
cca act att tca tca ggt cct att gat cga tat cgt aga ttt aag aaa	528	
Pro Thr Ile Ser Ser Gly Pro Ile Asp Arg Tyr Arg Arg Phe Lys Lys		
	165 170 175	
gat tac gat aaa gtt cct aca aga gac gca tat att aca gat tta caa	576	
Asp Tyr Asp Lys Val Pro Thr Arg Asp Ala Tyr Ile Thr Asp Leu Gln		
	180 185 190	
tat gct gta aga tat ttg ttc caa gga ttt tta tac aaa ttt att att	624	
Tyr Ala Val Arg Tyr Leu Phe Gln Gly Phe Leu Tyr Lys Phe Ile Ile		
	195 200 205	
ggt tgg ttc ttt ggt act tat tgg ctt cct aag att agt gcc gct gct	672	
Gly Trp Phe Phe Gly Thr Tyr Trp Leu Pro Lys Ile Ser Ala Ala Ala		
	210 215 220	
tta gcg gtg gga aat gct aat ggt ggt ttg aag tta tca tgg tgg ctt	720	
Leu Ala Val Gly Asn Ala Asn Gly Gly Leu Lys Leu Ser Trp Trp Leu		
	225 230 235 240	
ctt gct tac atg tat tgc tac agt atg tac ctg ttc ttt gac ttt gca	768	
Leu Ala Tyr Met Tyr Cys Tyr Ser Met Tyr Leu Phe Phe Asp Phe Ala		

245	250	255	
ggt tac tca cta ttt gct gta tca att tca tac ttc atg ggt att cat Gly Tyr Ser Leu Phe Ala Val Ser Ile Ser Tyr Phe Met Gly Ile His 260 265 270			816
acc cca atg aac ttc aac aaa cca ttt att tct aag aat att aaa gac Thr Pro Met Asn Phe Asn Lys Pro Phe Ile Ser Lys Asn Ile Lys Asp 275 280 285			864
ttc tgg aac cgt tgg cac att aca ctt tca ttc tgg ttc cgt gat tat Phe Trp Asn Arg Trp His Ile Thr Leu Ser Phe Trp Phe Arg Asp Tyr 290 295 300			912
atc tac atg cga ttc act ttc ttt gca atg aaa aaa aag ttg ttt aag Ile Tyr Met Arg Phe Thr Phe Phe Ala Met Lys Lys Lys Leu Phe Lys 305 310 315 320			960
aat cgt att aga ttg tca cag gta tca tat ttc cta tta ttc ttg ata Asn Arg Ile Arg Leu Ser Gln Val Ser Tyr Phe Leu Leu Phe Leu Ile 325 330 335			1008
atg gga ttc tgg cat ggg tta aca tgg tat tat att gtt tat ggt ata Met Gly Phe Trp His Gly Leu Thr Trp Tyr Tyr Ile Val Tyr Gly Ile 340 345 350			1056
ttc cat gcc act gct atc tgt gtc aac gat atg tgg cta aga ttt aag Phe His Ala Thr Ala Ile Cys Val Asn Asp Met Trp Leu Arg Phe Lys 355 360 365			1104
aga aag cat aag aaa caa att cca cat aac aag ttt act gaa tgg ttt Arg Lys His Lys Lys Gln Ile Pro His Asn Lys Phe Thr Glu Trp Phe 370 375 380			1152
gcc att ttc tta act ttc aat atg gta tgt ttc agt ttc ttg att ttc Ala Ile Phe Leu Thr Phe Asn Met Val Cys Phe Ser Phe Leu Ile Phe 385 390 395 400			1200
tca gga ttc ctt agt caa ttg tgg ttt ggc tgg aag Ser Gly Phe Leu Ser Gln Leu Trp Phe Gly Trp Lys 405 410			1236

<210> 150

<211> 412

<212> PRT

<213> Lactobacillus acidophilus

<400> 150

Met Asn Phe Asn Phe Ile Asn Leu Gln Pro Tyr Ser Asn Pro Gln Tyr			
1 5 10 15			
Phe Val Tyr Leu Met Ile Ala Leu Ile Pro Ile Ile Ile Gly Leu Tyr			
20 25 30			
Tyr Gly His Arg Leu Lys Thr Tyr Glu Ala Ile Phe Ser Ile Val Phe			
35 40 45			
Leu Phe Leu Ile Phe Asp Gly Ser His Trp Gln Gln Gly Val Asn Leu			
50 55 60			

```

Leu Ile Trp Leu Val Tyr Glu Phe Ala Leu Thr Phe Ala Tyr Gln Tyr
65      70      75      80
Tyr Arg His His Gly Lys Asn Lys Thr Trp Val Phe Ser Leu Ala Val
      85      90      95
Ile Leu Ala Ile Ile Pro Leu Ala Ala Val Lys Tyr Leu Thr Ala Phe
      100      105      110
Pro Leu Asn Ser Ile Asn Phe Val Ile Gly Phe Leu Gly Ile Ser Tyr
      115      120      125
Val Thr Phe Lys Thr Val Gln Val Ile Met Glu Met Arg Asp Gly Ala
      130      135      140
Ile Lys Lys Val Asp Pro Val Thr Tyr Ala Arg Phe Leu Leu Phe Phe
145      150      155      160
Pro Thr Ile Ser Ser Gly Pro Ile Asp Arg Tyr Arg Arg Phe Lys Lys
      165      170      175
Asp Tyr Asp Lys Val Pro Thr Arg Asp Ala Tyr Ile Thr Asp Leu Gln
      180      185      190
Tyr Ala Val Arg Tyr Leu Phe Gln Gly Phe Leu Tyr Lys Phe Ile Ile
      195      200      205
Gly Trp Phe Phe Gly Thr Tyr Trp Leu Pro Lys Ile Ser Ala Ala Ala
      210      215      220
Leu Ala Val Gly Asn Ala Asn Gly Gly Leu Lys Leu Ser Trp Trp Leu
225      230      235      240
Leu Ala Tyr Met Tyr Cys Tyr Ser Met Tyr Leu Phe Phe Asp Phe Ala
      245      250      255
Gly Tyr Ser Leu Phe Ala Val Ser Ile Ser Tyr Phe Met Gly Ile His
      260      265      270
Thr Pro Met Asn Phe Asn Lys Pro Phe Ile Ser Lys Asn Ile Lys Asp
      275      280      285
Phe Trp Asn Arg Trp His Ile Thr Leu Ser Phe Trp Phe Arg Asp Tyr
      290      295      300
Ile Tyr Met Arg Phe Thr Phe Phe Ala Met Lys Lys Lys Leu Phe Lys
305      310      315      320
Asn Arg Ile Arg Leu Ser Gln Val Ser Tyr Phe Leu Leu Phe Leu Ile
      325      330      335
Met Gly Phe Trp His Gly Leu Thr Trp Tyr Tyr Ile Val Tyr Gly Ile
      340      345      350
Phe His Ala Thr Ala Ile Cys Val Asn Asp Met Trp Leu Arg Phe Lys
      355      360      365
Arg Lys His Lys Lys Gln Ile Pro His Asn Lys Phe Thr Glu Trp Phe
      370      375      380
Ala Ile Phe Leu Thr Phe Asn Met Val Cys Phe Ser Phe Leu Ile Phe
385      390      395      400
Ser Gly Phe Leu Ser Gln Leu Trp Phe Gly Trp Lys
      405      410

```

<210> 151

<211> 237

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1924 - DltC D-alanyl carrier protein

<220>

<221> CDS

<222> (1)...(237)

<400> 151

```

atg gac act aaa caa ggc gta tta gac att tta aac gat tta act ggt 48
Met Asp Thr Lys Gln Gly Val Leu Asp Ile Leu Asn Asp Leu Thr Gly
1      5      10      15

```

```

gaa gat tta tca gat caa atg gat gaa aac atc ttt gat aat ggt ttg 96
Glu Asp Leu Ser Asp Gln Met Asp Glu Asn Ile Phe Asp Asn Gly Leu
      20      25      30

```

```

atg gac tca atg gca agt gta caa atg ctt ttg agt tta caa gaa aaa 144
Met Asp Ser Met Ala Ser Val Gln Met Leu Leu Ser Leu Gln Glu Lys
      35      40      45

```

```

ttt gat att gat gtt cct gta tca gaa ttt aat cgt gaa gaa tgg gac 192
Phe Asp Ile Asp Val Pro Val Ser Glu Phe Asn Arg Glu Glu Trp Asp
      50      55      60

```

```

act cct aac aag att gtt gca aag gtg gaa agc tta gaa aat gag 237
Thr Pro Asn Lys Ile Val Ala Lys Val Glu Ser Leu Glu Asn Glu
      65      70      75

```

<210> 152

<211> 79

<212> PRT

<213> Lactobacillus acidophilus

<400> 152

```

Met Asp Thr Lys Gln Gly Val Leu Asp Ile Leu Asn Asp Leu Thr Gly
1      5      10      15

```

```

Glu Asp Leu Ser Asp Gln Met Asp Glu Asn Ile Phe Asp Asn Gly Leu
      20      25      30

```

```

Met Asp Ser Met Ala Ser Val Gln Met Leu Leu Ser Leu Gln Glu Lys
      35      40      45

```

```

Phe Asp Ile Asp Val Pro Val Ser Glu Phe Asn Arg Glu Glu Trp Asp
      50      55      60

```

```

Thr Pro Asn Lys Ile Val Ala Lys Val Glu Ser Leu Glu Asn Glu
      65      70      75

```

<210> 153

<211> 1284

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1923 - DltD extramembranal transfer protein

<220>

<221> CDS

<222> (1)...(1284)

<400> 153

atg agt aat aaa cgc cgg ctg tgg caa att ttt ggc cca gtt ctt tgc	48
Met Ser Asn Lys Arg Arg Leu Trp Gln Ile Phe Gly Pro Val Leu Cys	
1 5 10 15	
gct ttt atc ctt tta tta gtt gta ttt ctt att ccc tgg gaa aga act	96
Ala Phe Ile Leu Leu Leu Val Val Phe Leu Ile Pro Trp Glu Arg Thr	
20 25 30	
ttt tct aag caa act atc tat gaa gca gct gcc tca caa aat agt act	144
Phe Ser Lys Gln Thr Ile Tyr Glu Ala Ala Ala Ser Gln Asn Ser Thr	
35 40 45	
gta ttt aag ggc agt aca atg aag caa gaa gct tat aaa gat ggt tat	192
Val Phe Lys Gly Ser Thr Met Lys Gln Glu Ala Tyr Lys Asp Gly Tyr	
50 55 60	
gta cca ttc tat ggt tca agt gaa ttg tct aga ttt gat cca ctt cac	240
Val Pro Phe Tyr Gly Ser Ser Glu Leu Ser Arg Phe Asp Pro Leu His	
65 70 75 80	
cct agt gtt att gct gaa aag tat cac aga aat tac cgt cca ttt ctt	288
Pro Ser Val Ile Ala Glu Lys Tyr His Arg Asn Tyr Arg Pro Phe Leu	
85 90 95	
cta ggt gga cca ggt agt caa tct ttg gct caa ttc ttg ggg atg cag	336
Leu Gly Gly Pro Gly Ser Gln Ser Leu Ala Gln Phe Leu Gly Met Gln	
100 105 110	
ggt aca act aaa cag ctt aaa aac aaa aag gct gta gtg att att tca	384
Gly Thr Thr Lys Gln Leu Lys Asn Lys Lys Ala Val Val Ile Ile Ser	
115 120 125	
cca caa tgg ttt acc aag aaa ggc caa gat cct aat gca ttt gct tta	432
Pro Gln Trp Phe Thr Lys Lys Gly Gln Asp Pro Asn Ala Phe Ala Leu	
130 135 140	
tat tat tca cca ctt caa gca tgt aac ttc ttg tta agt gct aag aat	480
Tyr Tyr Ser Pro Leu Gln Ala Cys Asn Phe Leu Leu Ser Ala Lys Asn	
145 150 155 160	
aat aag act gat cgt tat gct gct aag cgt ctg ctt gat atg cca gat	528
Asn Lys Thr Asp Arg Tyr Ala Ala Lys Arg Leu Leu Asp Met Pro Asp	
165 170 175	
gta aag ggt gaa att aga aac agt ctt aag caa att gct gca ggt aaa	576
Val Lys Gly Glu Ile Arg Asn Ser Leu Lys Gln Ile Ala Ala Gly Lys	
180 185 190	
aag cta act act ttt gaa aga ttt tat tta gaa aat cgt cgt aga atg	624
Lys Leu Thr Thr Phe Glu Arg Phe Tyr Leu Glu Asn Arg Arg Arg Met	
195 200 205	
tta cgt aac gaa gat aac ttc ttt agt tca ttc caa tta cgc gat cgt	672

Leu	Arg	Asn	Glu	Asp	Asn	Phe	Phe	Ser	Ser	Phe	Gln	Leu	Arg	Asp	Arg		
210						215					220						
gta	aat	aag	att	caa	aat	aga	gct	aaa	gta	tta	cct	aat	act	tat	tct	720	
Val	Asn	Lys	Ile	Gln	Asn	Arg	Ala	Lys	Val	Leu	Pro	Asn	Thr	Tyr	Ser		
225					230					235					240		
gta	gct	gct	ttg	aac	aag	gtg	gct	gaa	gaa	cag	gct	gca	gca	cat	act	768	
Val	Ala	Ala	Leu	Asn	Lys	Val	Ala	Glu	Glu	Gln	Ala	Ala	Ala	His	Thr		
				245					250					255			
act	tca	aat	aac	ttg	gga	att	gac	aat	act	ttc	tat	aga	act	cgt	ttg	816	
Thr	Ser	Asn	Asn	Leu	Gly	Ile	Asp	Asn	Thr	Phe	Tyr	Arg	Thr	Arg	Leu		
			260					265						270			
cct	aga	aag	gta	tta	aag	aga	ctc	aag	ggt	agt	caa	cgt	cac	ttt	gat	864	
Pro	Arg	Lys	Val	Leu	Lys	Arg	Leu	Lys	Gly	Ser	Gln	Arg	His	Phe	Asp		
		275					280					285					
tac	gtt	aga	tct	gtt	gaa	tat	ggc	gac	ttc	cag	tta	atg	ctg	gaa	caa	912	
Tyr	Val	Arg	Ser	Val	Glu	Tyr	Gly	Asp	Phe	Gln	Leu	Met	Leu	Glu	Gln		
	290					295					300						
ttt	gcc	aag	caa	cat	act	aat	gtg	ttg	ttc	att	att	cca	cca	att	aat	960	
Phe	Ala	Lys	Gln	His	Thr	Asn	Val	Leu	Phe	Ile	Ile	Pro	Pro	Ile	Asn		
305					310					315					320		
ggt	aag	tgg	atg	aag	tat	act	ggt	tta	tca	caa	aaa	atg	tat	caa	gaa	1008	
Gly	Lys	Trp	Met	Lys	Tyr	Thr	Gly	Leu	Ser	Gln	Lys	Met	Tyr	Gln	Glu		
				325					330					335			
tca	gtt	gct	aaa	att	gaa	caa	caa	ttg	act	agt	caa	ggt	ttt	gaa	aat	1056	
Ser	Val	Ala	Lys	Ile	Glu	Gln	Gln	Leu	Thr	Ser	Gln	Gly	Phe	Glu	Asn		
			340					345						350			
att	gca	gat	ctt	tct	aaa	cgt	ggt	aat	gaa	aag	tac	ttc	atg	caa	gat	1104	
Ile	Ala	Asp	Leu	Ser	Lys	Arg	Gly	Asn	Glu	Lys	Tyr	Phe	Met	Gln	Asp		
		355					360					365					
act	att	cac	ctt	ggt	tgg	aaa	ggc	tgg	gta	gct	gtt	gat	caa	gct	gtt	1152	
Thr	Ile	His	Leu	Gly	Trp	Lys	Gly	Trp	Val	Ala	Val	Asp	Gln	Ala	Val		
			370				375					380					
aga	cca	ttt	atg	aag	ttg	cct	aac	gaa	cgt	tac	aac	tat	gat	atg	tct	1200	
Arg	Pro	Phe	Met	Lys	Leu	Pro	Asn	Glu	Arg	Tyr	Asn	Tyr	Asp	Met	Ser		
385					390					395					400		
aac	tac	tac	ttc	tca	aag	aag	tgg	cag	aat	aaa	gat	aac	gtt	aaa	cgt	1248	
Asn	Tyr	Tyr	Phe	Ser	Lys	Lys	Trp	Gln	Asn	Lys	Asp	Asn	Val	Lys	Arg		
				405					410					415			
gta	aat	tta	aat	aat	aaa	gat	cgt	tta	aaa	gtg	aag					1284	
Val	Asn	Leu	Asn	Asn	Lys	Asp	Arg	Leu	Lys	Val	Lys						
				420					425								

<210> 154

<211> 428

<212> PRT

<213> Lactobacillus acidophilus

<400> 154

```

Met Ser Asn Lys Arg Arg Leu Trp Gln Ile Phe Gly Pro Val Leu Cys
 1          5          10          15
Ala Phe Ile Leu Leu Leu Val Val Phe Leu Ile Pro Trp Glu Arg Thr
      20          25          30
Phe Ser Lys Gln Thr Ile Tyr Glu Ala Ala Ala Ser Gln Asn Ser Thr
      35          40          45
Val Phe Lys Gly Ser Thr Met Lys Gln Glu Ala Tyr Lys Asp Gly Tyr
      50          55          60
Val Pro Phe Tyr Gly Ser Ser Glu Leu Ser Arg Phe Asp Pro Leu His
      65          70          75          80
Pro Ser Val Ile Ala Glu Lys Tyr His Arg Asn Tyr Arg Pro Phe Leu
      85          90          95
Leu Gly Gly Pro Gly Ser Gln Ser Leu Ala Gln Phe Leu Gly Met Gln
      100          105          110
Gly Thr Thr Lys Gln Leu Lys Asn Lys Lys Ala Val Val Ile Ile Ser
      115          120          125
Pro Gln Trp Phe Thr Lys Lys Gly Gln Asp Pro Asn Ala Phe Ala Leu
      130          135          140
Tyr Tyr Ser Pro Leu Gln Ala Cys Asn Phe Leu Leu Ser Ala Lys Asn
      145          150          155          160
Asn Lys Thr Asp Arg Tyr Ala Ala Lys Arg Leu Leu Asp Met Pro Asp
      165          170          175
Val Lys Gly Glu Ile Arg Asn Ser Leu Lys Gln Ile Ala Ala Gly Lys
      180          185          190
Lys Leu Thr Thr Phe Glu Arg Phe Tyr Leu Glu Asn Arg Arg Arg Met
      195          200          205
Leu Arg Asn Glu Asp Asn Phe Phe Ser Ser Phe Gln Leu Arg Asp Arg
      210          215          220
Val Asn Lys Ile Gln Asn Arg Ala Lys Val Leu Pro Asn Thr Tyr Ser
      225          230          235          240
Val Ala Ala Leu Asn Lys Val Ala Glu Glu Gln Ala Ala Ala His Thr
      245          250          255
Thr Ser Asn Asn Leu Gly Ile Asp Asn Thr Phe Tyr Arg Thr Arg Leu
      260          265          270
Pro Arg Lys Val Leu Lys Arg Leu Lys Gly Ser Gln Arg His Phe Asp
      275          280          285
Tyr Val Arg Ser Val Glu Tyr Gly Asp Phe Gln Leu Met Leu Glu Gln
      290          295          300
Phe Ala Lys Gln His Thr Asn Val Leu Phe Ile Ile Pro Pro Ile Asn
      305          310          315          320
Gly Lys Trp Met Lys Tyr Thr Gly Leu Ser Gln Lys Met Tyr Gln Glu
      325          330          335
Ser Val Ala Lys Ile Glu Gln Gln Leu Thr Ser Gln Gly Phe Glu Asn
      340          345          350
Ile Ala Asp Leu Ser Lys Arg Gly Asn Glu Lys Tyr Phe Met Gln Asp
      355          360          365
Thr Ile His Leu Gly Trp Lys Gly Trp Val Ala Val Asp Gln Ala Val
      370          375          380
Arg Pro Phe Met Lys Leu Pro Asn Glu Arg Tyr Asn Tyr Asp Met Ser
      385          390          395          400
Asn Tyr Tyr Phe Ser Lys Lys Trp Gln Asn Lys Asp Asn Val Lys Arg
      405          410          415

```

Val Asn Leu Asn Asn Lys Asp Arg Leu Lys Val Lys
 420 425

<210> 155

<211> 1431

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1724 - oligosaccharide repeat unit transporter

<220>

<221> CDS

<222> (1)...(1431)

<400> 155

atg aag gtt gta aga aat tac ctt tat aat gtt gga tat caa gta cta	48
Met Lys Val Val Arg Asn Tyr Leu Tyr Asn Val Gly Tyr Gln Val Leu	
1 5 10 15	
gca att att gta cct tta att aca tca gct tat gtt agt cgg gta ctt	96
Ala Ile Ile Val Pro Leu Ile Thr Ser Ala Tyr Val Ser Arg Val Leu	
20 25 30	
aga cct gaa ggt gtt ggt gca aat gca ttt act aat tca ata att caa	144
Arg Pro Glu Gly Val Gly Ala Asn Ala Phe Thr Asn Ser Ile Ile Gln	
35 40 45	
tat ttt ata ctt ttt gca agt atg ggc ata ggc tat tat ggt aat cgt	192
Tyr Phe Ile Leu Phe Ala Ser Met Gly Ile Gly Tyr Tyr Gly Asn Arg	
50 55 60	
cag att gct tat gta cgt gaa gat tca cat aag atg gcg caa aca ttt	240
Gln Ile Ala Tyr Val Arg Glu Asp Ser His Lys Met Ala Gln Thr Phe	
65 70 75 80	
tgg gaa att caa ata gta aaa aca atg atg aca ctt ttg tct att att	288
Trp Glu Ile Gln Ile Val Lys Thr Met Met Thr Leu Leu Ser Ile Ile	
85 90 95	
gca ttt gaa att ttc atg atg ttc tat aca aga caa cct gaa tat atg	336
Ala Phe Glu Ile Phe Met Met Phe Tyr Thr Arg Gln Pro Glu Tyr Met	
100 105 110	
atc gct caa tcc att aat tta gtg gca gtt gca ttt gat ata tct tgg	384
Ile Ala Gln Ser Ile Asn Leu Val Ala Val Ala Phe Asp Ile Ser Trp	
115 120 125	
ttt tac gaa gga ata gaa gac ttt aag gtt aca gtc tta aaa aat tct	432
Phe Tyr Glu Gly Ile Glu Asp Phe Lys Val Thr Val Leu Lys Asn Ser	
130 135 140	
ttt gtt aaa tta ata tct atg gca gca att ttc cta tta att aag gga	480

Phe Val Lys Leu Ile Ser Met Ala Ala Ile Phe Leu Leu Ile Lys Gly	
145 150 155 160	
cca tat gat gtg act tta tat att gtt gtt tta gcg gtt tca aca tta	528
Pro Tyr Asp Val Thr Leu Tyr Ile Val Val Leu Ala Val Ser Thr Leu	
165 170 175	
tta gga aat ttg act tta tgg cct aat att aaa aaa gat ctt cct aaa	576
Leu Gly Asn Leu Thr Leu Trp Pro Asn Ile Lys Lys Asp Leu Pro Lys	
180 185 190	
att aac ata aat att tta aat cca tgg cga cat ttt ttg cct atg gca	624
Ile Asn Ile Asn Ile Leu Asn Pro Trp Arg His Phe Leu Pro Met Ala	
195 200 205	
gaa tta ttt att cca caa att gct aca caa gta tat gtt caa tta aat	672
Glu Leu Phe Ile Pro Gln Ile Ala Thr Gln Val Tyr Val Gln Leu Asn	
210 215 220	
aaa act atg ctt ggt ggt atg gta agt gaa act tcc gcg gga tac tat	720
Lys Thr Met Leu Gly Gly Met Val Ser Glu Thr Ser Ala Gly Tyr Tyr	
225 230 235 240	
caa tac tct gat aat ctg gtt aaa ctg att tta gct cta gta act gca	768
Gln Tyr Ser Asp Asn Leu Val Lys Leu Ile Leu Ala Leu Val Thr Ala	
245 250 255	
aca ggt act gtc atg ctt cct cat gtt gct aat gcc gtg tca aaa gga	816
Thr Gly Thr Val Met Leu Pro His Val Ala Asn Ala Val Ser Lys Gly	
260 265 270	
aat atg cga gaa gtc aat caa atg tta tat aaa tca ttt gat ttt gtt	864
Asn Met Arg Glu Val Asn Gln Met Leu Tyr Lys Ser Phe Asp Phe Val	
275 280 285	
tcg gct gtg tca tat cca atg atg ttt ggc tta gct gca att tct tta	912
Ser Ala Val Ser Tyr Pro Met Met Phe Gly Leu Ala Ala Ile Ser Leu	
290 295 300	
aca tta gca cca aaa tat tat ggc cca ggg tat gat cct gtt ggc cca	960
Thr Leu Ala Pro Lys Tyr Tyr Gly Pro Gly Tyr Asp Pro Val Gly Pro	
305 310 315 320	
gct atg atg ata gaa tct att gtt ata ttg atg att gcc tgg agc aat	1008
Ala Met Met Ile Glu Ser Ile Val Ile Leu Met Ile Ala Trp Ser Asn	
325 330 335	
gta ctt gga gtt caa tat ttg tta cct att aat cat caa cgt gat ttt	1056
Val Leu Gly Val Gln Tyr Leu Leu Pro Ile Asn His Gln Arg Asp Phe	
340 345 350	
aca gtt tca gta aca gta ggt gcg gtt gtt aat gtt att tta aat ata	1104
Thr Val Ser Val Thr Val Gly Ala Val Val Asn Val Ile Leu Asn Ile	
355 360 365	
ccg tta att cat aat tgg ggt tta gat ggt gca atg tgg tct act gtt	1152
Pro Leu Ile His Asn Trp Gly Leu Asp Gly Ala Met Trp Ser Thr Val	

370	375	380	
att tct gaa att tca gtt act ttg tat caa cta tgg gct gtt aaa gga			1200
Ile Ser Glu Ile Ser Val Thr Leu Tyr Gln Leu Trp Ala Val Lys Gly			
385	390	395	400
tta cta aat tat aga caa ctt ttt tta aat tct tgg aaa tat tta ttg			1248
Leu Leu Asn Tyr Arg Gln Leu Phe Leu Asn Ser Trp Lys Tyr Leu Leu			
	405	410	415
tca ggg ata att atg ttt gtt ctt gta ttt tgg atg aat cag cat ttc			1296
Ser Gly Ile Ile Met Phe Val Leu Val Phe Trp Met Asn Gln His Phe			
	420	425	430
caa gat agt tgg cta atg atg gga tta gaa att att att ggt gta ata			1344
Gln Asp Ser Trp Leu Met Met Gly Leu Glu Ile Ile Ile Gly Val Ile			
	435	440	445
ata tat ggt gta atg att ata ttt ttt aag gca cct att att gat cag			1392
Ile Tyr Gly Val Met Ile Ile Phe Phe Lys Ala Pro Ile Ile Asp Gln			
	450	455	460
gca aag aaa ata gtt aat gat aaa ttg aaa aat gta aaa			1431
Ala Lys Lys Ile Val Asn Asp Lys Leu Lys Asn Val Lys			
465	470	475	

<210> 156

<211> 477

<212> PRT

<213> Lactobacillus acidophilus

<400> 156

Met Lys Val Val Arg Asn Tyr Leu Tyr Asn Val Gly Tyr Gln Val Leu			
1	5	10	15
Ala Ile Ile Val Pro Leu Ile Thr Ser Ala Tyr Val Ser Arg Val Leu			
	20	25	30
Arg Pro Glu Gly Val Gly Ala Asn Ala Phe Thr Asn Ser Ile Ile Gln			
	35	40	45
Tyr Phe Ile Leu Phe Ala Ser Met Gly Ile Gly Tyr Tyr Gly Asn Arg			
	50	55	60
Gln Ile Ala Tyr Val Arg Glu Asp Ser His Lys Met Ala Gln Thr Phe			
	65	70	75
Trp Glu Ile Gln Ile Val Lys Thr Met Met Thr Leu Leu Ser Ile Ile			
	85	90	95
Ala Phe Glu Ile Phe Met Met Phe Tyr Thr Arg Gln Pro Glu Tyr Met			
	100	105	110
Ile Ala Gln Ser Ile Asn Leu Val Ala Val Ala Phe Asp Ile Ser Trp			
	115	120	125
Phe Tyr Glu Gly Ile Glu Asp Phe Lys Val Thr Val Leu Lys Asn Ser			
	130	135	140
Phe Val Lys Leu Ile Ser Met Ala Ala Ile Phe Leu Leu Ile Lys Gly			
	145	150	155
Pro Tyr Asp Val Thr Leu Tyr Ile Val Val Leu Ala Val Ser Thr Leu			
	165	170	175
Leu Gly Asn Leu Thr Leu Trp Pro Asn Ile Lys Lys Asp Leu Pro Lys			
	180	185	190

```

Ile Asn Ile Asn Ile Leu Asn Pro Trp Arg His Phe Leu Pro Met Ala
    195                200                205
Glu Leu Phe Ile Pro Gln Ile Ala Thr Gln Val Tyr Val Gln Leu Asn
    210                215                220
Lys Thr Met Leu Gly Gly Met Val Ser Glu Thr Ser Ala Gly Tyr Tyr
    225                230                235                240
Gln Tyr Ser Asp Asn Leu Val Lys Leu Ile Leu Ala Leu Val Thr Ala
    245                250                255
Thr Gly Thr Val Met Leu Pro His Val Ala Asn Ala Val Ser Lys Gly
    260                265                270
Asn Met Arg Glu Val Asn Gln Met Leu Tyr Lys Ser Phe Asp Phe Val
    275                280                285
Ser Ala Val Ser Tyr Pro Met Met Phe Gly Leu Ala Ala Ile Ser Leu
    290                295                300
Thr Leu Ala Pro Lys Tyr Tyr Gly Pro Gly Tyr Asp Pro Val Gly Pro
    305                310                315                320
Ala Met Met Ile Glu Ser Ile Val Ile Leu Met Ile Ala Trp Ser Asn
    325                330                335
Val Leu Gly Val Gln Tyr Leu Leu Pro Ile Asn His Gln Arg Asp Phe
    340                345                350
Thr Val Ser Val Thr Val Gly Ala Val Val Asn Val Ile Leu Asn Ile
    355                360                365
Pro Leu Ile His Asn Trp Gly Leu Asp Gly Ala Met Trp Ser Thr Val
    370                375                380
Ile Ser Glu Ile Ser Val Thr Leu Tyr Gln Leu Trp Ala Val Lys Gly
    385                390                395                400
Leu Leu Asn Tyr Arg Gln Leu Phe Leu Asn Ser Trp Lys Tyr Leu Leu
    405                410                415
Ser Gly Ile Ile Met Phe Val Leu Val Phe Trp Met Asn Gln His Phe
    420                425                430
Gln Asp Ser Trp Leu Met Met Gly Leu Glu Ile Ile Ile Gly Val Ile
    435                440                445
Ile Tyr Gly Val Met Ile Ile Phe Phe Lys Ala Pro Ile Ile Asp Gln
    450                455                460
Ala Lys Lys Ile Val Asn Asp Lys Leu Lys Asn Val Lys
    465                470                475

```

<210> 157

<211> 522

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1725 - UDP-galactopyranose mutase

<220>

<221> CDS

<222> (1)...(522)

<400> 157

```

atg gtt gaa aat atg ttg ggt gat cct gat atc aca gtt aaa tta aat 48
Met Val Glu Asn Met Leu Gly Asp Pro Asp Ile Thr Val Lys Leu Asn
  1              5              10              15

```

act gat ttt ttt gat aat aaa gat gat tac tta aag aac ttt gac aag 96
 Thr Asp Phe Phe Asp Asn Lys Asp Asp Tyr Leu Lys Asn Phe Asp Lys
 20 25 30

att att tat act ggt atg att gat aaa ttc ttt gat tat aaa tta ggt 144
 Ile Ile Tyr Thr Gly Met Ile Asp Lys Phe Phe Asp Tyr Lys Leu Gly
 35 40 45

gaa cta gaa tac cgt tca ctt cgt ttt gaa act gaa gaa aaa gat gta 192
 Glu Leu Glu Tyr Arg Ser Leu Arg Phe Glu Thr Glu Glu Lys Asp Val
 50 55 60

aat aat tac caa gga aat gca gtg atc aat tat act gaa gca gaa att 240
 Asn Asn Tyr Gln Gly Asn Ala Val Ile Asn Tyr Thr Glu Ala Glu Ile
 65 70 75 80

cca tat act cgt gta att gaa cac aag cat ttt gaa ttt gga aaa ggt 288
 Pro Tyr Thr Arg Val Ile Glu His Lys His Phe Glu Phe Gly Lys Gly
 85 90 95

gac aat gat aaa aca atc atc act cga gaa tac cca gct gat tgg aaa 336
 Asp Asn Asp Lys Thr Ile Ile Thr Arg Glu Tyr Pro Ala Asp Trp Lys
 100 105 110

cgt ggt gat gaa cct tat tat cca ata aat aat aag cgt aat aat gac 384
 Arg Gly Asp Glu Pro Tyr Tyr Pro Ile Asn Asn Lys Arg Asn Asn Asp
 115 120 125

tta tat gct aag tat gca gaa tta gct aaa aag cag gat aaa gtt att 432
 Leu Tyr Ala Lys Tyr Ala Glu Leu Ala Lys Lys Gln Asp Lys Val Ile
 130 135 140

ttt ggt gga cgt ctt ggt caa tat aag tat tac aat atg gat caa gtt 480
 Phe Gly Gly Arg Leu Gly Gln Tyr Lys Tyr Tyr Asn Met Asp Gln Val
 145 150 155 160

att gca gca gcg ctt gat acc gtt aat agt gaa ttt ggt gat 522
 Ile Ala Ala Ala Leu Asp Thr Val Asn Ser Glu Phe Gly Asp
 165 170

<210> 158

<211> 174

<212> PRT

<213> Lactobacillus acidophilus

<400> 158

Met Val Glu Asn Met Leu Gly Asp Pro Asp Ile Thr Val Lys Leu Asn
 1 5 10 15
 Thr Asp Phe Phe Asp Asn Lys Asp Asp Tyr Leu Lys Asn Phe Asp Lys
 20 25 30
 Ile Ile Tyr Thr Gly Met Ile Asp Lys Phe Phe Asp Tyr Lys Leu Gly
 35 40 45
 Glu Leu Glu Tyr Arg Ser Leu Arg Phe Glu Thr Glu Glu Lys Asp Val
 50 55 60

```

Asn Asn Tyr Gln Gly Asn Ala Val Ile Asn Tyr Thr Glu Ala Glu Ile
65          70          75          80
Pro Tyr Thr Arg Val Ile Glu His Lys His Phe Glu Phe Gly Lys Gly
      85          90          95
Asp Asn Asp Lys Thr Ile Ile Thr Arg Glu Tyr Pro Ala Asp Trp Lys
      100        105        110
Arg Gly Asp Glu Pro Tyr Tyr Pro Ile Asn Asn Lys Arg Asn Asn Asp
      115        120        125
Leu Tyr Ala Lys Tyr Ala Glu Leu Ala Lys Lys Gln Asp Lys Val Ile
      130        135        140
Phe Gly Gly Arg Leu Gly Gln Tyr Lys Tyr Tyr Asn Met Asp Gln Val
145          150          155          160
Ile Ala Ala Ala Leu Asp Thr Val Asn Ser Glu Phe Gly Asp
      165          170

```

<210> 159

<211> 399

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1726 - UDP-galactopyranose mutase

<220>

<221> CDS

<222> (1)...(399)

<400> 159

```

gtg aag aca tat tta gtt gta ggt tct ggt ctt ttt gca gct gtg ttt 48
Met Lys Thr Tyr Leu Val Val Gly Ser Gly Leu Phe Ala Ala Val Phe
1      5      10      15

gct cac gag gct gca aaa cgt gga aat aaa gtt aag gta att gaa aaa 96
Ala His Glu Ala Ala Lys Arg Gly Asn Lys Val Lys Val Ile Glu Lys
      20      25      30

aga gac cat att gca ggc aac atc tat act aaa gaa ata gat ggc att 144
Arg Asp His Ile Ala Gly Asn Ile Tyr Thr Lys Glu Ile Asp Gly Ile
      35      40      45

caa gtt cat aaa tat ggt gct cat att ttc cat act tct aat aag aag 192
Gln Val His Lys Tyr Gly Ala His Ile Phe His Thr Ser Asn Lys Lys
      50      55      60

gtt tgg gat tat gtt cat caa ttt gcg gat ttt aat cgc tat act aat 240
Val Trp Asp Tyr Val His Gln Phe Ala Asp Phe Asn Arg Tyr Thr Asn
      65      70      75      80

agt cct gtt gcc aat tat aag gga cat atg tat aac tta cct ttc aat 288
Ser Pro Val Ala Asn Tyr Lys Gly His Met Tyr Asn Leu Pro Phe Asn
      85      90      95

atg aat acc ttt agt gaa atg tgg ggt gtt aga aca cca caa gaa gct 336

```

```

Met Asn Thr Phe Ser Glu Met Trp Gly Val Arg Thr Pro Gln Glu Ala
      100                      105                      110

atg gct aag atc aat gag caa cgt caa gaa atg gct gga aaa gaa ccg   384
Met Ala Lys Ile Asn Glu Gln Arg Gln Glu Met Ala Gly Lys Glu Pro
      115                      120                      125

caa aat tta gaa gag                                           399
Gln Asn Leu Glu Glu
      130

```

<210> 160
 <211> 133
 <212> PRT
 <213> Lactobacillus acidophilus

```

<400> 160
Met Lys Thr Tyr Leu Val Val Gly Ser Gly Leu Phe Ala Ala Val Phe
  1                      5                      10                      15
Ala His Glu Ala Ala Lys Arg Gly Asn Lys Val Lys Val Ile Glu Lys
      20                      25                      30
Arg Asp His Ile Ala Gly Asn Ile Tyr Thr Lys Glu Ile Asp Gly Ile
      35                      40                      45
Gln Val His Lys Tyr Gly Ala His Ile Phe His Thr Ser Asn Lys Lys
      50                      55                      60
Val Trp Asp Tyr Val His Gln Phe Ala Asp Phe Asn Arg Tyr Thr Asn
      65                      70                      75                      80
Ser Pro Val Ala Asn Tyr Lys Gly His Met Tyr Asn Leu Pro Phe Asn
      85                      90                      95
Met Asn Thr Phe Ser Glu Met Trp Gly Val Arg Thr Pro Gln Glu Ala
      100                      105                      110
Met Ala Lys Ile Asn Glu Gln Arg Gln Glu Met Ala Gly Lys Glu Pro
      115                      120                      125
Gln Asn Leu Glu Glu
      130

```

<210> 161
 <211> 1293
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1727 - polysaccharide polymerase

<220>
 <221> CDS
 <222> (1)...(1293)

```

<400> 161
atg att tta tta gtc att act ctc tta ggg tta tct ata aca tct tat   48
Met Ile Leu Leu Val Ile Thr Leu Leu Gly Leu Ser Ile Thr Ser Tyr
  1                      5                      10                      15

```

tat tta aat aat aga aat tta gtt tct cca gca ttt ctt tta agc aca	96
Tyr Leu Asn Asn Arg Asn Leu Val Ser Pro Ala Phe Leu Leu Ser Thr	
20 25 30	
act ttt ttt att tgt tct ttg gtt gct tta att aat caa aat aaa tgg	144
Thr Phe Phe Ile Cys Ser Leu Val Ala Leu Ile Asn Gln Asn Lys Trp	
35 40 45	
caa ctt att tta aat aga aaa aca tac tta gtt att tgt ggt gcc ata	192
Gln Leu Ile Leu Asn Arg Lys Thr Tyr Leu Val Ile Cys Gly Ala Ile	
50 55 60	
tta gaa ttt att ata gtg aca tat tta gtt aat aaa ctg ttg tct gta	240
Leu Glu Phe Ile Ile Val Thr Tyr Leu Val Asn Lys Leu Leu Ser Val	
65 70 75 80	
gtt aaa ttt caa tat aaa aat agt aaa aaa tca aaa tta aat gcg cct	288
Val Lys Phe Gln Tyr Lys Asn Ser Lys Lys Ser Lys Leu Asn Ala Pro	
85 90 95	
tat att agc acg aga aaa tca tac ata ttg ttt gct ata cag tta tta	336
Tyr Ile Ser Thr Arg Lys Ser Tyr Ile Leu Phe Ala Ile Gln Leu Leu	
100 105 110	
tta att att tat gta att agg aat cta aaa gaa gtt act aaa ata aat	384
Leu Ile Ile Tyr Val Ile Arg Asn Leu Lys Glu Val Thr Lys Ile Asn	
115 120 125	
aat att ttt caa gct gct tcg gca tta aac caa tct agt ttg ccc aat	432
Asn Ile Phe Gln Ala Ala Ser Ala Leu Asn Gln Ser Ser Leu Pro Asn	
130 135 140	
tat ata ggg cag cct att gca tta tcg aaa att gct aat att ttc ttg	480
Tyr Ile Gly Gln Pro Ile Ala Leu Ser Lys Ile Ala Asn Ile Phe Leu	
145 150 155 160	
gca ttc ata tta gca agt ggt tta tat aca ggt tat gtt ttt ttt cta	528
Ala Phe Ile Leu Ala Ser Gly Leu Tyr Thr Gly Tyr Val Phe Phe Leu	
165 170 175	
tat att att gta aag aaa aac ttt aga ttt gac tta ttt att aat atg	576
Tyr Ile Ile Val Lys Lys Asn Phe Arg Phe Asp Leu Phe Ile Asn Met	
180 185 190	
ttt att agt ata tta gct cca ttt gtt act gga tcg cgt ggc aat tct	624
Phe Ile Ser Ile Leu Ala Pro Phe Val Thr Gly Ser Arg Gly Asn Ser	
195 200 205	
att tat atg atc att tct tgg gtt ata tat tgt tac ttg ata ttg tgg	672
Ile Tyr Met Ile Ile Ser Trp Val Ile Tyr Cys Tyr Leu Ile Leu Trp	
210 215 220	
aaa aac aat aaa ttg aat ttt aaa atg cag ttt aaa ttt gtt atg aga	720
Lys Asn Asn Lys Leu Asn Phe Lys Met Gln Phe Lys Phe Val Met Arg	
225 230 235 240	

ata acc cta gtt ttg att ata tta ctt ttg tta ttg ccc cta aca gcc 768
 Ile Thr Leu Val Leu Ile Ile Leu Leu Leu Leu Leu Pro Leu Thr Ala
 245 250 255

gtt tta ttt ggt aga aga atg gat aat tgg gat gaa tat ctt agt att 816
 Val Leu Phe Gly Arg Arg Met Asp Asn Trp Asp Glu Tyr Leu Ser Ile
 260 265 270

tat ata ggt gca caa ata aag aat tta aat gaa ttc atc tta aat aat 864
 Tyr Ile Gly Ala Gln Ile Lys Asn Leu Asn Glu Phe Ile Leu Asn Asn
 275 280 285

aat ttt cca ttg caa aca agt ata ttt gga cag caa aca ttt ttt aca 912
 Asn Phe Pro Leu Gln Thr Ser Ile Phe Gly Gln Gln Thr Phe Phe Thr
 290 295 300

ata att cct ttg gtt tca aaa tta att gga cta aat att cct agt tat 960
 Ile Ile Pro Leu Val Ser Lys Leu Ile Gly Leu Asn Ile Pro Ser Tyr
 305 310 315 320

aag ttg gat tta cca tat caa gca atc gga agt tta tct tta gga aat 1008
 Lys Leu Asp Leu Pro Tyr Gln Ala Ile Gly Ser Leu Ser Leu Gly Asn
 325 330 335

gtg tat acg aca ttt tac cct tgg tta tat gat ttt ggt tat aaa ggt 1056
 Val Tyr Thr Thr Phe Tyr Pro Trp Leu Tyr Asp Phe Gly Tyr Lys Gly
 340 345 350

gtt ttt ctt tta aca tta atc atg gca ata gtc gta gaa ttt ata tat 1104
 Val Phe Leu Leu Thr Leu Ile Met Ala Ile Val Val Glu Phe Ile Tyr
 355 360 365

cat tta gca tta cat agt aaa ttg caa ttc gga tta agt ata ctg tta 1152
 His Leu Ala Leu His Ser Lys Leu Gln Phe Gly Leu Ser Ile Leu Leu
 370 375 380

tat gga tat tta gga agc ttt gta gca tta ttg ttt ttc tct aat aag 1200
 Tyr Gly Tyr Leu Gly Ser Phe Val Ala Leu Leu Phe Phe Ser Asn Lys
 385 390 395 400

ttt tat gaa gga cta aat tct act ttg att tta ata ata atg tca tgg 1248
 Phe Tyr Glu Gly Leu Asn Ser Thr Leu Ile Leu Ile Ile Met Ser Trp
 405 410 415

ata cta cta att tac att ttt aag caa aag aaa ggg aaa ata aag 1293
 Ile Leu Leu Ile Tyr Ile Phe Lys Gln Lys Lys Gly Lys Ile Lys
 420 425 430

<210> 162

<211> 431

<212> PRT

<213> Lactobacillus acidophilus

<400> 162

Met Ile Leu Leu Val Ile Thr Leu Leu Gly Leu Ser Ile Thr Ser Tyr

1		5		10		15									
Tyr	Leu	Asn	Asn	Arg	Asn	Leu	Val	Ser	Pro	Ala	Phe	Leu	Leu	Ser	Thr
		20						25					30		
Thr	Phe	Phe	Ile	Cys	Ser	Leu	Val	Ala	Leu	Ile	Asn	Gln	Asn	Lys	Trp
		35					40					45			
Gln	Leu	Ile	Leu	Asn	Arg	Lys	Thr	Tyr	Leu	Val	Ile	Cys	Gly	Ala	Ile
	50					55					60				
Leu	Glu	Phe	Ile	Ile	Val	Thr	Tyr	Leu	Val	Asn	Lys	Leu	Leu	Ser	Val
65					70					75					80
Val	Lys	Phe	Gln	Tyr	Lys	Asn	Ser	Lys	Lys	Ser	Lys	Leu	Asn	Ala	Pro
			85					90						95	
Tyr	Ile	Ser	Thr	Arg	Lys	Ser	Tyr	Ile	Leu	Phe	Ala	Ile	Gln	Leu	Leu
			100					105					110		
Leu	Ile	Ile	Tyr	Val	Ile	Arg	Asn	Leu	Lys	Glu	Val	Thr	Lys	Ile	Asn
		115					120					125			
Asn	Ile	Phe	Gln	Ala	Ala	Ser	Ala	Leu	Asn	Gln	Ser	Ser	Leu	Pro	Asn
		130				135					140				
Tyr	Ile	Gly	Gln	Pro	Ile	Ala	Leu	Ser	Lys	Ile	Ala	Asn	Ile	Phe	Leu
145					150					155					160
Ala	Phe	Ile	Leu	Ala	Ser	Gly	Leu	Tyr	Thr	Gly	Tyr	Val	Phe	Phe	Leu
			165						170						175
Tyr	Ile	Ile	Val	Lys	Lys	Asn	Phe	Arg	Phe	Asp	Leu	Phe	Ile	Asn	Met
			180					185						190	
Phe	Ile	Ser	Ile	Leu	Ala	Pro	Phe	Val	Thr	Gly	Ser	Arg	Gly	Asn	Ser
		195					200					205			
Ile	Tyr	Met	Ile	Ile	Ser	Trp	Val	Ile	Tyr	Cys	Tyr	Leu	Ile	Leu	Trp
	210					215					220				
Lys	Asn	Asn	Lys	Leu	Asn	Phe	Lys	Met	Gln	Phe	Lys	Phe	Val	Met	Arg
225					230					235					240
Ile	Thr	Leu	Val	Leu	Ile	Ile	Leu	Leu	Leu	Leu	Pro	Leu	Thr	Ala	
			245						250					255	
Val	Leu	Phe	Gly	Arg	Arg	Met	Asp	Asn	Trp	Asp	Glu	Tyr	Leu	Ser	Ile
			260					265						270	
Tyr	Ile	Gly	Ala	Gln	Ile	Lys	Asn	Leu	Asn	Glu	Phe	Ile	Leu	Asn	Asn
		275					280					285			
Asn	Phe	Pro	Leu	Gln	Thr	Ser	Ile	Phe	Gly	Gln	Gln	Thr	Phe	Phe	Thr
		290				295					300				
Ile	Ile	Pro	Leu	Val	Ser	Lys	Leu	Ile	Gly	Leu	Asn	Ile	Pro	Ser	Tyr
305					310					315					320
Lys	Leu	Asp	Leu	Pro	Tyr	Gln	Ala	Ile	Gly	Ser	Leu	Ser	Leu	Gly	Asn
			325						330					335	
Val	Tyr	Thr	Thr	Phe	Tyr	Pro	Trp	Leu	Tyr	Asp	Phe	Gly	Tyr	Lys	Gly
			340					345					350		
Val	Phe	Leu	Leu	Thr	Leu	Ile	Met	Ala	Ile	Val	Val	Glu	Phe	Ile	Tyr
			355				360					365			
His	Leu	Ala	Leu	His	Ser	Lys	Leu	Gln	Phe	Gly	Leu	Ser	Ile	Leu	Leu
		370				375					380				
Tyr	Gly	Tyr	Leu	Gly	Ser	Phe	Val	Ala	Leu	Leu	Phe	Phe	Ser	Asn	Lys
385					390					395					400
Phe	Tyr	Glu	Gly	Leu	Asn	Ser	Thr	Leu	Ile	Leu	Ile	Ile	Met	Ser	Trp
			405						410					415	
Ile	Leu	Leu	Ile	Tyr	Ile	Phe	Lys	Gln	Lys	Lys	Gly	Lys	Ile	Lys	
			420					425					430		

<210> 163

<211> 1038

<212> DNA
 <213> Lactobacillus acidophilus
 <220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1728 - glycosyl transferase

<220>
 <221> CDS
 <222> (1)...(1038)

<400> 163
 ttg aag aaa aaa aca tta act atc ggg gta gct gca tat aat gcg gca 48
 Met Lys Lys Lys Thr Leu Thr Ile Gly Val Ala Ala Tyr Asn Ala Ala
 1 5 10 15
 aaa att att tct aat tgt tta gat agt tta ctc att gat gaa gta aaa 96
 Lys Ile Ile Ser Asn Cys Leu Asp Ser Leu Leu Ile Asp Glu Val Lys
 20 25 30
 aat gat ata gaa gtt tta gtt att aat gat ggc tcc aca gat aac ata 144
 Asn Asp Ile Glu Val Leu Val Ile Asn Asp Gly Ser Thr Asp Asn Ile
 35 40 45
 caa agt gtt gta gct acg tat gaa aat aga tat cct aat agt ata cgg 192
 Gln Ser Val Val Ala Thr Tyr Glu Asn Arg Tyr Pro Asn Ser Ile Arg
 50 55 60
 tta att aat aaa aaa aat gga gga cat ggt tct aca att aat aag aca 240
 Leu Ile Asn Lys Lys Asn Gly Gly His Gly Ser Thr Ile Asn Lys Thr
 65 70 75 80
 ata gaa gaa gct aag ggc gag tat tta aaa atg gtg gat gct gat gat 288
 Ile Glu Glu Ala Lys Gly Glu Tyr Leu Lys Met Val Asp Ala Asp Asp
 85 90 95
 agt gtt gaa aaa caa ggt ttc ata gca tta gta cgt cat ctg aag aaa 336
 Ser Val Glu Lys Gln Gly Phe Ile Ala Leu Val Arg His Leu Lys Lys
 100 105 110
 acc aat gct gat gtt gtt atg tca ccg tat tat aga gta aat att gtt 384
 Thr Asn Ala Asp Val Val Met Ser Pro Tyr Tyr Arg Val Asn Ile Val
 115 120 125
 aat aat cat aaa aaa tta ata ggt tat tta aag tct tcg aat aag gag 432
 Asn Asn His Lys Lys Leu Ile Gly Tyr Leu Lys Ser Ser Asn Lys Glu
 130 135 140
 agt att gtt gat aat aaa ctc gta aat ctg cag gat att tat caa gac 480
 Ser Ile Val Asp Asn Lys Leu Val Asn Leu Gln Asp Ile Tyr Gln Asp
 145 150 155 160
 tta ttg gta gca atg cat agt ttg act tac agg act act ttg tta aag 528
 Leu Leu Val Ala Met His Ser Leu Thr Tyr Arg Thr Thr Leu Leu Lys
 165 170 175

gaa aat aat tat aaa ata gat gaa cat tgt ttt tat gtg gat gtt gaa 576
 Glu Asn Asn Tyr Lys Ile Asp Glu His Cys Phe Tyr Val Asp Val Glu
 180 185 190

tat tct att tac tat ttc tta aaa gct aag aat gta tta tta ctt aat 624
 Tyr Ser Ile Tyr Tyr Phe Leu Lys Ala Lys Asn Val Leu Leu Leu Asn
 195 200 205

gaa cct gta tat aac tat aat ata ggt tcc tct gat caa agt gtt aat 672
 Glu Pro Val Tyr Asn Tyr Asn Ile Gly Ser Ser Asp Gln Ser Val Asn
 210 215 220

ata gat aat atg aga gct aga agg gcg caa cac tta agg gta gca aaa 720
 Ile Asp Asn Met Arg Ala Arg Arg Ala Gln His Leu Arg Val Ala Lys
 225 230 235 240

agt atg gtg aac ttt tat aaa aaa gaa aga aat aaa att cct tca tat 768
 Ser Met Val Asn Phe Tyr Lys Lys Glu Arg Asn Lys Ile Pro Ser Tyr
 245 250 255

atg aaa agc ttt ttt aaa aat aat ata gtt aat atg atc tta gtt aat 816
 Met Lys Ser Phe Phe Lys Asn Asn Ile Val Asn Met Ile Leu Val Asn
 260 265 270

gaa tat aag tta tta atg tca cta aaa tca agt aaa aac tca aaa ata 864
 Glu Tyr Lys Leu Leu Met Ser Leu Lys Ser Ser Lys Asn Ser Lys Ile
 275 280 285

gaa ttg ata aaa ttc gat aaa tat tta aaa aag aat tct att gag tta 912
 Glu Leu Ile Lys Phe Asp Lys Tyr Leu Lys Lys Asn Ser Ile Glu Leu
 290 295 300

tat gag ggt gtc aca acc ttt aat aat agt aaa aaa ata aaa cta ctt 960
 Tyr Glu Gly Val Thr Phe Asn Asn Ser Lys Lys Ile Lys Leu Leu
 305 310 315 320

aaa ata ttg aga aaa ata aat ttt aat gga tat acc ata gtt cat aat 1008
 Lys Ile Leu Arg Lys Ile Asn Phe Asn Gly Tyr Thr Ile Val His Asn
 325 330 335

tta tgt aaa aag tcg ttg act act cat ata 1038
 Leu Cys Lys Lys Ser Leu Thr Thr His Ile
 340 345

<210> 164

<211> 346

<212> PRT

<213> Lactobacillus acidophilus

<400> 164

Met Lys Lys Lys Thr Leu Thr Ile Gly Val Ala Ala Tyr Asn Ala Ala
 1 5 10 15
 Lys Ile Ile Ser Asn Cys Leu Asp Ser Leu Leu Ile Asp Glu Val Lys
 20 25 30
 Asn Asp Ile Glu Val Leu Val Ile Asn Asp Gly Ser Thr Asp Asn Ile

```

      35      40      45
Gln Ser Val Val Ala Thr Tyr Glu Asn Arg Tyr Pro Asn Ser Ile Arg
  50      55      60
Leu Ile Asn Lys Lys Asn Gly Gly His Gly Ser Thr Ile Asn Lys Thr
  65      70      75      80
Ile Glu Glu Ala Lys Gly Glu Tyr Leu Lys Met Val Asp Ala Asp Asp
      85      90      95
Ser Val Glu Lys Gln Gly Phe Ile Ala Leu Val Arg His Leu Lys Lys
      100      105      110
Thr Asn Ala Asp Val Val Met Ser Pro Tyr Tyr Arg Val Asn Ile Val
      115      120      125
Asn Asn His Lys Lys Leu Ile Gly Tyr Leu Lys Ser Ser Asn Lys Glu
      130      135      140
Ser Ile Val Asp Asn Lys Leu Val Asn Leu Gln Asp Ile Tyr Gln Asp
  145      150      155      160
Leu Leu Val Ala Met His Ser Leu Thr Tyr Arg Thr Thr Leu Leu Lys
      165      170      175
Glu Asn Asn Tyr Lys Ile Asp Glu His Cys Phe Tyr Val Asp Val Glu
      180      185      190
Tyr Ser Ile Tyr Tyr Phe Leu Lys Ala Lys Asn Val Leu Leu Leu Asn
      195      200      205
Glu Pro Val Tyr Asn Tyr Asn Ile Gly Ser Ser Asp Gln Ser Val Asn
      210      215      220
Ile Asp Asn Met Arg Ala Arg Arg Ala Gln His Leu Arg Val Ala Lys
  225      230      235      240
Ser Met Val Asn Phe Tyr Lys Lys Glu Arg Asn Lys Ile Pro Ser Tyr
      245      250      255
Met Lys Ser Phe Phe Lys Asn Asn Ile Val Asn Met Ile Leu Val Asn
      260      265      270
Glu Tyr Lys Leu Leu Met Ser Leu Lys Ser Ser Lys Asn Ser Lys Ile
      275      280      285
Glu Leu Ile Lys Phe Asp Lys Tyr Leu Lys Lys Asn Ser Ile Glu Leu
      290      295      300
Tyr Glu Gly Val Thr Thr Phe Asn Asn Ser Lys Lys Ile Lys Leu Leu
  305      310      315      320
Lys Ile Leu Arg Lys Ile Asn Phe Asn Gly Tyr Thr Ile Val His Asn
      325      330      335
Leu Cys Lys Lys Ser Leu Thr Thr His Ile
      340      345

```

<210> 165

<211> 654

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1729

<220>

<221> CDS

<222> (1)...(654)

<400> 165

ttg aaa aaa ctc cta aaa ttt tac cca aat aaa cca tat aaa att aac	48
Met Lys Lys Leu Leu Lys Phe Tyr Pro Asn Lys Pro Tyr Lys Ile Asn	
1 5 10 15	
ttt gaa aat aaa gat gat gat act tca aga ata tca gat att ata gag	96
Phe Glu Asn Lys Asp Asp Asp Thr Ser Arg Ile Ser Asp Ile Ile Glu	
20 25 30	
aca atg cga agt gat caa cga tta aaa ata tta tat caa ggt gta ttt	144
Thr Met Arg Ser Asp Gln Arg Leu Lys Ile Leu Tyr Gln Gly Val Phe	
35 40 45	
gat aaa gat aga aaa tta gat gaa ttt gca aag aca att gaa aat gaa	192
Asp Lys Asp Arg Lys Leu Asp Glu Phe Ala Lys Thr Ile Glu Asn Glu	
50 55 60	
agt gat aaa ttt tgt ctt tat ata atg gga aaa caa aat aaa tat agt	240
Ser Asp Lys Phe Cys Leu Tyr Ile Met Gly Lys Gln Asn Lys Tyr Ser	
65 70 75 80	
aaa gaa ctt tgt aaa aaa tat ccc cat att cga tat ata cca tat ata	288
Lys Glu Leu Cys Lys Lys Tyr Pro His Ile Arg Tyr Ile Pro Tyr Ile	
85 90 95	
aca tca ccg aat cat ttg aaa ata aca aga gaa gca gat att gga tta	336
Thr Ser Pro Asn His Leu Lys Ile Thr Arg Glu Ala Asp Ile Gly Leu	
100 105 110	
cta cca tat ttt cca gta aga gtt ggt aat aat tca ata tta aat gcg	384
Leu Pro Tyr Phe Pro Val Arg Val Gly Asn Asn Ser Ile Leu Asn Ala	
115 120 125	
tta tat tgt gca ccg aat aaa att tat gaa tac tct gca ttt ggt aag	432
Leu Tyr Cys Ala Pro Asn Lys Ile Tyr Glu Tyr Ser Ala Phe Gly Lys	
130 135 140	
cca atg cta gga act gat gtc tta ggg tta aaa tat cct ttt gaa aag	480
Pro Met Leu Gly Thr Asp Val Leu Gly Leu Lys Tyr Pro Phe Glu Lys	
145 150 155 160	
tat aaa atg ggg tat acg gtt tca aaa tta gaa gaa aaa gaa att tta	528
Tyr Lys Met Gly Tyr Thr Val Ser Lys Leu Glu Glu Lys Glu Ile Leu	
165 170 175	
gaa aaa tta aat aaa ata ctt gtc aat tat cag aag atg agt gaa aat	576
Glu Lys Leu Asn Lys Ile Leu Val Asn Tyr Gln Lys Met Ser Glu Asn	
180 185 190	
tcc aga cgt ttc ttt caa tct gtt aat tgg gat aag aaa att gat gaa	624
Ser Arg Arg Phe Phe Gln Ser Val Asn Trp Asp Lys Lys Ile Asp Glu	
195 200 205	
att ttg gag att aaa gaa gag gaa aaa gat	654
Ile Leu Glu Ile Lys Glu Glu Glu Lys Asp	
210 215	

<210> 166
 <211> 218
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 166
 Met Lys Lys Leu Leu Lys Phe Tyr Pro Asn Lys Pro Tyr Lys Ile Asn
 1 5 10 15
 Phe Glu Asn Lys Asp Asp Asp Thr Ser Arg Ile Ser Asp Ile Ile Glu
 20 25 30
 Thr Met Arg Ser Asp Gln Arg Leu Lys Ile Leu Tyr Gln Gly Val Phe
 35 40 45
 Asp Lys Asp Arg Lys Leu Asp Glu Phe Ala Lys Thr Ile Glu Asn Glu
 50 55 60
 Ser Asp Lys Phe Cys Leu Tyr Ile Met Gly Lys Gln Asn Lys Tyr Ser
 65 70 75 80
 Lys Glu Leu Cys Lys Lys Tyr Pro His Ile Arg Tyr Ile Pro Tyr Ile
 85 90 95
 Thr Ser Pro Asn His Leu Lys Ile Thr Arg Glu Ala Asp Ile Gly Leu
 100 105 110
 Leu Pro Tyr Phe Pro Val Arg Val Gly Asn Asn Ser Ile Leu Asn Ala
 115 120 125
 Leu Tyr Cys Ala Pro Asn Lys Ile Tyr Glu Tyr Ser Ala Phe Gly Lys
 130 135 140
 Pro Met Leu Gly Thr Asp Val Leu Gly Leu Lys Tyr Pro Phe Glu Lys
 145 150 155 160
 Tyr Lys Met Gly Tyr Thr Val Ser Lys Leu Glu Glu Lys Glu Ile Leu
 165 170 175
 Glu Lys Leu Asn Lys Ile Leu Val Asn Tyr Gln Lys Met Ser Glu Asn
 180 185 190
 Ser Arg Arg Phe Phe Gln Ser Val Asn Trp Asp Lys Lys Ile Asp Glu
 195 200 205
 Ile Leu Glu Ile Lys Glu Glu Glu Lys Asp
 210 215

<210> 167
 <211> 519
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1730

<220>
 <221> CDS
 <222> (1)...(519)

<400> 167
 atg aga gtt tta att gta cat aat aga gaa att agc gat ttt ccg cct 48
 Met Arg Val Leu Ile Val His Asn Arg Glu Ile Ser Asp Phe Pro Pro
 1 5 10 15
 gtt aga agt ctg gtt gat gct tta ata gct aat aaa gtt aaa acc act 96

```

Val Arg Ser Leu Val Asp Ala Leu Ile Ala Asn Lys Val Lys Thr Thr
      20                      25                      30

ata att act cga gat gaa aat aat gta tta gat agt tat ggt gat aaa 144
Ile Ile Thr Arg Asp Glu Asn Asn Val Leu Asp Ser Tyr Gly Asp Lys
      35                      40                      45

tta aaa gtt ttg gaa tta ttg cca tat gct tca aat ggt aat ttt aaa 192
Leu Lys Val Leu Glu Leu Leu Pro Tyr Ala Ser Asn Gly Asn Phe Lys
      50                      55                      60

aat act tat aaa ttt ttt gaa aat aga aag cta att aga aaa tgg gta 240
Asn Thr Tyr Lys Phe Phe Glu Asn Arg Lys Leu Ile Arg Lys Trp Val
      65                      70                      75                      80

aag aag gag atg aaa aat aat gat att att tgg aca act acg gat gca 288
Lys Lys Glu Met Lys Asn Asn Asp Ile Ile Trp Thr Thr Thr Asp Ala
      85                      90                      95

act gtt cga gaa att gga cct gat ttg ctt aat tac aaa cat gtt atg 336
Thr Val Arg Glu Ile Gly Pro Asp Leu Leu Asn Tyr Lys His Val Met
      100                      105                      110

caa tta atg gaa tta gtt gaa tac gtg cca aaa ttc cct tta att cct 384
Gln Leu Met Glu Leu Val Glu Tyr Val Pro Lys Phe Pro Leu Ile Pro
      115                      120                      125

aaa aaa aat tta ttt aaa ttc aat ata act aaa tat gcc cat cat gct 432
Lys Lys Asn Leu Phe Lys Phe Asn Ile Thr Lys Tyr Ala His His Ala
      130                      135                      140

tgg aag ata gtg gta cct gaa ata aat aga gct tat att caa aag gta 480
Trp Lys Ile Val Val Pro Glu Ile Asn Arg Ala Tyr Ile Gln Lys Val
      145                      150                      155                      160

tgg tgg gat ctt gaa aaa act cct aaa att tta ccc aaa 519
Trp Trp Asp Leu Glu Lys Thr Pro Lys Ile Leu Pro Lys
      165                      170

```

<210> 168

<211> 173

<212> PRT

<213> Lactobacillus acidophilus

<400> 168

```

Met Arg Val Leu Ile Val His Asn Arg Glu Ile Ser Asp Phe Pro Pro
  1      5      10      15
Val Arg Ser Leu Val Asp Ala Leu Ile Ala Asn Lys Val Lys Thr Thr
      20      25      30
Ile Ile Thr Arg Asp Glu Asn Asn Val Leu Asp Ser Tyr Gly Asp Lys
      35      40      45
Leu Lys Val Leu Glu Leu Leu Pro Tyr Ala Ser Asn Gly Asn Phe Lys
      50      55      60
Asn Thr Tyr Lys Phe Phe Glu Asn Arg Lys Leu Ile Arg Lys Trp Val
      65      70      75      80
Lys Lys Glu Met Lys Asn Asn Asp Ile Ile Trp Thr Thr Thr Asp Ala

```

<400> 169																	
atg	aat	aat	ata	gca	gcg	ata	gta	gtt	aca	tat	aat	aga	aaa	aaa	tta	48	
Met	Asn	Asn	Ile	Ala	Ala	Ile	Val	Val	Thr	Tyr	Asn	Arg	Lys	Lys	Leu		
1				5					10					15			
tta	aaa	aaa	tgt	att	aaa	gga	cta	aaa	gag	caa	aca	gaa	aaa	gct	gat	96	
Leu	Lys	Lys	Cys	Ile	Lys	Gly	Leu	Lys	Glu	Gln	Thr	Glu	Lys	Ala	Asp		
			20					25					30				
atc	att	att	att	gat	aat	atg	agt	act	gat	ggg	act	tta	gaa	atg	tta	144	
Ile	Ile	Ile	Ile	Asp	Asn	Met	Ser	Thr	Asp	Gly	Thr	Leu	Glu	Met	Leu		
			35				40					45					
cag	cct	tta	att	aat	tca	aac	gaa	ata	att	tat	cac	tcg	act	gga	aaa	192	
Gln	Pro	Leu	Ile	Asn	Ser	Asn	Glu	Ile	Ile	Tyr	His	Ser	Thr	Gly	Lys		
	50					55					60						
aat	att	ggg	ggg	gct	ggg	ggc	ttt	tat	gag	gga	ata	aaa	cta	gct	tat	240	
Asn	Ile	Gly	Gly	Ala	Gly	Gly	Phe	Tyr	Glu	Gly	Ile	Lys	Leu	Ala	Tyr		
65					70					75					80		
gaa	atg	gga	tat	aaa	tat	ttt	tgg	tta	atg	gat	gat	gat	tgt	att	cca	288	
Glu	Met	Gly	Tyr	Lys	Tyr	Phe	Trp	Leu	Met	Asp	Asp	Asp	Cys	Ile	Pro		
				85					90					95			
act	tct	tcc	gct	tta	gaa	aaa	tta	atg	aat	gta	gta	aat	gag	aaa	aaa	336	
Thr	Ser	Ser	Ala	Leu	Glu	Lys	Leu	Met	Asn	Val	Val	Asn	Glu	Lys	Lys		
			100					105					110				

```

aat ttt ggt ttt ttg gta agt aaa gcc cta tgg aaa gat gga gaa gta   384
Asn Phe Gly Phe Leu Val Ser Lys Ala Leu Trp Lys Asp Gly Glu Val
      115                      120                      125

tgt aaa atg aat ata cct aag ata aaa ctt acc aag caa gta aat gat   432
Cys Lys Met Asn Ile Pro Lys Ile Lys Leu Thr Lys Gln Val Asn Asp
      130                      135                      140

ttc tca aaa aag gtt att caa att aaa atg gga aca ttc gtt tcg ttt   480
Phe Ser Lys Lys Val Ile Gln Ile Lys Met Gly Thr Phe Val Ser Phe
      145                      150                      155                      160

cta acc tca aga gaa gta gta gaa aaa gta gga tta cct ata aaa gaa   528
Leu Thr Ser Arg Glu Val Val Glu Lys Val Gly Leu Pro Ile Lys Glu
      165                      170                      175

ttc ttt att tgg ggg gat gat ttg gaa tat agc caa aga att tcc caa   576
Phe Phe Ile Trp Gly Asp Asp Leu Glu Tyr Ser Gln Arg Ile Ser Gln
      180                      185                      190

aaa ttt cca tct tat ttg gtt aca aat agt ctt gtg tat cat gaa act   624
Lys Phe Pro Ser Tyr Leu Val Thr Asn Ser Leu Val Tyr His Glu Thr
      195                      200                      205

aaa ttg aat gaa ggg tct aat att gca tta gat agc gtt gat cgt tta   672
Lys Leu Asn Glu Gly Ser Asn Ile Ala Leu Asp Ser Val Asp Arg Leu
      210                      215                      220

aaa cga tat aaa ctt gca tat aga aat gaa gtt gtt ttg ttt aaa gaa   720
Lys Arg Tyr Lys Leu Ala Tyr Arg Asn Glu Val Val Leu Phe Lys Glu
      225                      230                      235                      240

atg gga ttg caa ggg caa atg tat caa tat ttt cgt tta gtt ctg cat   768
Met Gly Leu Gln Gly Gln Met Tyr Gln Tyr Phe Arg Leu Val Leu His
      245                      250                      255

tgt gga cgg att ctg ttt aag agc aaa gat cat aaa aaa gaa cga ttg   816
Cys Gly Arg Ile Leu Phe Lys Ser Lys Asp His Lys Lys Glu Arg Leu
      260                      265                      270

aat att att ttt caa ggc aca cga gct gga tat aat ttc cat ccc gta   864
Asn Ile Ile Phe Gln Gly Thr Arg Ala Gly Tyr Asn Phe His Pro Val
      275                      280                      285

ata aaa aat atc aaa                                           879
Ile Lys Asn Ile Lys
      290

```

<210> 170

<211> 293

<212> PRT

<213> Lactobacillus acidophilus

<400> 170

```

Met Asn Asn Ile Ala Ala Ile Val Val Thr Tyr Asn Arg Lys Lys Leu
  1              5              10              15

```

Leu Lys Lys Cys Ile Lys Gly Leu Lys Glu Gln Thr Glu Lys Ala Asp
 20 25 30
 Ile Ile Ile Ile Asp Asn Met Ser Thr Asp Gly Thr Leu Glu Met Leu
 35 40 45
 Gln Pro Leu Ile Asn Ser Asn Glu Ile Ile Tyr His Ser Thr Gly Lys
 50 55 60
 Asn Ile Gly Gly Ala Gly Gly Phe Tyr Glu Gly Ile Lys Leu Ala Tyr
 65 70 75 80
 Glu Met Gly Tyr Lys Tyr Phe Trp Leu Met Asp Asp Asp Cys Ile Pro
 85 90 95
 Thr Ser Ser Ala Leu Glu Lys Leu Met Asn Val Val Asn Glu Lys Lys
 100 105 110
 Asn Phe Gly Phe Leu Val Ser Lys Ala Leu Trp Lys Asp Gly Glu Val
 115 120 125
 Cys Lys Met Asn Ile Pro Lys Ile Lys Leu Thr Lys Gln Val Asn Asp
 130 135 140
 Phe Ser Lys Lys Val Ile Gln Ile Lys Met Gly Thr Phe Val Ser Phe
 145 150 155 160
 Leu Thr Ser Arg Glu Val Val Glu Lys Val Gly Leu Pro Ile Lys Glu
 165 170 175
 Phe Phe Ile Trp Gly Asp Asp Leu Glu Tyr Ser Gln Arg Ile Ser Gln
 180 185 190
 Lys Phe Pro Ser Tyr Leu Val Thr Asn Ser Leu Val Tyr His Glu Thr
 195 200 205
 Lys Leu Asn Glu Gly Ser Asn Ile Ala Leu Asp Ser Val Asp Arg Leu
 210 215 220
 Lys Arg Tyr Lys Leu Ala Tyr Arg Asn Glu Val Val Leu Phe Lys Glu
 225 230 235 240
 Met Gly Leu Gln Gly Gln Met Tyr Gln Tyr Phe Arg Leu Val Leu His
 245 250 255
 Cys Gly Arg Ile Leu Phe Lys Ser Lys Asp His Lys Lys Glu Arg Leu
 260 265 270
 Asn Ile Ile Phe Gln Gly Thr Arg Ala Gly Tyr Asn Phe His Pro Val
 275 280 285
 Ile Lys Asn Ile Lys
 290

<210> 171

<211> 771

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1732 - galactosyl transferase

<220>

<221> CDS

<222> (1)...(771)

<400> 171

atg aaa ata aaa att tta gtt gct gca cat aag aaa ttt cca atg cca 48
 Met Lys Ile Lys Ile Leu Val Ala Ala His Lys Lys Phe Pro Met Pro
 1 5 10 15

aat act gat gga tat atg cct gtg tta gta ggt gca gct aaa aat tat	96
Asn Thr Asp Gly Tyr Met Pro Val Leu Val Gly Ala Ala Lys Asn Tyr	
20 25 30	
aaa cca gac att aaa tat caa aga gac gac gag ggt gat aat ata tct	144
Lys Pro Asp Ile Lys Tyr Gln Arg Asp Asp Glu Gly Asp Asn Ile Ser	
35 40 45	
ttt aag aat cca aat tat aat gaa ctg acc gct gtt tat tgg gct tgg	192
Phe Lys Asn Pro Asn Tyr Asn Glu Leu Thr Ala Val Tyr Trp Ala Trp	
50 55 60	
aag aat ttg gaa aat gta gat gca gta ggt ctt gtc cac tat cgt cgt	240
Lys Asn Leu Glu Asn Val Asp Ala Val Gly Leu Val His Tyr Arg Arg	
65 70 75 80	
ctc ttt ttt gat acg aaa ccg tat acg tta agt aat gtt att agt atc	288
Leu Phe Phe Asp Thr Lys Pro Tyr Thr Leu Ser Asn Val Ile Ser Ile	
85 90 95	
aaa aaa ata gaa gaa tta cta act caa tat gat gta atc ctt cct aaa	336
Lys Lys Ile Glu Glu Leu Leu Thr Gln Tyr Asp Val Ile Leu Pro Lys	
100 105 110	
aaa aga aac tat tat att gag aca aat tat tct cat tat ata cat gct	384
Lys Arg Asn Tyr Tyr Ile Glu Thr Asn Tyr Ser His Tyr Ile His Ala	
115 120 125	
cat cat cgg gaa cct tta gat aga acg aga gat gta gtt gcc caa aat	432
His His Arg Glu Pro Leu Asp Arg Thr Arg Asp Val Val Ala Gln Asn	
130 135 140	
tat cca caa tat tta tca aat ttt gat aaa gca atg cat aga aga aaa	480
Tyr Pro Gln Tyr Leu Ser Asn Phe Asp Lys Ala Met His Arg Arg Lys	
145 150 155 160	
gcg cat atg ttt aat atg ttc ata atg cgt aaa aag gtt ttt gaa tca	528
Ala His Met Phe Asn Met Phe Ile Met Arg Lys Lys Val Phe Glu Ser	
165 170 175	
tat tgt aat ttt gtt ttt ggt gta ttg agt aaa tta gaa aat ata ata	576
Tyr Cys Asn Phe Val Phe Gly Val Leu Ser Lys Leu Glu Asn Ile Ile	
180 185 190	
gat att tca aat tat tct gta caa gaa gca aga gta tat gga tat att	624
Asp Ile Ser Asn Tyr Ser Val Gln Glu Ala Arg Val Tyr Gly Tyr Ile	
195 200 205	
tca gaa ttg tta atg gat gtt tgg ctt gaa act aat gga atc aaa tat	672
Ser Glu Leu Leu Met Asp Val Trp Leu Glu Thr Asn Gly Ile Lys Tyr	
210 215 220	
gtt gaa atg cca tgg gga cag att ggc ggt aag aat aat gtg aaa aag	720
Val Glu Met Pro Trp Gly Gln Ile Gly Gly Lys Asn Asn Val Lys Lys	
225 230 235 240	

gct att ttt ctt ata aaa aga aag atg gga ata aag act aaa aca cac 768
 Ala Ile Phe Leu Ile Lys Arg Lys Met Gly Ile Lys Thr Lys Thr His
 245 250 255

ttt 771
 Phe

<210> 172

<211> 257

<212> PRT

<213> Lactobacillus acidophilus

<400> 172

Met Lys Ile Lys Ile Leu Val Ala Ala His Lys Lys Phe Pro Met Pro
 1 5 10 15
 Asn Thr Asp Gly Tyr Met Pro Val Leu Val Gly Ala Ala Lys Asn Tyr
 20 25 30
 Lys Pro Asp Ile Lys Tyr Gln Arg Asp Asp Glu Gly Asp Asn Ile Ser
 35 40 45
 Phe Lys Asn Pro Asn Tyr Asn Glu Leu Thr Ala Val Tyr Trp Ala Trp
 50 55 60
 Lys Asn Leu Glu Asn Val Asp Ala Val Gly Leu Val His Tyr Arg Arg
 65 70 75 80
 Leu Phe Phe Asp Thr Lys Pro Tyr Thr Leu Ser Asn Val Ile Ser Ile
 85 90 95
 Lys Lys Ile Glu Glu Leu Leu Thr Gln Tyr Asp Val Ile Leu Pro Lys
 100 105 110
 Lys Arg Asn Tyr Tyr Ile Glu Thr Asn Tyr Ser His Tyr Ile His Ala
 115 120 125
 His His Arg Glu Pro Leu Asp Arg Thr Arg Asp Val Val Ala Gln Asn
 130 135 140
 Tyr Pro Gln Tyr Leu Ser Asn Phe Asp Lys Ala Met His Arg Arg Lys
 145 150 155 160
 Ala His Met Phe Asn Met Phe Ile Met Arg Lys Lys Val Phe Glu Ser
 165 170 175
 Tyr Cys Asn Phe Val Phe Gly Val Leu Ser Lys Leu Glu Asn Ile Ile
 180 185 190
 Asp Ile Ser Asn Tyr Ser Val Gln Glu Ala Arg Val Tyr Gly Tyr Ile
 195 200 205
 Ser Glu Leu Leu Met Asp Val Trp Leu Glu Thr Asn Gly Ile Lys Tyr
 210 215 220
 Val Glu Met Pro Trp Gly Gln Ile Gly Gly Lys Asn Asn Val Lys Lys
 225 230 235 240
 Ala Ile Phe Leu Ile Lys Arg Lys Met Gly Ile Lys Thr Lys Thr His
 245 250 255
 Phe

<210> 173

<211> 651

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1733 - phospho-glucosyltransferase epse

<220>

<221> CDS

<222> (1)...(651)

<400> 173

atg atg gcg atg gaa aga ctg aaa gtt aat cct aag aag gta tat aat	48
Met Met Ala Met Glu Arg Leu Lys Val Asn Pro Lys Lys Val Tyr Asn	
1 5 10 15	
cga cct ttt tat cac aca gtt aag cgg tta ttt gat atc gta gcc agt	96
Arg Pro Phe Tyr His Thr Val Lys Arg Leu Phe Asp Ile Val Ala Ser	
20 25 30	
gcg att gga tta gtt ctt cta tca cca tta ttt ttg tat cta att att	144
Ala Ile Gly Leu Val Leu Leu Ser Pro Leu Phe Leu Tyr Leu Ile Ile	
35 40 45	
aga att aga cac gaa gat ggt ggc cca gca ttt tat tcg caa gag cga	192
Arg Ile Arg His Glu Asp Gly Gly Pro Ala Phe Tyr Ser Gln Glu Arg	
50 55 60	
att ggt aag aat gaa aag cca ttt aga atg tgg aag ttt cgt tcc atg	240
Ile Gly Lys Asn Glu Lys Pro Phe Arg Met Trp Lys Phe Arg Ser Met	
65 70 75 80	
gtt gtt aat gca gat aag atg ctg gat aaa tta gaa gat caa aat gaa	288
Val Val Asn Ala Asp Lys Met Leu Asp Lys Leu Glu Asp Gln Asn Glu	
85 90 95	
gtc aat gga gct atg ttt aag att aaa gat gat cca aga att acc aaa	336
Val Asn Gly Ala Met Phe Lys Ile Lys Asp Asp Pro Arg Ile Thr Lys	
100 105 110	
att ggg cat atg att cgt aaa tat agt ctt gat gaa tta cca caa tta	384
Ile Gly His Met Ile Arg Lys Tyr Ser Leu Asp Glu Leu Pro Gln Leu	
115 120 125	
tac aat gtt ctg atc gga gac atg tcg tta gta gga cca cgt cca cct	432
Tyr Asn Val Leu Ile Gly Asp Met Ser Leu Val Gly Pro Arg Pro Pro	
130 135 140	
ctt cct tct gaa gtt gaa gag tat acg gat tat gat aaa caa cgt cta	480
Leu Pro Ser Glu Val Glu Glu Tyr Thr Asp Tyr Asp Lys Gln Arg Leu	
145 150 155 160	
tta gtt atg cct ggg tgt act gga ctt tgg caa gta acg cgt aga aat	528
Leu Val Met Pro Gly Cys Thr Gly Leu Trp Gln Val Thr Arg Arg Asn	
165 170 175	
gaa gca gac ttt gat gaa atg gta tgg ctt gat att gtt tat atc aat	576
Glu Ala Asp Phe Asp Glu Met Val Trp Leu Asp Ile Val Tyr Ile Asn	
180 185 190	

cat tct gga ttg tgg gaa gac ttt aaa ttg att att aag acc gta tta 624
 His Ser Gly Leu Trp Glu Asp Phe Lys Leu Ile Ile Lys Thr Val Leu
 195 200 205

gtt atg att cat ccg aat ggg gct tat 651
 Val Met Ile His Pro Asn Gly Ala Tyr
 210 215

<210> 174

<211> 217

<212> PRT

<213> Lactobacillus acidophilus

<400> 174

Met Met Ala Met Glu Arg Leu Lys Val Asn Pro Lys Lys Val Tyr Asn
 1 5 10 15
 Arg Pro Phe Tyr His Thr Val Lys Arg Leu Phe Asp Ile Val Ala Ser
 20 25 30
 Ala Ile Gly Leu Val Leu Leu Ser Pro Leu Phe Leu Tyr Leu Ile Ile
 35 40 45
 Arg Ile Arg His Glu Asp Gly Gly Pro Ala Phe Tyr Ser Gln Glu Arg
 50 55 60
 Ile Gly Lys Asn Glu Lys Pro Phe Arg Met Trp Lys Phe Arg Ser Met
 65 70 75 80
 Val Val Asn Ala Asp Lys Met Leu Asp Lys Leu Glu Asp Gln Asn Glu
 85 90 95
 Val Asn Gly Ala Met Phe Lys Ile Lys Asp Asp Pro Arg Ile Thr Lys
 100 105 110
 Ile Gly His Met Ile Arg Lys Tyr Ser Leu Asp Glu Leu Pro Gln Leu
 115 120 125
 Tyr Asn Val Leu Ile Gly Asp Met Ser Leu Val Gly Pro Arg Pro Pro
 130 135 140
 Leu Pro Ser Glu Val Glu Glu Tyr Thr Asp Tyr Asp Lys Gln Arg Leu
 145 150 155 160
 Leu Val Met Pro Gly Cys Thr Gly Leu Trp Gln Val Thr Arg Arg Asn
 165 170 175
 Glu Ala Asp Phe Asp Glu Met Val Trp Leu Asp Ile Val Tyr Ile Asn
 180 185 190
 His Ser Gly Leu Trp Glu Asp Phe Lys Leu Ile Ile Lys Thr Val Leu
 195 200 205
 Val Met Ile His Pro Asn Gly Ala Tyr
 210 215

<210> 175

<211> 768

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1734 - epsD

<220>

<221> CDS

<222> (1)...(768)

<400> 175

atg act tta gtt gat att cac tgt cac att ttg cca gga att gat gat	48
Met Thr Leu Val Asp Ile His Cys His Ile Leu Pro Gly Ile Asp Asp	
1 5 10 15	
gga tca aaa gat tgg gaa aca tca att aag ttg gca agg gat gct gta	96
Gly Ser Lys Asp Trp Glu Thr Ser Ile Lys Leu Ala Arg Asp Ala Val	
20 25 30	
aaa gat ggt ata aca cat gca gta tgt aca cca cat acg tta aat gga	144
Lys Asp Gly Ile Thr His Ala Val Cys Thr Pro His Thr Leu Asn Gly	
35 40 45	
aaa tat ctt aat cac aaa gat gat gtg att cga tta act gag aac ttt	192
Lys Tyr Leu Asn His Lys Asp Asp Val Ile Arg Leu Thr Glu Asn Phe	
50 55 60	
caa gat atg ctt gat gaa gca aag att cca tta aca gta ttt cct ggg	240
Gln Asp Met Leu Asp Glu Ala Lys Ile Pro Leu Thr Val Phe Pro Gly	
65 70 75 80	
caa gaa gtg cgt att tca ggc gat ttg cct gat gca tta gat aat gat	288
Gln Glu Val Arg Ile Ser Gly Asp Leu Pro Asp Ala Leu Asp Asn Asp	
85 90 95	
gac att ctc ttc tta gat gaa gag gga caa tac atg tta ttg gaa ttt	336
Asp Ile Leu Phe Leu Asp Glu Glu Gly Gln Tyr Met Leu Leu Glu Phe	
100 105 110	
cca agt gat gat gta cca act tat gct aaa gat atg atc ttt agc att	384
Pro Ser Asp Asp Val Pro Thr Tyr Ala Lys Asp Met Ile Phe Ser Ile	
115 120 125	
caa caa cgt ggt att aca cca att gtt gtg cat ccg gaa cgt aac agt	432
Gln Gln Arg Gly Ile Thr Pro Ile Val Val His Pro Glu Arg Asn Ser	
130 135 140	
aga atc tta aaa gag cca cat atc ttg caa gaa tta att gag caa ggt	480
Arg Ile Leu Lys Glu Pro His Ile Leu Gln Glu Leu Ile Glu Gln Gly	
145 150 155 160	
tgt cta gtt caa att act gct agt tca tat gtt gga aca ttt ggc cag	528
Cys Leu Val Gln Ile Thr Ala Ser Ser Tyr Val Gly Thr Phe Gly Gln	
165 170 175	
aaa ata gaa gaa atg agt aga cgc ttc att gaa gct gga caa tgt gct	576
Lys Ile Glu Glu Met Ser Arg Arg Phe Ile Glu Ala Gly Gln Cys Ala	
180 185 190	
tgc ttt gca tcc gat gct cat gat ctg cct aag aga caa tat gaa tat	624
Cys Phe Ala Ser Asp Ala His Asp Leu Pro Lys Arg Gln Tyr Glu Tyr	
195 200 205	

```

agt gca gca tta aag aag ttg agc aat gaa ttt gga agt gga cgt gct 672
Ser Ala Ala Leu Lys Lys Leu Ser Asn Glu Phe Gly Ser Gly Arg Ala
    210                215                220

caa gaa ttc gaa gat aat gct cgc gca att gtg aac ggc gat aat gtt 720
Gln Glu Phe Glu Asp Asn Ala Arg Ala Ile Val Asn Gly Asp Asn Val
    225                230                235                240

caa ttg aat tgg cga cca ctt aag aaa aag aag aag ttt tgg tta ttt 768
Gln Leu Asn Trp Arg Pro Leu Lys Lys Lys Lys Lys Phe Trp Leu Phe
    245                250                255

```

```

<210> 176
<211> 256
<212> PRT
<213> Lactobacillus acidophilus

```

```

<400> 176
Met Thr Leu Val Asp Ile His Cys His Ile Leu Pro Gly Ile Asp Asp
 1      5      10
Gly Ser Lys Asp Trp Glu Thr Ser Ile Lys Leu Ala Arg Asp Ala Val
    20      25      30
Lys Asp Gly Ile Thr His Ala Val Cys Thr Pro His Thr Leu Asn Gly
    35      40      45
Lys Tyr Leu Asn His Lys Asp Val Ile Arg Leu Thr Glu Asn Phe
    50      55      60
Gln Asp Met Leu Asp Glu Ala Lys Ile Pro Leu Thr Val Phe Pro Gly
    65      70      75      80
Gln Glu Val Arg Ile Ser Gly Asp Leu Pro Asp Ala Leu Asp Asn Asp
    85      90      95
Asp Ile Leu Phe Leu Asp Glu Glu Gly Gln Tyr Met Leu Leu Glu Phe
    100     105     110
Pro Ser Asp Asp Val Pro Thr Tyr Ala Lys Asp Met Ile Phe Ser Ile
    115     120     125
Gln Gln Arg Gly Ile Thr Pro Ile Val Val His Pro Glu Arg Asn Ser
    130     135     140
Arg Ile Leu Lys Glu Pro His Ile Leu Gln Glu Leu Ile Glu Gln Gly
    145     150     155     160
Cys Leu Val Gln Ile Thr Ala Ser Ser Tyr Val Gly Thr Phe Gly Gln
    165     170     175
Lys Ile Glu Glu Met Ser Arg Arg Phe Ile Glu Ala Gly Gln Cys Ala
    180     185     190
Cys Phe Ala Ser Asp Ala His Asp Leu Pro Lys Arg Gln Tyr Glu Tyr
    195     200     205
Ser Ala Ala Leu Lys Lys Leu Ser Asn Glu Phe Gly Ser Gly Arg Ala
    210     215     220
Gln Glu Phe Glu Asp Asn Ala Arg Ala Ile Val Asn Gly Asp Asn Val
    225     230     235     240
Gln Leu Asn Trp Arg Pro Leu Lys Lys Lys Lys Phe Trp Leu Phe
    245     250     255

```

```

<210> 177
<211> 780
<212> DNA

```

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1735 - epsC

<220>

<221> CDS

<222> (1)...(780)

<400> 177

```

atg cca tta ttt aag aaa aag cgt ggt aca gat gaa act att aaa cat 48
Met Pro Leu Phe Lys Lys Lys Arg Gly Thr Asp Glu Thr Ile Lys His
1 5 10 15

ggt gct aag tta atc act gta gct aag cca aag agt cca ata gct gaa 96
Gly Ala Lys Leu Ile Thr Val Ala Lys Pro Lys Ser Pro Ile Ala Glu
20 25 30

caa ttc cgt act gtt cgt act aat att aac ttt atg gca gtg gat cat 144
Gln Phe Arg Thr Val Arg Thr Asn Ile Asn Phe Met Ala Val Asp His
35 40 45

gac att aag tct tta gca ttt act tct gct aat att agt gaa ggt aaa 192
Asp Ile Lys Ser Leu Ala Phe Thr Ser Ala Asn Ile Ser Glu Gly Lys
50 55 60

tct act gtg gct gct aac gtt gct gtt act tat gct caa gca ggt cgt 240
Ser Thr Val Ala Ala Asn Val Ala Val Thr Tyr Ala Gln Ala Gly Arg
65 70 75 80

aaa gtc tta ttg gtc gat gcc gac tta cgt aga cct aca gtg cac tca 288
Lys Val Leu Leu Val Asp Ala Asp Leu Arg Arg Pro Thr Val His Ser
85 90 95

acc ttt aac tta agt aat cat gtt ggt ctt agt acg gtt atc tct tca 336
Thr Phe Asn Leu Ser Asn His Val Gly Leu Ser Thr Val Ile Ser Ser
100 105 110

act gct aag gaa gtt gat ctt gat agc gta gta caa gag agc ggc gta 384
Thr Ala Lys Glu Val Asp Leu Asp Ser Val Val Gln Glu Ser Gly Val
115 120 125

gat aat ctt tac gtg tta acg gct ggt ccg atg cca cct aac ccg gca 432
Asp Asn Leu Tyr Val Leu Thr Ala Gly Pro Met Pro Pro Asn Pro Ala
130 135 140

gaa ctg ata ggt tct aag cgt atg cgt gac ttt gtt aaa ctt act gaa 480
Glu Leu Ile Gly Ser Lys Arg Met Arg Asp Phe Val Lys Leu Thr Glu
145 150 155 160

gaa cac tac gat tta gtt att atc gac tta gct cct gtt ctt gaa gta 528
Glu His Tyr Asp Leu Val Ile Ile Asp Leu Ala Pro Val Leu Glu Val
165 170 175

```

```

tct gat aca caa gaa ctt gct agt cac tta gat ggg gtt gtc tta gta 576
Ser Asp Thr Gln Glu Leu Ala Ser His Leu Asp Gly Val Val Leu Val
      180                      185                      190

gtt cgc caa ggg aag acg caa aag atg gcc att aag cgt gct gtt gaa 624
Val Arg Gln Gly Lys Thr Gln Lys Met Ala Ile Lys Arg Ala Val Glu
      195                      200                      205

atg ctt gaa ttt gca aag gca cgt atc ttg ggt tac atc atg aat gat 672
Met Leu Glu Phe Ala Lys Ala Arg Ile Leu Gly Tyr Ile Met Asn Asp
      210                      215                      220

gta agt tct gat aat gcg ggt tat ggc tat ggt tac ggc tac ggc tat 720
Val Ser Ser Asp Asn Ala Gly Tyr Gly Tyr Gly Tyr Gly Tyr Gly Tyr
      225                      230                      235                      240

ggg tat ggc tac gga gaa gaa gat aca aag aaa aaa gga ttg ttc tct 768
Gly Tyr Gly Tyr Gly Glu Glu Asp Thr Lys Lys Lys Gly Leu Phe Ser
      245                      250                      255

aaa ttt agg aag 780
Lys Phe Arg Lys
      260

```

<210> 178

<211> 260

<212> PRT

<213> Lactobacillus acidophilus

<400> 178

```

Met Pro Leu Phe Lys Lys Lys Arg Gly Thr Asp Glu Thr Ile Lys His
1      5      10      15
Gly Ala Lys Leu Ile Thr Val Ala Lys Pro Lys Ser Pro Ile Ala Glu
      20      25      30
Gln Phe Arg Thr Val Arg Thr Asn Ile Asn Phe Met Ala Val Asp His
      35      40      45
Asp Ile Lys Ser Leu Ala Phe Thr Ser Ala Asn Ile Ser Glu Gly Lys
      50      55      60
Ser Thr Val Ala Ala Asn Val Ala Val Thr Tyr Ala Gln Ala Gly Arg
65      70      75      80
Lys Val Leu Leu Val Asp Ala Asp Leu Arg Arg Pro Thr Val His Ser
      85      90      95
Thr Phe Asn Leu Ser Asn His Val Gly Leu Ser Thr Val Ile Ser Ser
      100     105     110
Thr Ala Lys Glu Val Asp Leu Asp Ser Val Val Gln Glu Ser Gly Val
      115     120     125
Asp Asn Leu Tyr Val Leu Thr Ala Gly Pro Met Pro Pro Asn Pro Ala
130     135     140
Glu Leu Ile Gly Ser Lys Arg Met Arg Asp Phe Val Lys Leu Thr Glu
145     150     155     160
Glu His Tyr Asp Leu Val Ile Ile Asp Leu Ala Pro Val Leu Glu Val
      165     170     175
Ser Asp Thr Gln Glu Leu Ala Ser His Leu Asp Gly Val Val Leu Val
      180     185     190
Val Arg Gln Gly Lys Thr Gln Lys Met Ala Ile Lys Arg Ala Val Glu
195     200     205

```

Met Leu Glu Phe Ala Lys Ala Arg Ile Leu Gly Tyr Ile Met Asn Asp
 210 215 220
 Val Ser Ser Asp Asn Ala Gly Tyr Gly Tyr Gly Tyr Gly Tyr Gly Tyr
 225 230 235 240
 Gly Tyr Gly Tyr Gly Glu Glu Asp Thr Lys Lys Lys Gly Leu Phe Ser
 245 250 255
 Lys Phe Arg Lys
 260

<210> 179

<211> 873

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1736 - epsB

<220>

<221> CDS

<222> (1)...(873)

<400> 179

atg gaa caa aaa caa gaa caa gaa aat aca atc gat ctt acc caa tta 48
 Met Glu Gln Lys Gln Glu Gln Glu Asn Thr Ile Asp Leu Thr Gln Leu
 1 5 10 15
 tta cgc att tgc cgt aag cat atc tgg gca ttg att ctt tgg agt gta 96
 Leu Arg Ile Cys Arg Lys His Ile Trp Ala Leu Ile Leu Trp Ser Val
 20 25 30
 ggt ctt gcc tta gtg ggc tgg gga gtt tca gaa ttt gta att tct cct 144
 Gly Leu Ala Leu Val Gly Trp Gly Val Ser Glu Phe Val Ile Ser Pro
 35 40 45
 aaa tat act tca act gct caa tta tta gtt aac caa aag agt cgt aac 192
 Lys Tyr Thr Ser Thr Ala Gln Leu Leu Val Asn Gln Lys Ser Arg Asn
 50 55 60
 aat gat cca aac gca gct tat gcg act caa caa gct aac atg cag atg 240
 Asn Asp Pro Asn Ala Ala Tyr Ala Thr Gln Gln Ala Asn Met Gln Met
 65 70 75 80
 gtt act act tat aaa gac att gta aca agt aac aag atc tta aca gaa 288
 Val Thr Thr Tyr Lys Asp Ile Val Thr Ser Asn Lys Ile Leu Thr Glu
 85 90 95
 gct tct aat cgt ttg gcc aat cca act gtt gtt gtg aaa aaa gca caa 336
 Ala Ser Asn Arg Leu Ala Asn Pro Thr Val Val Val Lys Lys Ala Gln
 100 105 110
 aaa gca gtg tac aga act gat gaa aat ggt aga aga aga tta gta aga 384
 Lys Ala Val Tyr Arg Thr Asp Glu Asn Gly Arg Arg Arg Leu Val Arg
 115 120 125

```

aaa gct caa cca gct gta att gaa cga agc ggt aag agt tat tca gtt 432
Lys Ala Gln Pro Ala Val Ile Glu Arg Ser Gly Lys Ser Tyr Ser Val
130 135 140

tct gca agt gaa ctt gct aag agt atc tca gta ggt acc caa caa caa 480
Ser Ala Ser Glu Leu Ala Lys Ser Ile Ser Val Gly Thr Gln Gln Gln
145 150 155 160

tca caa gtc ttc tca att tca gcg gaa gcc gat aca cca gct aag gcg 528
Ser Gln Val Phe Ser Ile Ser Ala Glu Ala Asp Thr Pro Ala Lys Ala
165 170 175

aag gca gaa gta aat gca gta gct gaa acg ttc cgt aaa gaa att cct 576
Lys Ala Glu Val Asn Ala Val Ala Glu Thr Phe Arg Lys Glu Ile Pro
180 185 190

act att atg agc gtt aat aac gta acg att gtg gca aat ggt act aat 624
Thr Ile Met Ser Val Asn Asn Val Thr Ile Val Ala Asn Gly Thr Asn
195 200 205

ggg gtt caa tcc tca cct aac gtt aag ttg ttc act cta gct gga ttt 672
Gly Val Gln Ser Ser Pro Asn Val Lys Leu Phe Thr Leu Ala Gly Phe
210 215 220

gta gtt ggg tta gta ttg agc ttt gct gta gtt att att cgt gaa atg 720
Val Val Gly Leu Val Leu Ser Phe Ala Val Val Ile Ile Arg Glu Met
225 230 235 240

agt aat act act gtt cgt gac gat gaa ttc tta act cgt gaa tta ggc 768
Ser Asn Thr Thr Val Arg Asp Asp Glu Phe Leu Thr Arg Glu Leu Gly
245 250 255

tta act aac tta ggt caa att gct cac ttc cac ttg tca tct tca ttt 816
Leu Thr Asn Leu Gly Gln Ile Ala His Phe His Leu Ser Ser Ser Phe
260 265 270

act att aaa aag agt gca aat atg act aat cgt gga caa gct aag aga 864
Thr Ile Lys Lys Ser Ala Asn Met Thr Asn Arg Gly Gln Ala Lys Arg
275 280 285

cgt aga gta 873
Arg Arg Val
290

```

<210> 180

<211> 291

<212> PRT

<213> Lactobacillus acidophilus

<400> 180

```

Met Glu Gln Lys Gln Glu Gln Glu Asn Thr Ile Asp Leu Thr Gln Leu
1 5 10 15
Leu Arg Ile Cys Arg Lys His Ile Trp Ala Leu Ile Leu Trp Ser Val
20 25 30
Gly Leu Ala Leu Val Gly Trp Gly Val Ser Glu Phe Val Ile Ser Pro

```

```

      35      40      45
Lys Tyr Thr Ser Thr Ala Gln Leu Leu Val Asn Gln Lys Ser Arg Asn
  50      55      60
Asn Asp Pro Asn Ala Ala Tyr Ala Thr Gln Gln Ala Asn Met Gln Met
  65      70      75      80
Val Thr Thr Tyr Lys Asp Ile Val Thr Ser Asn Lys Ile Leu Thr Glu
      85      90      95
Ala Ser Asn Arg Leu Ala Asn Pro Thr Val Val Val Lys Lys Ala Gln
      100      105      110
Lys Ala Val Tyr Arg Thr Asp Glu Asn Gly Arg Arg Arg Leu Val Arg
      115      120      125
Lys Ala Gln Pro Ala Val Ile Glu Arg Ser Gly Lys Ser Tyr Ser Val
      130      135      140
Ser Ala Ser Glu Leu Ala Lys Ser Ile Ser Val Gly Thr Gln Gln Gln
      145      150      155      160
Ser Gln Val Phe Ser Ile Ser Ala Glu Ala Asp Thr Pro Ala Lys Ala
      165      170      175
Lys Ala Glu Val Asn Ala Val Ala Glu Thr Phe Arg Lys Glu Ile Pro
      180      185      190
Thr Ile Met Ser Val Asn Asn Val Thr Ile Val Ala Asn Gly Thr Asn
      195      200      205
Gly Val Gln Ser Ser Pro Asn Val Lys Leu Phe Thr Leu Ala Gly Phe
      210      215      220
Val Val Gly Leu Val Leu Ser Phe Ala Val Val Ile Ile Arg Glu Met
      225      230      235      240
Ser Asn Thr Thr Val Arg Asp Asp Glu Phe Leu Thr Arg Glu Leu Gly
      245      250      255
Leu Thr Asn Leu Gly Gln Ile Ala His Phe His Leu Ser Ser Ser Phe
      260      265      270
Thr Ile Lys Lys Ser Ala Asn Met Thr Asn Arg Gly Gln Ala Lys Arg
      275      280      285
Arg Arg Val
      290

```

```

<210> 181
<211> 1053
<212> DNA
<213> Lactobacillus acidophilus

```

```

<220>
<221> misc_feature
<222> (0)...(0)
<223> ORF 1737 - epsA

```

```

<220>
<221> CDS
<222> (1)...(1053)

```

```

<400> 181
atg gca gaa aat aat caa cca aat aat gat gta cgt cgc cat cac cac   48
Met Ala Glu Asn Asn Gln Pro Asn Asn Asp Val Arg Arg His His His
  1          5          10          15

cat aga cat cac cgt cat cac cat cgt aag ttt tgg cat tgg ttc tgg   96
His Arg His His Arg His His His Arg Lys Phe Trp His Trp Phe Trp

```

	20	25	30	
att gtg atc ggc gtt att gta gtc att gta ctt ttt gtt tgt ggt atg				144
Ile Val Ile Gly Val Ile Val Val Ile Val Leu Phe Val Cys Gly Met				
	35	40	45	
ggt tat aag aat tta cgc gat acc acg caa aat atg tat act ccc gtt				192
Val Tyr Lys Asn Leu Arg Asp Thr Thr Gln Asn Met Tyr Thr Pro Val				
	50	55	60	
gct aag aca act aag agc aac aag gga cgt aat ctt gat aat ttg cta				240
Ala Lys Thr Thr Lys Ser Asn Lys Gly Arg Asn Leu Asp Asn Leu Leu				
	65	70	75	80
gcg cag aaa aaa cca atc aat att ctt ttg ctc ggt act gat act gga				288
Ala Gln Lys Lys Pro Ile Asn Ile Leu Leu Leu Gly Thr Asp Thr Gly				
	85	90	95	
gca atg gga cgt agc tgg aaa gga cgt act gat acc atc atg atg atg				336
Ala Met Gly Arg Ser Trp Lys Gly Arg Thr Asp Thr Ile Met Met Met				
	100	105	110	
gca att aat cct aag act aat agt acg tca att gta tct att cca cgt				384
Ala Ile Asn Pro Lys Thr Asn Ser Thr Ser Ile Val Ser Ile Pro Arg				
	115	120	125	
gat tca aat gca atc ttc cca gat ttc cca caa tat gga gta acg aag				432
Asp Ser Asn Ala Ile Phe Pro Asp Phe Pro Gln Tyr Gly Val Thr Lys				
	130	135	140	
att aac tct gct tat aca cta ggc gga gtt ggt gaa aca gtt aag aca				480
Ile Asn Ser Ala Tyr Thr Leu Gly Gly Val Gly Glu Thr Val Lys Thr				
	145	150	155	160
ttg gat aaa tac tat agt gtg cca att gac ggt tac att atg atc aac				528
Leu Asp Lys Tyr Tyr Ser Val Pro Ile Asp Gly Tyr Ile Met Ile Asn				
	165	170	175	
atg ggt ggt ctt aag aag gct att gat caa gtt ggt ggt att gat gta				576
Met Gly Gly Leu Lys Lys Ala Ile Asp Gln Val Gly Gly Ile Asp Val				
	180	185	190	
act tca cca ttg act ttc gac aat atg gga tac cac ttc caa gaa ggt				624
Thr Ser Pro Leu Thr Phe Asp Asn Met Gly Tyr His Phe Gln Glu Gly				
	195	200	205	
aag acc tac cat atg gat ggt aag aag gca tta gcc ttt gct caa ctt				672
Lys Thr Tyr His Met Asp Gly Lys Lys Ala Leu Ala Phe Ala Gln Leu				
	210	215	220	
aga cat ggg gat cca cgt caa gat tat ggt cgt caa gac cgt gat cgc				720
Arg His Gly Asp Pro Arg Gln Asp Tyr Gly Arg Gln Asp Arg Asp Arg				
	225	230	235	240
cgt gtt gtc atg gca ctt ctt aag aag tct atc tca cct act aca tta				768
Arg Val Val Met Ala Leu Leu Lys Lys Ser Ile Ser Pro Thr Thr Leu				
	245	250	255	

```

ctt aat act aaa ttc ttg aat tca atc tca agt gaa atg caa act gac 816
Leu Asn Thr Lys Phe Leu Asn Ser Ile Ser Ser Glu Met Gln Thr Asp
                260                      265                      270

ttg act atg aat caa atg tac aag atc ggg atg gat tat aga cat gca 864
Leu Thr Met Asn Gln Met Tyr Lys Ile Gly Met Asp Tyr Arg His Ala
                275                      280                      285

aca gat aac ttg tca caa gat cat gct caa ggt gta agt aag caa act 912
Thr Asp Asn Leu Ser Gln Asp His Ala Gln Gly Val Ser Lys Gln Thr
                290                      295                      300

cag aat cct aag ttt ggt act atg gaa atc gaa gta gta agt aga caa 960
Gln Asn Pro Lys Phe Gly Thr Met Glu Ile Glu Val Val Ser Arg Gln
305                      310                      315                      320

gaa agg caa aga gtg tct gat aaa tta aga gca gca tta ggt ctt cct 1008
Glu Arg Gln Arg Val Ser Asp Lys Leu Arg Ala Ala Leu Gly Leu Pro
                325                      330                      335

aag gta cga gtt gct gct aat agt gcc agc tat gtc atg aat caa 1053
Lys Val Arg Val Ala Ala Asn Ser Ala Ser Tyr Val Met Asn Gln
                340                      345                      350

```

<210> 182

<211> 351

<212> PRT

<213> Lactobacillus acidophilus

<400> 182

```

Met Ala Glu Asn Asn Gln Pro Asn Asn Asp Val Arg Arg His His His
1          5          10          15
His Arg His His Arg His His His Arg Lys Phe Trp His Trp Phe Trp
                20          25          30
Ile Val Ile Gly Val Ile Val Val Ile Val Leu Phe Val Cys Gly Met
35          40          45
Val Tyr Lys Asn Leu Arg Asp Thr Thr Gln Asn Met Tyr Thr Pro Val
50          55          60
Ala Lys Thr Thr Lys Ser Asn Lys Gly Arg Asn Leu Asp Asn Leu Leu
65          70          75          80
Ala Gln Lys Lys Pro Ile Asn Ile Leu Leu Leu Gly Thr Asp Thr Gly
85          90          95
Ala Met Gly Arg Ser Trp Lys Gly Arg Thr Asp Thr Ile Met Met Met
100         105         110
Ala Ile Asn Pro Lys Thr Asn Ser Thr Ser Ile Val Ser Ile Pro Arg
115         120         125
Asp Ser Asn Ala Ile Phe Pro Asp Phe Pro Gln Tyr Gly Val Thr Lys
130         135         140
Ile Asn Ser Ala Tyr Thr Leu Gly Gly Val Gly Glu Thr Val Lys Thr
145         150         155         160
Leu Asp Lys Tyr Tyr Ser Val Pro Ile Asp Gly Tyr Ile Met Ile Asn
165         170         175
Met Gly Gly Leu Lys Lys Ala Ile Asp Gln Val Gly Gly Ile Asp Val
180         185         190

```

Thr Ser Pro Leu Thr Phe Asp Asn Met Gly Tyr His Phe Gln Glu Gly
 195 200 205
 Lys Thr Tyr His Met Asp Gly Lys Lys Ala Leu Ala Phe Ala Gln Leu
 210 215 220
 Arg His Gly Asp Pro Arg Gln Asp Tyr Gly Arg Gln Asp Arg Asp Arg
 225 230 235 240
 Arg Val Val Met Ala Leu Leu Lys Lys Ser Ile Ser Pro Thr Thr Leu
 245 250 255
 Leu Asn Thr Lys Phe Leu Asn Ser Ile Ser Ser Glu Met Gln Thr Asp
 260 265 270
 Leu Thr Met Asn Gln Met Tyr Lys Ile Gly Met Asp Tyr Arg His Ala
 275 280 285
 Thr Asp Asn Leu Ser Gln Asp His Ala Gln Gly Val Ser Lys Gln Thr
 290 295 300
 Gln Asn Pro Lys Phe Gly Thr Met Glu Ile Glu Val Val Ser Arg Gln
 305 310 315 320
 Glu Arg Gln Arg Val Ser Asp Lys Leu Arg Ala Ala Leu Gly Leu Pro
 325 330 335
 Lys Val Arg Val Ala Ala Asn Ser Ala Ser Tyr Val Met Asn Gln
 340 345 350

<210> 183

<211> 1263

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1738 - GTP-binding protein (HflX)

<220>

<221> CDS

<222> (1)...(1263)

<400> 183

atg ata gat aat caa cct aaa aaa act aag gcc tat atc gca ggc gtt 48
 Met Ile Asp Asn Gln Pro Lys Lys Thr Lys Ala Tyr Ile Ala Gly Val
 1 5 10 15

aac ttg aag gat cct aac ttc gac tac tac atg act gaa ctt gct aac 96
 Asn Leu Lys Asp Pro Asn Phe Asp Tyr Tyr Met Thr Glu Leu Ala Asn
 20 25 30

tta act gaa gca aat aat atg gaa gta gtt ggt caa agc tca caa aac 144
 Leu Thr Glu Ala Asn Asn Met Glu Val Val Gly Gln Ser Ser Gln Asn
 35 40 45

gcg gaa tca atc gtt gcc gga act tac ttc ggt gtc ggc aag att aac 192
 Ala Glu Ser Ile Val Ala Gly Thr Tyr Phe Gly Val Gly Lys Ile Asn
 50 55 60

gag att aag tcg atg gcc caa ggc ttg aaa gct aaa gtc ttg gtc tta 240
 Glu Ile Lys Ser Met Ala Gln Gly Leu Lys Ala Lys Val Leu Val Leu
 65 70 75 80

aat gat gaa tta act cca gta cag atc cgt aat ctt gag aag tta acc	288
Asn Asp Glu Leu Thr Pro Val Gln Ile Arg Asn Leu Glu Lys Leu Thr	
85 90 95	
aag atg cgc gtg att gat cga act gaa tta atc tta gaa atc ttc gcc	336
Lys Met Arg Val Ile Asp Arg Thr Glu Leu Ile Leu Glu Ile Phe Ala	
100 105 110	
agt cgt gca aga act aag caa gct aag cta caa gtt caa ctc gcc aga	384
Ser Arg Ala Arg Thr Lys Gln Ala Lys Leu Gln Val Gln Leu Ala Arg	
115 120 125	
ttg cag tac gaa ttg cca cgt ctt cac cct tcc gag aac aac ctg gac	432
Leu Gln Tyr Glu Leu Pro Arg Leu His Pro Ser Glu Asn Asn Leu Asp	
130 135 140	
cag caa cgt ggt ggt ggc ttc tcc aac cgt ggt gcc ggt gaa agt aaa	480
Gln Gln Arg Gly Gly Gly Phe Ser Asn Arg Gly Ala Gly Glu Ser Lys	
145 150 155 160	
ctt gaa tta aat cgt cgg aca atc ggt aag caa atc tct gct att aag	528
Leu Glu Leu Asn Arg Arg Thr Ile Gly Lys Gln Ile Ser Ala Ile Lys	
165 170 175	
aaa gaa ctc aag gct gtt gcc agc caa gaa gag att aaa tca gct cgc	576
Lys Glu Leu Lys Ala Val Ala Ser Gln Glu Glu Ile Lys Ser Ala Arg	
180 185 190	
cgt aat caa agt cgc atc cct aaa gtt gct ctt gtc ggc tac acc aac	624
Arg Asn Gln Ser Arg Ile Pro Lys Val Ala Leu Val Gly Tyr Thr Asn	
195 200 205	
gcc ggc aag tcc aca aca atg aac ggc cta ctc cgc gaa ttc tct aaa	672
Ala Gly Lys Ser Thr Thr Met Asn Gly Leu Leu Arg Glu Phe Ser Lys	
210 215 220	
gaa ggc agc gac aag gaa gtt ttc gtt aag aac atg ctc ttt gcc act	720
Glu Gly Ser Asp Lys Glu Val Phe Val Lys Asn Met Leu Phe Ala Thr	
225 230 235 240	
ctg gac acc agc gtg cgt cgt att gat tta aaa gat aat ttc agt ttt	768
Leu Asp Thr Ser Val Arg Arg Ile Asp Leu Lys Asp Asn Phe Ser Phe	
245 250 255	
atc ttg tct gac acc gtt ggt ttt att tct aag tta cca cac aac tta	816
Ile Leu Ser Asp Thr Val Gly Phe Ile Ser Lys Leu Pro His Asn Leu	
260 265 270	
gtt gaa tca ttc aag gca acc ttg caa gaa aca cgc gac gct gat ctt	864
Val Glu Ser Phe Lys Ala Thr Leu Gln Glu Thr Arg Asp Ala Asp Leu	
275 280 285	
ttg att aac gtg gtt gat gca tcc gac cct aac atg gtc cag atg atc	912
Leu Ile Asn Val Val Asp Ala Ser Asp Pro Asn Met Val Gln Met Ile	
290 295 300	

```

cgc act aca cag aac gtg cta gac gag atc ggc gtt aaa ggc att cca 960
Arg Thr Thr Gln Asn Val Leu Asp Glu Ile Gly Val Lys Gly Ile Pro
305 310 315 320

atg atc acc gcc tac aac aag gcc gac aag acc gac cgc aat tat cca 1008
Met Ile Thr Ala Tyr Asn Lys Ala Asp Lys Thr Asp Arg Asn Tyr Pro
325 330 335

cag atc gaa ggt agc gac att ctt tat tca gca act gat ccc aag tca 1056
Gln Ile Glu Gly Ser Asp Ile Leu Tyr Ser Ala Thr Asp Pro Lys Ser
340 345 350

att aag ctc ttg gct gat ctc atc act aag cgt gtc ttc tct gat tat 1104
Ile Lys Leu Leu Ala Asp Leu Ile Thr Lys Arg Val Phe Ser Asp Tyr
355 360 365

ggc aag ttc aac ctc aca ctt cct ttg agt gca ggt aag gaa ctg gcc 1152
Gly Lys Phe Asn Leu Thr Leu Pro Leu Ser Ala Gly Lys Glu Leu Ala
370 375 380

tac tta cac gag aat gct cag atc ttg agt gaa aac tat gaa gac gac 1200
Tyr Leu His Glu Asn Ala Gln Ile Leu Ser Glu Asn Tyr Glu Asp Asp
385 390 395 400

ggc gtc cac atc gaa gcc aac att gca ccg gat gat caa ggt cgt ttt 1248
Gly Val His Ile Glu Ala Asn Ile Ala Pro Asp Asp Gln Gly Arg Phe
405 410 415

aaa gaa tat cta gtc 1263
Lys Glu Tyr Leu Val
420

```

<210> 184

<211> 421

<212> PRT

<213> Lactobacillus acidophilus

<400> 184

```

Met Ile Asp Asn Gln Pro Lys Lys Thr Lys Ala Tyr Ile Ala Gly Val
1 5 10 15
Asn Leu Lys Asp Pro Asn Phe Asp Tyr Tyr Met Thr Glu Leu Ala Asn
20 25 30
Leu Thr Glu Ala Asn Asn Met Glu Val Val Gly Gln Ser Ser Gln Asn
35 40 45
Ala Glu Ser Ile Val Ala Gly Thr Tyr Phe Gly Val Gly Lys Ile Asn
50 55 60
Glu Ile Lys Ser Met Ala Gln Gly Leu Lys Ala Lys Val Leu Val Leu
65 70 75 80
Asn Asp Glu Leu Thr Pro Val Gln Ile Arg Asn Leu Glu Lys Leu Thr
85 90 95
Lys Met Arg Val Ile Asp Arg Thr Glu Leu Ile Leu Glu Ile Phe Ala
100 105 110
Ser Arg Ala Arg Thr Lys Gln Ala Lys Leu Gln Val Gln Leu Ala Arg
115 120 125
Leu Gln Tyr Glu Leu Pro Arg Leu His Pro Ser Glu Asn Asn Leu Asp
130 135 140

```

Gln Gln Arg Gly Gly Gly Phe Ser Asn Arg Gly Ala Gly Glu Ser Lys
 145 150 155 160
 Leu Glu Leu Asn Arg Arg Thr Ile Gly Lys Gln Ile Ser Ala Ile Lys
 165 170 175
 Lys Glu Leu Lys Ala Val Ala Ser Gln Glu Glu Ile Lys Ser Ala Arg
 180 185 190
 Arg Asn Gln Ser Arg Ile Pro Lys Val Ala Leu Val Gly Tyr Thr Asn
 195 200 205
 Ala Gly Lys Ser Thr Thr Met Asn Gly Leu Leu Arg Glu Phe Ser Lys
 210 215 220
 Glu Gly Ser Asp Lys Glu Val Phe Val Lys Asn Met Leu Phe Ala Thr
 225 230 235 240
 Leu Asp Thr Ser Val Arg Arg Ile Asp Leu Lys Asp Asn Phe Ser Phe
 245 250 255
 Ile Leu Ser Asp Thr Val Gly Phe Ile Ser Lys Leu Pro His Asn Leu
 260 265 270
 Val Glu Ser Phe Lys Ala Thr Leu Gln Glu Thr Arg Asp Ala Asp Leu
 275 280 285
 Leu Ile Asn Val Val Asp Ala Ser Asp Pro Asn Met Val Gln Met Ile
 290 295 300
 Arg Thr Thr Gln Asn Val Leu Asp Glu Ile Gly Val Lys Gly Ile Pro
 305 310 315 320
 Met Ile Thr Ala Tyr Asn Lys Ala Asp Lys Thr Asp Arg Asn Tyr Pro
 325 330 335
 Gln Ile Glu Gly Ser Asp Ile Leu Tyr Ser Ala Thr Asp Pro Lys Ser
 340 345 350
 Ile Lys Leu Leu Ala Asp Leu Ile Thr Lys Arg Val Phe Ser Asp Tyr
 355 360 365
 Gly Lys Phe Asn Leu Thr Leu Pro Leu Ser Ala Gly Lys Glu Leu Ala
 370 375 380
 Tyr Leu His Glu Asn Ala Gln Ile Leu Ser Glu Asn Tyr Glu Asp Asp
 385 390 395 400
 Gly Val His Ile Glu Ala Asn Ile Ala Pro Asp Asp Gln Gly Arg Phe
 405 410 415
 Lys Glu Tyr Leu Val
 420

<210> 185
 <211> 1008
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1739

<220>
 <221> CDS
 <222> (1)...(1008)

<400> 185
 atg aaa aaa cat aat ttg ctg gta atc gct gtt gcg tta ttc ggg tgt 48
 Met Lys Lys His Asn Leu Leu Val Ile Ala Val Ala Leu Phe Gly Cys
 1 5 10 15

gtt gca ctt agc agt gaa cct gtt caa gca gcc aaa tat tct aaa tca	96
Val Ala Leu Ser Ser Glu Pro Val Gln Ala Ala Lys Tyr Ser Lys Ser	
20 25 30	
gaa gct aag aaa gtt aag tat ttc cag cgc gaa tat cgc ggc ttg agt	144
Glu Ala Lys Lys Val Lys Tyr Phe Gln Arg Glu Tyr Arg Gly Leu Ser	
35 40 45	
aag acc aaa tac aac cgc aat acc att tac cag caa gca ccc aac ttt	192
Lys Thr Lys Tyr Asn Arg Asn Thr Ile Tyr Gln Gln Ala Pro Asn Phe	
50 55 60	
gcc gat cct ttt tca cca ggg acg tta act cct aca tat att cct gat	240
Ala Asp Pro Phe Ser Pro Gly Thr Leu Thr Pro Thr Tyr Ile Pro Asp	
65 70 75 80	
acg atg ggc tac att aat tac tat cgt gaa tta gca gga ctg ccg gct	288
Thr Met Gly Tyr Ile Asn Tyr Tyr Arg Glu Leu Ala Gly Leu Pro Ala	
85 90 95	
gaa gct aat cat aac gaa gac aat caa agc gcc caa atc ggg gca gta	336
Glu Ala Asn His Asn Glu Asp Asn Gln Ser Ala Gln Ile Gly Ala Val	
100 105 110	
gcg tta gct tcc gtt aac gcg gcc gcc aac ttg aag gcc cat ggc cta	384
Ala Leu Ala Ser Val Asn Ala Ala Ala Asn Leu Lys Ala His Gly Leu	
115 120 125	
ctt gac tat ctt cgc cct agt tat att agt gaa tct gat tgg gat atc	432
Leu Asp Tyr Leu Arg Pro Ser Tyr Ile Ser Glu Ser Asp Trp Asp Ile	
130 135 140	
gct gaa agt tct act tta ggt aat atc aac ttc ttg gat aac gcc ggt	480
Ala Glu Ser Ser Thr Leu Gly Asn Ile Asn Phe Leu Asp Asn Ala Gly	
145 150 155 160	
agt acc tca gct ggt gag ata gta acg gat ctg att cgc gag gat aat	528
Ser Thr Ser Ala Gly Glu Ile Val Thr Asp Leu Ile Arg Glu Asp Asn	
165 170 175	
aat atc gca ggt act ggg aac atc gcc cac cgg gcc atg atc tta tct	576
Asn Ile Ala Gly Thr Gly Asn Ile Gly His Arg Ala Met Ile Leu Ser	
180 185 190	
act cgc gca acg cgg atg gga atc ggt gcg gca tac ggc tta agc aac	624
Thr Arg Ala Thr Arg Met Gly Ile Gly Ala Ala Tyr Gly Leu Ser Asn	
195 200 205	
gat atg ctc tat tct gtg gaa tac gga cta ttt gcc gat gac atc ttg	672
Asp Met Leu Tyr Ser Val Glu Tyr Gly Leu Phe Ala Asp Asp Ile Leu	
210 215 220	
cgt acg ccc gtg aag aag caa gtt gtt tat ccc gct acc acg gtc ttt	720
Arg Thr Pro Val Lys Lys Gln Val Val Tyr Pro Ala Thr Thr Val Phe	
225 230 235 240	

```

ccc tat gaa tta att ggc agg aat act cca tgg tcg tat gca aca acg   768
Pro Tyr Glu Leu Ile Gly Arg Asn Thr Pro Trp Ser Tyr Ala Thr Thr
                245                250                255

aag aag atc tct ggt aca ccg aag att tat att act gat tta tcc acc   816
Lys Lys Ile Ser Gly Thr Pro Lys Ile Tyr Ile Thr Asp Leu Ser Thr
                260                265                270

aaa aag aag aaa cgt tat cgc gca aca caa gta cgc aat ttt aac acg   864
Lys Lys Lys Lys Arg Tyr Arg Ala Thr Gln Val Arg Asn Phe Asn Thr
                275                280                285

atg ttt tac ggt gaa ggt tat acc aca acg atc acg tat cgc cca ggt   912
Met Phe Tyr Gly Glu Gly Tyr Thr Thr Thr Ile Thr Tyr Arg Pro Gly
                290                295                300

aag att aag tta gtt aat aca cat aag tac aag gta cag att ggc aag   960
Lys Ile Lys Leu Val Asn Thr His Lys Tyr Lys Val Gln Ile Gly Lys
305                310                315                320

cat tat aca tac tca ttt aga ttt ttt aga cag aac gga aaa tta aag   1008
His Tyr Thr Tyr Ser Phe Arg Phe Phe Arg Gln Asn Gly Lys Leu Lys
                325                330                335

```

<210> 186

<211> 336

<212> PRT

<213> Lactobacillus acidophilus

<400> 186

```

Met Lys Lys His Asn Leu Leu Val Ile Ala Val Ala Leu Phe Gly Cys
 1          5          10          15
Val Ala Leu Ser Glu Pro Val Gln Ala Ala Lys Tyr Ser Lys Ser
 20          25          30
Glu Ala Lys Lys Val Lys Tyr Phe Gln Arg Glu Tyr Arg Gly Leu Ser
 35          40          45
Lys Thr Lys Tyr Asn Arg Asn Thr Ile Tyr Gln Gln Ala Pro Asn Phe
 50          55          60
Ala Asp Pro Phe Ser Pro Gly Thr Leu Thr Pro Thr Tyr Ile Pro Asp
 65          70          75          80
Thr Met Gly Tyr Ile Asn Tyr Tyr Arg Glu Leu Ala Gly Leu Pro Ala
 85          90          95
Glu Ala Asn His Asn Glu Asp Asn Gln Ser Ala Gln Ile Gly Ala Val
100          105          110
Ala Leu Ala Ser Val Asn Ala Ala Asn Leu Lys Ala His Gly Leu
115          120          125
Leu Asp Tyr Leu Arg Pro Ser Tyr Ile Ser Glu Ser Asp Trp Asp Ile
130          135          140
Ala Glu Ser Ser Thr Leu Gly Asn Ile Asn Phe Leu Asp Asn Ala Gly
145          150          155          160
Ser Thr Ser Ala Gly Glu Ile Val Thr Asp Leu Ile Arg Glu Asp Asn
165          170          175
Asn Ile Ala Gly Thr Gly Asn Ile Gly His Arg Ala Met Ile Leu Ser
180          185          190
Thr Arg Ala Thr Arg Met Gly Ile Gly Ala Ala Tyr Gly Leu Ser Asn

```

```
<210> 187
<211> 4146
<212> DNA
<213> Lactobacillus acidophilus
```

```
<220>
<221> misc_feature
<222> (0)...(0)
<223> ORF 1740
```

```
<220>
<221> CDS
<222> (1) ... (4146)
```

<400> 187																	
atg	agg	aga	cga	tgc	gaa	atg	tta	tct	aaa	aac	aac	ttt	aat	gag	aaa	48	
Met	Arg	Arg	Arg	Cys	Glu	Met	Leu	Ser	Lys	Asn	Asn	Phe	Asn	Glu	Lys		
1				5					10					15			
ctt	atg	caa	atg	aac	aat	caa	aaa	gct	cat	ttt	tca	att	cgt	aaa	tta	96	
Leu	Met	Gln	Met	Asn	Asn	Gln	Lys	Ala	His	Phe	Ser	Ile	Arg	Lys	Leu		
			20					25					30				
act	att	ggg	gct	gct	tca	gta	tta	ata	ggg	atc	act	ttt	atg	gga	att	144	
Thr	Ile	Gly	Ala	Ala	Ser	Val	Leu	Ile	Gly	Ile	Thr	Phe	Met	Gly	Ile		
		35					40					45					
aac	ggg	caa	aca	gta	aac	gct	gat	gaa	atg	act	ggg	aat	act	caa	cct	192	
Asn	Gly	Gln	Thr	Val	Asn	Ala	Asp	Glu	Met	Thr	Gly	Asn	Thr	Gln	Pro		
	50					55					60						
gaa	gca	atg	caa	gtt	tca	acg	gat	aaa	tct	act	gat	gcc	act	acc	act	240	
Glu	Ala	Met	Gln	Val	Ser	Thr	Asp	Lys	Ser	Thr	Asp	Ala	Thr	Thr	Thr		
65					70					75					80		
caa	cag	aat	gat	tca	gat	agt	agt	gct	caa	aag	aat	gct	gct	caa	aca	288	
Gln	Gln	Asn	Asp	Ser	Asp	Ser	Ser	Ala	Gln	Lys	Asn	Ala	Ala	Gln	Thr		

85										90					95									
gta	gaa	gtt	cct	caa	aat	agt	aaa	caa	gat	aat	aca	gga	gaa	act	tct	336								
Val	Glu	Val	Pro	Gln	Asn	Ser	Lys	Gln	Asp	Asn	Thr	Gly	Glu	Thr	Ser									
100										105					110									
caa	tca	act	aca	gat	aaa	aaa	gat	aca	caa	gtt	caa	aaa	aca	gaa	tct	384								
Gln	Ser	Thr	Thr	Asp	Lys	Lys	Asp	Thr	Gln	Val	Gln	Lys	Thr	Glu	Ser									
115										120					125									
agt	gaa	aca	aag	gct	gat	act	gct	caa	agt	caa	gta	ccc	cca	gct	gcc	432								
Ser	Glu	Thr	Lys	Ala	Asp	Thr	Ala	Gln	Ser	Gln	Val	Pro	Pro	Ala	Ala									
130										135					140									
aac	caa	act	caa	aaa	tca	gct	gac	caa	aat	gta	gaa	aat	aca	caa	tca	480								
Asn	Gln	Thr	Gln	Lys	Ser	Ala	Asp	Gln	Asn	Val	Glu	Asn	Thr	Gln	Ser									
145										150					155					160				
cca	gtt	gct	agc	aat	act	act	caa	cct	aaa	aca	caa	aat	gac	agc	aaa	528								
Pro	Val	Ala	Ser	Asn	Thr	Thr	Gln	Pro	Lys	Thr	Gln	Asn	Asp	Ser	Lys									
165										170					175									
tat	aac	gtt	gct	gac	tgg	ggg	ggg	agt	ctc	aat	gat	gaa	act	cac	gag	576								
Tyr	Asn	Val	Ala	Asp	Trp	Gly	Gly	Ser	Leu	Asn	Asp	Glu	Thr	His	Glu									
180										185					190									
tac	acc	tta	aat	aaa	tac	aat	ggg	agt	gat	aaa	gaa	aat	atc	tac	att	624								
Tyr	Thr	Leu	Asn	Lys	Tyr	Asn	Gly	Ser	Asp	Lys	Glu	Asn	Ile	Tyr	Ile									
195										200					205									
cca	aat	aca	gaa	gat	ttt	atc	aag	gct	gga	aag	att	aca	gat	atc	gac	672								
Pro	Asn	Thr	Glu	Asp	Phe	Ile	Lys	Ala	Gly	Lys	Ile	Thr	Asp	Ile	Asp									
210										215					220									
aaa	gtt	ttc	att	act	aag	gat	tta	att	caa	aac	att	act	aaa	aat	ggc	720								
Lys	Val	Phe	Ile	Thr	Lys	Asp	Leu	Ile	Gln	Asn	Ile	Thr	Lys	Asn	Gly									
225										230					235					240				
gca	acc	agt	att	gtg	att	gat	gat	caa	ggc	agt	gaa	gat	aaa	aat	aaa	768								
Ala	Thr	Ser	Ile	Val	Ile	Asp	Asp	Gln	Gly	Ser	Glu	Asp	Lys	Asn	Lys									
245										250					255									
gtc	tat	gct	aaa	gga	gac	tgg	agc	aat	gct	ttt	gct	ggc	tct	acc	aaa	816								
Val	Tyr	Ala	Lys	Gly	Asp	Trp	Ser	Asn	Ala	Phe	Ala	Gly	Ser	Thr	Lys									
260										265					270									
tta	aag	agt	gtc	gat	tta	agt	cat	tta	gat	aca	agc	caa	gtt	act	agt	864								
Leu	Lys	Ser	Val	Asp	Leu	Ser	His	Leu	Asp	Thr	Ser	Gln	Val	Thr	Ser									
275										280					285									
atg	gct	ggg	gca	ttt	aat	ggg	gat	act	ggc	tta	aat	gat	gct	aac	tta	912								
Met	Ala	Gly	Ala	Phe	Asn	Gly	Asp	Thr	Gly	Leu	Asn	Asp	Ala	Asn	Leu									
290										295					300									
agt	ggg	tgg	aat	att	caa	aat	atg	act	aac	ttg	tcc	tca	tta	ttt	tat	960								
Ser	Gly	Trp	Asn	Ile	Gln	Asn	Met	Thr	Asn	Leu	Ser	Ser	Leu	Phe	Tyr									
305										310					315					320				

ggt gca aat aat ttg tac aat gtg gac atg agt ggt tgg aat ttt att	1008
Gly Ala Asn Asn Leu Tyr Asn Val Asp Met Ser Gly Trp Asn Phe Ile	
325 330 335	
aac aac cct aat aca aat agc atg ttt tca tat gca gac tac aat tta	1056
Asn Asn Pro Asn Thr Asn Ser Met Phe Ser Tyr Ala Asp Tyr Asn Leu	
340 345 350	
aag agc gta aat ctt aaa aat gct aaa aat gtt act gat gat ata tta	1104
Lys Ser Val Asn Leu Lys Asn Ala Lys Asn Val Thr Asp Asp Ile Leu	
355 360 365	
aga att tac gct aga gca att aag aac tct aac gca acc act gct gac	1152
Arg Ile Tyr Ala Arg Ala Ile Lys Asn Ser Asn Ala Thr Thr Ala Asp	
370 375 380	
cta agt gat atc aat tta tca cca aat gtt act agt tta cat ggc ttg	1200
Leu Ser Asp Ile Asn Leu Ser Pro Asn Val Thr Ser Leu His Gly Leu	
385 390 395 400	
ttt tct aac atg cct gac ctt aag aac gtt aac tta agc ggt ctt gat	1248
Phe Ser Asn Met Pro Asp Leu Lys Asn Val Asn Leu Ser Gly Leu Asp	
405 410 415	
att agt cat att aca gat atg ggt ggc atg ttt tct gga gat agt aat	1296
Ile Ser His Ile Thr Asp Met Gly Gly Met Phe Ser Gly Asp Ser Asn	
420 425 430	
cta gaa agt tta gat tta agc ggc ttg gat tta agt aaa gta acc aac	1344
Leu Glu Ser Leu Asp Leu Ser Gly Leu Asp Leu Ser Lys Val Thr Asn	
435 440 445	
acc aat aat atg ttt gac tgg gtt ggt gga aag ata aag agt gta aac	1392
Thr Asn Asn Met Phe Asp Trp Val Gly Gly Lys Ile Lys Ser Val Asn	
450 455 460	
att act aac act aag agt att cca cgt agc atc tta gat ata tat cta	1440
Ile Thr Asn Thr Lys Ser Ile Pro Arg Ser Ile Leu Asp Ile Tyr Leu	
465 470 475 480	
aag gca ctc agc aat aca ggt aca acg act gtt gat ctg agc ggt att	1488
Lys Ala Leu Ser Asn Thr Gly Thr Thr Thr Val Asp Leu Ser Gly Ile	
485 490 495	
aat ctt tca cca aat gtt act agc tta cat ggt tta ttt gct aac atg	1536
Asn Leu Ser Pro Asn Val Thr Ser Leu His Gly Leu Phe Ala Asn Met	
500 505 510	
cct aac ctt ggg agc gct aac tta agc ggt ctt gat att agc cat att	1584
Pro Asn Leu Gly Ser Ala Asn Leu Ser Gly Leu Asp Ile Ser His Ile	
515 520 525	
aca gat atg ggc ggt atg ttc ttt aat gat act tca ttg aag agt gtt	1632
Thr Asp Met Gly Gly Met Phe Phe Asn Asp Thr Ser Leu Lys Ser Val	
530 535 540	

aac tta tct ggt ctt aac tta gaa aaa gta aaa gat ctt agc aca atg Asn Leu Ser Gly Leu Asn Leu Glu Lys Val Lys Asp Leu Ser Thr Met 545 550 555 560	1680
ttt tac ggt gca aat aac ttg gaa aat gtt gat ttt agt aat acc aag Phe Tyr Gly Ala Asn Asn Leu Glu Asn Val Asp Phe Ser Asn Thr Lys 565 570 575	1728
ttt gca cca gat gct aat aca aac gta atg ttt gct ttt gca gat act Phe Ala Pro Asp Ala Asn Thr Asn Val Met Phe Ala Phe Ala Asp Thr 580 585 590	1776
aaa tta caa agc gta aat att aat ggt act aaa aat att acc cgt gaa Lys Leu Gln Ser Val Asn Ile Asn Gly Thr Lys Asn Ile Thr Arg Glu 595 600 605	1824
gtt tta gat gcc gtt att aga gca gct aag aat tcc aac gca act act Val Leu Asp Ala Val Ile Arg Ala Ala Lys Asn Ser Asn Ala Thr Thr 610 615 620	1872
ctt gat tta agc ggt gtt agc ttt tca cca agt atc acc agt ttt aat Leu Asp Leu Ser Gly Val Ser Phe Ser Pro Ser Ile Thr Ser Phe Asn 625 630 635 640	1920
aat cta ttc tct aat atg ccg aat att gaa agt ata gac cta act ggc Asn Leu Phe Ser Asn Met Pro Asn Ile Glu Ser Ile Asp Leu Thr Gly 645 650 655	1968
tgg gac act agt cat att acc gat atg agt tac atg ttc ttt aat gat Trp Asp Thr Ser His Ile Thr Asp Met Ser Tyr Met Phe Phe Asn Asp 660 665 670	2016
cca aag ctt aaa att att aaa gga ctt gaa gat ttc aat acc tca aat Pro Lys Leu Lys Ile Ile Lys Gly Leu Glu Asp Phe Asn Thr Ser Asn 675 680 685	2064
gta act aat atg gca tac atg ttt gct gct ttt aac aat cca aca aca Val Thr Asn Met Ala Tyr Met Phe Ala Ala Phe Asn Asn Pro Thr Thr 690 695 700	2112
gat aat tat gat cca aaa ggt ctt gag agt tta gga cat ttg act aaa Asp Asn Tyr Asp Pro Lys Gly Leu Glu Ser Leu Gly His Leu Thr Lys 705 710 715 720	2160
ctt gat tta agc aat tgg gat act tcc aat gta act aat atg cta tat Leu Asp Leu Ser Asn Trp Asp Thr Ser Asn Val Thr Asn Met Leu Tyr 725 730 735	2208
atg ttt gcc gga cag act aat tta act agt ttg ggt gac ctt tct aag Met Phe Ala Gly Gln Thr Asn Leu Thr Ser Leu Gly Asp Leu Ser Lys 740 745 750	2256
tgg aat act agc aag gta act aat atg gcc tac atg ttc tat gat tta Trp Asn Thr Ser Lys Val Thr Asn Met Ala Tyr Met Phe Tyr Asp Leu 755 760 765	2304
aaa aat ata gat gac ggt aaa tta gat cta acc ggt tgg gat act tcc	2352

Lys	Asn	Ile	Asp	Asp	Gly	Lys	Leu	Asp	Leu	Thr	Gly	Trp	Asp	Thr	Ser		
770						775					780						
aat	gta	act	gac	atg	agc	tac	atg	ttc	ttt	aac	atg	ttc	tta	caa	aaa	2400	
Asn	Val	Thr	Asp	Met	Ser	Tyr	Met	Phe	Phe	Asn	Met	Phe	Leu	Gln	Lys		
785					790					795					800		
gat	tta	agc	ttc	gtt	aat	gat	tgg	aac	act	ggt	aaa	gta	act	gat	atg	2448	
Asp	Leu	Ser	Phe	Val	Asn	Asp	Trp	Asn	Thr	Gly	Lys	Val	Thr	Asp	Met		
				805					810					815			
agt	tac	atg	ttt	gcc	aat	gac	aag	aac	ctt	gaa	aaa	tta	gat	ctt	tct	2496	
Ser	Tyr	Met	Phe	Ala	Asn	Asp	Lys	Asn	Leu	Glu	Lys	Leu	Asp	Leu	Ser		
			820					825					830				
aaa	tgg	gat	gta	agt	agt	gtt	ggg	tta	aag	cat	act	gaa	caa	aac	tac	2544	
Lys	Trp	Asp	Val	Ser	Ser	Val	Gly	Leu	Lys	His	Thr	Glu	Gln	Asn	Tyr		
	835						840					845					
agt	ctg	gca	atg	atg	ttt	gcg	ggt	gat	act	tca	tta	act	act	gtt	ggt	2592	
Ser	Leu	Ala	Met	Met	Phe	Ala	Gly	Asp	Thr	Ser	Leu	Thr	Thr	Val	Gly		
	850					855					860						
gat	att	tct	cat	tgg	aat	acc	aag	aat	gtt	cat	gat	act	cgt	caa	atg	2640	
Asp	Ile	Ser	His	Trp	Asn	Thr	Lys	Asn	Val	His	Asp	Thr	Arg	Gln	Met		
865					870					875				880			
ttc	tat	aat	act	cct	aag	tta	act	aac	att	gac	ttg	agt	ggc	tgg	aat	2688	
Phe	Tyr	Asn	Thr	Pro	Lys	Leu	Thr	Asn	Ile	Asp	Leu	Ser	Gly	Trp	Asn		
				885					890					895			
aca	ggt	aaa	tta	caa	att	gct	gaa	ggg	atg	ttc	aac	tcc	tct	ggc	gct	2736	
Thr	Gly	Lys	Leu	Gln	Ile	Ala	Glu	Gly	Met	Phe	Asn	Ser	Ser	Gly	Ala		
			900					905					910				
aag	caa	att	aac	tta	gat	aat	tgg	gat	tta	agt	aat	att	aaa	cga	att	2784	
Lys	Gln	Ile	Asn	Leu	Asp	Asn	Trp	Asp	Leu	Ser	Asn	Ile	Lys	Arg	Ile		
	915						920					925					
act	cct	gct	ggt	tat	gtt	gaa	ggt	aag	gct	ggt	gta	gga	gtg	ctt	cgc	2832	
Thr	Pro	Ala	Gly	Tyr	Val	Glu	Gly	Lys	Ala	Gly	Val	Gly	Val	Leu	Arg		
	930					935					940						
ggc	gtt	gag	aat	atg	ttt	aag	aac	tta	acc	aat	cca	gct	gtt	atc	tca	2880	
Gly	Val	Glu	Asn	Met	Phe	Lys	Asn	Leu	Thr	Asn	Pro	Ala	Val	Ile	Ser		
945					950					955				960			
atg	aat	aag	gtc	atc	tta	cca	gat	gct	aga	aat	gct	ttt	gaa	att	aat	2928	
Met	Asn	Lys	Val	Ile	Leu	Pro	Asp	Ala	Arg	Asn	Ala	Phe	Glu	Ile	Asn		
				965					970					975			
gac	ttt	gaa	gga	aat	aaa	gca	att	gta	gtg	att	gct	aat	ggt	caa	aac	2976	
Asp	Phe	Glu	Gly	Asn	Lys	Ala	Ile	Val	Val	Ile	Ala	Asn	Gly	Gln	Asn		
			980					985					990				
ggt	gaa	gct	ctt	caa	gat	ttg	ctt	aag	att	aat	aat	caa	act	tgg	act	3024	
Gly	Glu	Ala	Leu	Gln	Asp	Leu	Leu	Lys	Ile	Asn	Asn	Gln	Thr	Trp	Thr		

995	1000	1005	
gat aaa tct gga aac aat gta act gga cgt caa aat tca gat tat gta Asp Lys Ser Gly Asn Asn Val Thr Gly Arg Gln Asn Ser Asp Tyr Val 1010 1015 1020			3072
act tac gtt aga gct gat gat aat tct aac caa att ggc caa cgc gga Thr Tyr Val Arg Ala Asp Asp Asn Ser Asn Gln Ile Gly Gln Arg Gly 1025 1030 1035 1040			3120
ttg aat ttc atc ttt act aac tta gat gac ttg cac caa tac ttc aat Leu Asn Phe Ile Phe Thr Asn Leu Asp Asp Leu His Gln Tyr Phe Asn 1045 1050 1055			3168
caa gta act aat gca gat aat gtt aaa aac gat att ggc gaa ttg agt Gln Val Thr Asn Ala Asp Asn Val Lys Asn Asp Ile Gly Glu Leu Ser 1060 1065 1070			3216
cat gat tgg gat gct cag caa gat act gat aat aat att gtt aaa atc His Asp Trp Asp Ala Gln Gln Asp Thr Asp Asn Asn Ile Val Lys Ile 1075 1080 1085			3264
aca ttg cgt ttg tct ccg gct agt tca tat gat cca tat agt gaa aat Thr Leu Arg Leu Ser Pro Ala Ser Ser Tyr Asp Pro Tyr Ser Glu Asn 1090 1095 1100			3312
atc cat gct gaa aaa gat ggc aat att tta gca gac tta atg acc agc Ile His Ala Glu Lys Asp Gly Asn Ile Leu Ala Asp Leu Met Thr Ser 1105 1110 1115 1120			3360
aaa tat caa tta cat att gtt gct cca act aac act act gaa act aag Lys Tyr Gln Leu His Ile Val Ala Pro Thr Asn Thr Thr Glu Thr Lys 1125 1130 1135			3408
aag cca acc aga aca att att att gaa aat cct gat ggc acc aca agt Lys Pro Thr Arg Thr Ile Ile Ile Glu Asn Pro Asp Gly Thr Thr Ser 1140 1145 1150			3456
act aaa gag caa act gta gag ttt aag cgt gaa gtc act aag cat gtc Thr Lys Glu Gln Thr Val Glu Phe Lys Arg Glu Val Thr Lys His Val 1155 1160 1165			3504
gat ggt act gaa gag gct acg tca tgg act cca aca agt ggt gaa tgg Asp Gly Thr Glu Glu Ala Thr Ser Trp Thr Pro Thr Ser Gly Glu Trp 1170 1175 1180			3552
act aaa ttt gat gtg cca caa att gct gga tat gat tct tac gta gat Thr Lys Phe Asp Val Pro Gln Ile Ala Gly Tyr Asp Ser Tyr Val Asp 1185 1190 1195 1200			3600
gga act cag agc aag tct gtt gct tca gaa cct gtt aat aaa gat act Gly Thr Gln Ser Lys Ser Val Ala Ser Glu Pro Val Asn Lys Asp Thr 1205 1210 1215			3648
gag aat gta act gta gta att act tat aag tca aat gcg gta aat cct Glu Asn Val Thr Val Val Ile Thr Tyr Lys Ser Asn Ala Val Asn Pro 1220 1225 1230			3696

gaa cca atc att cca gat cca gta aag cca gaa gtt gat ccg gat aaa 3744
 Glu Pro Ile Ile Pro Asp Pro Val Lys Pro Glu Val Asp Pro Asp Lys
 1235 1240 1245
 aaa gat cca caa gaa cca aag aca gat cct gta act cca aca cca gat 3792
 Lys Asp Pro Gln Glu Pro Lys Thr Asp Pro Val Thr Pro Thr Pro Asp
 1250 1255 1260
 gaa cca gaa aat cca aag cct gaa aag aaa cca agt aat cca gac aag 3840
 Glu Pro Glu Asn Pro Lys Pro Glu Lys Lys Pro Ser Asn Pro Asp Lys
 1265 1270 1275 1280
 cgt aag gat gat aat tct aaa gtt gtt aag cca cat ggt gaa aat aaa 3888
 Arg Lys Asp Asp Asn Ser Lys Val Val Lys Pro His Gly Glu Asn Lys
 1285 1290 1295
 gca gct aag aag aac cat agt agt gtt gaa cac aaa aag aca ggt act 3936
 Ala Ala Lys Lys Asn His Ser Ser Val Glu His Lys Lys Thr Gly Thr
 1300 1305 1310
 cac act att aag ctt tct cac aga gtt gca cca aag ggc act caa gca 3984
 His Thr Ile Lys Leu Ser His Arg Val Ala Pro Lys Gly Thr Gln Ala
 1315 1320 1325
 act aat ggt tca aag aaa tct act tca act gta aat aaa gca gct gac 4032
 Thr Asn Gly Ser Lys Lys Ser Thr Ser Thr Val Asn Lys Ala Ala Asp
 1330 1335 1340
 aac aat aag aat act ttg cca caa act ggt gaa aag aag agc aat gcc 4080
 Asn Asn Lys Asn Thr Leu Pro Gln Thr Gly Glu Lys Lys Ser Asn Ala
 1345 1350 1355 1360
 ggc tta atc ggc tta gcc tta att gca ctt gca agt tta gga tta att 4128
 Gly Leu Ile Gly Leu Ala Leu Ile Ala Leu Ala Ser Leu Gly Leu Ile
 1365 1370 1375
 gat cgt aaa cgt cgt gat 4146
 Asp Arg Lys Arg Arg Asp
 1380

<210> 188

<211> 1382

<212> PRT

<213> Lactobacillus acidophilus

<400> 188

Met Arg Arg Arg Cys Glu Met Leu Ser Lys Asn Asn Phe Asn Glu Lys
 1 5 10 15
 Leu Met Gln Met Asn Asn Gln Lys Ala His Phe Ser Ile Arg Lys Leu
 20 25 30
 Thr Ile Gly Ala Ala Ser Val Leu Ile Gly Ile Thr Phe Met Gly Ile
 35 40 45
 Asn Gly Gln Thr Val Asn Ala Asp Glu Met Thr Gly Asn Thr Gln Pro
 50 55 60
 Glu Ala Met Gln Val Ser Thr Asp Lys Ser Thr Asp Ala Thr Thr Thr

65					70					75					80
Gln	Gln	Asn	Asp	Ser	Asp	Ser	Ser	Ala	Gln	Lys	Asn	Ala	Ala	Gln	Thr
				85					90					95	
Val	Glu	Val	Pro	Gln	Asn	Ser	Lys	Gln	Asp	Asn	Thr	Gly	Glu	Thr	Ser
			100					105						110	
Gln	Ser	Thr	Thr	Asp	Lys	Lys	Asp	Thr	Gln	Val	Gln	Lys	Thr	Glu	Ser
			115				120					125			
Ser	Glu	Thr	Lys	Ala	Asp	Thr	Ala	Gln	Ser	Gln	Val	Pro	Pro	Ala	Ala
			130				135					140			
Asn	Gln	Thr	Gln	Lys	Ser	Ala	Asp	Gln	Asn	Val	Glu	Asn	Thr	Gln	Ser
					150					155					160
Pro	Val	Ala	Ser	Asn	Thr	Thr	Gln	Pro	Lys	Thr	Gln	Asn	Asp	Ser	Lys
				165					170					175	
Tyr	Asn	Val	Ala	Asp	Trp	Gly	Gly	Ser	Leu	Asn	Asp	Glu	Thr	His	Glu
			180					185					190		
Tyr	Thr	Leu	Asn	Lys	Tyr	Asn	Gly	Ser	Asp	Lys	Glu	Asn	Ile	Tyr	Ile
			195				200						205		
Pro	Asn	Thr	Glu	Asp	Phe	Ile	Lys	Ala	Gly	Lys	Ile	Thr	Asp	Ile	Asp
			210			215					220				
Lys	Val	Phe	Ile	Thr	Lys	Asp	Leu	Ile	Gln	Asn	Ile	Thr	Lys	Asn	Gly
				225		230				235					240
Ala	Thr	Ser	Ile	Val	Ile	Asp	Asp	Gln	Gly	Ser	Glu	Asp	Lys	Asn	Lys
				245					250					255	
Val	Tyr	Ala	Lys	Gly	Asp	Trp	Ser	Asn	Ala	Phe	Ala	Gly	Ser	Thr	Lys
			260					265					270		
Leu	Lys	Ser	Val	Asp	Leu	Ser	His	Leu	Asp	Thr	Ser	Gln	Val	Thr	Ser
			275				280					285			
Met	Ala	Gly	Ala	Phe	Asn	Gly	Asp	Thr	Gly	Leu	Asn	Asp	Ala	Asn	Leu
			290			295					300				
Ser	Gly	Trp	Asn	Ile	Gln	Asn	Met	Thr	Asn	Leu	Ser	Ser	Leu	Phe	Tyr
				305		310				315					320
Gly	Ala	Asn	Asn	Leu	Tyr	Asn	Val	Asp	Met	Ser	Gly	Trp	Asn	Phe	Ile
				325					330					335	
Asn	Asn	Pro	Asn	Thr	Asn	Ser	Met	Phe	Ser	Tyr	Ala	Asp	Tyr	Asn	Leu
			340					345					350		
Lys	Ser	Val	Asn	Leu	Lys	Asn	Ala	Lys	Asn	Val	Thr	Asp	Asp	Ile	Leu
			355				360					365			
Arg	Ile	Tyr	Ala	Arg	Ala	Ile	Lys	Asn	Ser	Asn	Ala	Thr	Thr	Ala	Asp
			370			375					380				
Leu	Ser	Asp	Ile	Asn	Leu	Ser	Pro	Asn	Val	Thr	Ser	Leu	His	Gly	Leu
				385		390				395					400
Phe	Ser	Asn	Met	Pro	Asp	Leu	Lys	Asn	Val	Asn	Leu	Ser	Gly	Leu	Asp
				405					410					415	
Ile	Ser	His	Ile	Thr	Asp	Met	Gly	Gly	Met	Phe	Ser	Gly	Asp	Ser	Asn
			420				425						430		
Leu	Glu	Ser	Leu	Asp	Leu	Ser	Gly	Leu	Asp	Leu	Ser	Lys	Val	Thr	Asn
			435				440					445			
Thr	Asn	Asn	Met	Phe	Asp	Trp	Val	Gly	Gly	Lys	Ile	Lys	Ser	Val	Asn
				450		455						460			
Ile	Thr	Asn	Thr	Lys	Ser	Ile	Pro	Arg	Ser	Ile	Leu	Asp	Ile	Tyr	Leu
				465		470				475					480
Lys	Ala	Leu	Ser	Asn	Thr	Gly	Thr	Thr	Thr	Val	Asp	Leu	Ser	Gly	Ile
				485					490					495	
Asn	Leu	Ser	Pro	Asn	Val	Thr	Ser	Leu	His	Gly	Leu	Phe	Ala	Asn	Met
			500					505					510		
Pro	Asn	Leu	Gly	Ser	Ala	Asn	Leu	Ser	Gly	Leu	Asp	Ile	Ser	His	Ile
			515				520					525			

Thr	Asp	Met	Gly	Gly	Met	Phe	Phe	Asn	Asp	Thr	Ser	Leu	Lys	Ser	Val
530						535					540				
Asn	Leu	Ser	Gly	Leu	Asn	Leu	Glu	Lys	Val	Lys	Asp	Leu	Ser	Thr	Met
545					550					555					560
Phe	Tyr	Gly	Ala	Asn	Asn	Leu	Glu	Asn	Val	Asp	Phe	Ser	Asn	Thr	Lys
				565					570						575
Phe	Ala	Pro	Asp	Ala	Asn	Thr	Asn	Val	Met	Phe	Ala	Phe	Ala	Asp	Thr
			580					585					590		
Lys	Leu	Gln	Ser	Val	Asn	Ile	Asn	Gly	Thr	Lys	Asn	Ile	Thr	Arg	Glu
595							600					605			
Val	Leu	Asp	Ala	Val	Ile	Arg	Ala	Ala	Lys	Asn	Ser	Asn	Ala	Thr	Thr
610						615					620				
Leu	Asp	Leu	Ser	Gly	Val	Ser	Phe	Ser	Pro	Ser	Ile	Thr	Ser	Phe	Asn
625					630					635					640
Asn	Leu	Phe	Ser	Asn	Met	Pro	Asn	Ile	Glu	Ser	Ile	Asp	Leu	Thr	Gly
				645					650						655
Trp	Asp	Thr	Ser	His	Ile	Thr	Asp	Met	Ser	Tyr	Met	Phe	Phe	Asn	Asp
			660					665					670		
Pro	Lys	Leu	Lys	Ile	Ile	Lys	Gly	Leu	Glu	Asp	Phe	Asn	Thr	Ser	Asn
			675				680					685			
Val	Thr	Asn	Met	Ala	Tyr	Met	Phe	Ala	Ala	Phe	Asn	Asn	Pro	Thr	Thr
690						695					700				
Asp	Asn	Tyr	Asp	Pro	Lys	Gly	Leu	Glu	Ser	Leu	Gly	His	Leu	Thr	Lys
705					710					715					720
Leu	Asp	Leu	Ser	Asn	Trp	Asp	Thr	Ser	Asn	Val	Thr	Asn	Met	Leu	Tyr
				725					730						735
Met	Phe	Ala	Gly	Gln	Thr	Asn	Leu	Thr	Ser	Leu	Gly	Asp	Leu	Ser	Lys
			740					745					750		
Trp	Asn	Thr	Ser	Lys	Val	Thr	Asn	Met	Ala	Tyr	Met	Phe	Tyr	Asp	Leu
			755				760					765			
Lys	Asn	Ile	Asp	Asp	Gly	Lys	Leu	Asp	Leu	Thr	Gly	Trp	Asp	Thr	Ser
			770			775					780				
Asn	Val	Thr	Asp	Met	Ser	Tyr	Met	Phe	Phe	Asn	Met	Phe	Leu	Gln	Lys
785					790					795					800
Asp	Leu	Ser	Phe	Val	Asn	Asp	Trp	Asn	Thr	Gly	Lys	Val	Thr	Asp	Met
				805					810					815	
Ser	Tyr	Met	Phe	Ala	Asn	Asp	Lys	Asn	Leu	Glu	Lys	Leu	Asp	Leu	Ser
			820					825					830		
Lys	Trp	Asp	Val	Ser	Ser	Val	Gly	Leu	Lys	His	Thr	Glu	Gln	Asn	Tyr
			835				840						845		
Ser	Leu	Ala	Met	Met	Phe	Ala	Gly	Asp	Thr	Ser	Leu	Thr	Thr	Val	Gly
			850			855					860				
Asp	Ile	Ser	His	Trp	Asn	Thr	Lys	Asn	Val	His	Asp	Thr	Arg	Gln	Met
865					870					875					880
Phe	Tyr	Asn	Thr	Pro	Lys	Leu	Thr	Asn	Ile	Asp	Leu	Ser	Gly	Trp	Asn
				885					890					895	
Thr	Gly	Lys	Leu	Gln	Ile	Ala	Glu	Gly	Met	Phe	Asn	Ser	Ser	Gly	Ala
			900					905						910	
Lys	Gln	Ile	Asn	Leu	Asp	Asn	Trp	Asp	Leu	Ser	Asn	Ile	Lys	Arg	Ile
			915				920						925		
Thr	Pro	Ala	Gly	Tyr	Val	Glu	Gly	Lys	Ala	Gly	Val	Gly	Val	Leu	Arg
						930						940			
Gly	Val	Glu	Asn	Met	Phe	Lys	Asn	Leu	Thr	Asn	Pro	Ala	Val	Ile	Ser
945					950					955					960
Met	Asn	Lys	Val	Ile	Leu	Pro	Asp	Ala	Arg	Asn	Ala	Phe	Glu	Ile	Asn
				965					970					975	
Asp	Phe	Glu	Gly	Asn	Lys	Ala	Ile	Val	Val	Ile	Ala	Asn	Gly	Gln	Asn

980 985 990
 Gly Glu Ala Leu Gln Asp Leu Leu Lys Ile Asn Asn Gln Thr Trp Thr
 995 1000 1005
 Asp Lys Ser Gly Asn Asn Val Thr Gly Arg Gln Asn Ser Asp Tyr Val
 1010 1015 1020
 Thr Tyr Val Arg Ala Asp Asp Asn Ser Asn Gln Ile Gly Gln Arg Gly
 1025 1030 1035 1040
 Leu Asn Phe Ile Phe Thr Asn Leu Asp Asp Leu His Gln Tyr Phe Asn
 1045 1050 1055
 Gln Val Thr Asn Ala Asp Asn Val Lys Asn Asp Ile Gly Glu Leu Ser
 1060 1065 1070
 His Asp Trp Asp Ala Gln Gln Asp Thr Asp Asn Asn Ile Val Lys Ile
 1075 1080 1085
 Thr Leu Arg Leu Ser Pro Ala Ser Ser Tyr Asp Pro Tyr Ser Glu Asn
 1090 1095 1100
 Ile His Ala Glu Lys Asp Gly Asn Ile Leu Ala Asp Leu Met Thr Ser
 1105 1110 1115 1120
 Lys Tyr Gln Leu His Ile Val Ala Pro Thr Asn Thr Thr Glu Thr Lys
 1125 1130 1135
 Lys Pro Thr Arg Thr Ile Ile Ile Glu Asn Pro Asp Gly Thr Thr Ser
 1140 1145 1150
 Thr Lys Glu Gln Thr Val Glu Phe Lys Arg Glu Val Thr Lys His Val
 1155 1160 1165
 Asp Gly Thr Glu Glu Ala Thr Ser Trp Thr Pro Thr Ser Gly Glu Trp
 1170 1175 1180
 Thr Lys Phe Asp Val Pro Gln Ile Ala Gly Tyr Asp Ser Tyr Val Asp
 1185 1190 1195 1200
 Gly Thr Gln Ser Lys Ser Val Ala Ser Glu Pro Val Asn Lys Asp Thr
 1205 1210 1215
 Glu Asn Val Thr Val Val Ile Thr Tyr Lys Ser Asn Ala Val Asn Pro
 1220 1225 1230
 Glu Pro Ile Ile Pro Asp Pro Val Lys Pro Glu Val Asp Pro Asp Lys
 1235 1240 1245
 Lys Asp Pro Gln Glu Pro Lys Thr Asp Pro Val Thr Pro Thr Pro Asp
 1250 1255 1260
 Glu Pro Glu Asn Pro Lys Pro Glu Lys Lys Pro Ser Asn Pro Asp Lys
 1265 1270 1275 1280
 Arg Lys Asp Asp Asn Ser Lys Val Val Lys Pro His Gly Glu Asn Lys
 1285 1290 1295
 Ala Ala Lys Lys Asn His Ser Ser Val Glu His Lys Lys Thr Gly Thr
 1300 1305 1310
 His Thr Ile Lys Leu Ser His Arg Val Ala Pro Lys Gly Thr Gln Ala
 1315 1320 1325
 Thr Asn Gly Ser Lys Lys Ser Thr Ser Thr Val Asn Lys Ala Ala Asp
 1330 1335 1340
 Asn Asn Lys Asn Thr Leu Pro Gln Thr Gly Glu Lys Lys Ser Asn Ala
 1345 1350 1355 1360
 Gly Leu Ile Gly Leu Ala Leu Ile Ala Leu Ala Ser Leu Gly Leu Ile
 1365 1370 1375
 Asp Arg Lys Arg Arg Asp
 1380

<210> 189

<211> 750

<212> DNA

<213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF1741 - cell wall-associated hydrolase

<220>
 <221> CDS
 <222> (1)...(750)

<400> 189
 ttg aat att tgg aca aat tat gaa aat ggt aag ttt atg ggc tat cgt 48
 Met Asn Ile Trp Thr Asn Tyr Glu Asn Gly Lys Phe Met Gly Tyr Arg
 1 5 10 15
 gct aaa gat ggc tct gtt tgg aat gta gct gcg aca gct gtc gat agt 96
 Ala Lys Asp Gly Ser Val Trp Asn Val Ala Ala Thr Ala Val Asp Ser
 20 25 30
 aag ggt aat cta tgg tat aaa gta ggg acg cgt gaa tgg att gaa gcg 144
 Lys Gly Asn Leu Trp Tyr Lys Val Gly Thr Arg Glu Trp Ile Glu Ala
 35 40 45
 cgt tat acc gtt gat gtc aat gaa gca act gaa tct act aag aca gct 192
 Arg Tyr Thr Val Asp Val Asn Glu Ala Thr Glu Ser Thr Lys Thr Ala
 50 55 60
 acg aag aaa aag aca tcg gta gct act tta gct aat aaa gtt aag aaa 240
 Thr Lys Lys Lys Thr Ser Val Ala Thr Leu Ala Asn Lys Val Lys Lys
 65 70 75 80
 aca act acg aat gtt aat aaa aaa att tct gcc gca tta aaa gat aat 288
 Thr Thr Thr Asn Val Asn Lys Lys Ile Ser Ala Ala Leu Lys Asp Asn
 85 90 95
 aat aca aat aag act aaa gaa gaa aaa gtt aaa aag gct aat caa atc 336
 Asn Thr Asn Lys Thr Lys Glu Glu Lys Val Lys Lys Ala Asn Gln Ile
 100 105 110
 gtt aat gag aca gtt aag aag aat gaa gaa aat aaa aat tct tca atg 384
 Val Asn Glu Thr Val Lys Lys Asn Glu Glu Asn Lys Asn Ser Ser Met
 115 120 125
 caa gct tca agt aaa gct gct tca att gta gcc ctt gct aaa gag cag 432
 Gln Ala Ser Ser Lys Ala Ala Ser Ile Val Ala Leu Ala Lys Glu Gln
 130 135 140
 gtg ggt aag ccc tat gtt tgg gca gct gca gga cct gat aaa ttt gac 480
 Val Gly Lys Pro Tyr Val Trp Ala Ala Ala Gly Pro Asp Lys Phe Asp
 145 150 155 160
 tgt tct ggc tta gtt caa tat gtt tac caa cat gct gca gga att aat 528
 Cys Ser Gly Leu Val Gln Tyr Val Tyr Gln His Ala Ala Gly Ile Asn
 165 170 175
 tta cct cgt act act tat gat cag gtt aaa gtg gga caa aca gtt cca 576

Leu Pro Arg Thr Thr Tyr Asp Gln Val Lys Val Gly Gln Thr Val Pro
 180 185 190
 ctt aac caa ctt caa gca ggg gat tta gta ttt tgg ggt tct gag acc 624
 Leu Asn Gln Leu Gln Ala Gly Asp Leu Val Phe Trp Gly Ser Glu Thr
 195 200 205
 gct cca tat cac gtt gca att tat att ggt aat aat caa tat gtc aat 672
 Ala Pro Tyr His Val Ala Ile Tyr Ile Gly Asn Asn Gln Tyr Val Asn
 210 215 220
 gcg gct act cct gaa caa gga acc att ttg caa aat gta tct agt tat 720
 Ala Ala Thr Pro Glu Gln Gly Thr Ile Leu Gln Asn Val Ser Ser Tyr
 225 230 235 240
 aat gag cct aca att gct aag aga ata tta 750
 Asn Glu Pro Thr Ile Ala Lys Arg Ile Leu
 245 250

<210> 190

<211> 250

<212> PRT

<213> Lactobacillus acidophilus

<400> 190

Met Asn Ile Trp Thr Asn Tyr Glu Asn Gly Lys Phe Met Gly Tyr Arg
 1 5 10 15
 Ala Lys Asp Gly Ser Val Trp Asn Val Ala Ala Thr Ala Val Asp Ser
 20 25 30
 Lys Gly Asn Leu Trp Tyr Lys Val Gly Thr Arg Glu Trp Ile Glu Ala
 35 40 45
 Arg Tyr Thr Val Asp Val Asn Glu Ala Thr Glu Ser Thr Lys Thr Ala
 50 55 60
 Thr Lys Lys Lys Thr Ser Val Ala Thr Leu Ala Asn Lys Val Lys Lys
 65 70 75 80
 Thr Thr Thr Asn Val Asn Lys Lys Ile Ser Ala Ala Leu Lys Asp Asn
 85 90 95
 Asn Thr Asn Lys Thr Lys Glu Glu Lys Val Lys Lys Ala Asn Gln Ile
 100 105 110
 Val Asn Glu Thr Val Lys Lys Asn Glu Glu Asn Lys Asn Ser Ser Met
 115 120 125
 Gln Ala Ser Ser Lys Ala Ala Ser Ile Val Ala Leu Ala Lys Glu Gln
 130 135 140
 Val Gly Lys Pro Tyr Val Trp Ala Ala Ala Gly Pro Asp Lys Phe Asp
 145 150 155 160
 Cys Ser Gly Leu Val Gln Tyr Val Tyr Gln His Ala Ala Gly Ile Asn
 165 170 175
 Leu Pro Arg Thr Thr Tyr Asp Gln Val Lys Val Gly Gln Thr Val Pro
 180 185 190
 Leu Asn Gln Leu Gln Ala Gly Asp Leu Val Phe Trp Gly Ser Glu Thr
 195 200 205
 Ala Pro Tyr His Val Ala Ile Tyr Ile Gly Asn Asn Gln Tyr Val Asn
 210 215 220
 Ala Ala Thr Pro Glu Gln Gly Thr Ile Leu Gln Asn Val Ser Ser Tyr
 225 230 235 240
 Asn Glu Pro Thr Ile Ala Lys Arg Ile Leu

245

250

<210> 191
 <211> 126
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1742

<220>
 <221> CDS
 <222> (1)...(126)

<400> 191
 atg gca gta aag ttt gct gca cgg aca gtt tta agt gat gtt att gca 48
 Met Ala Val Lys Phe Ala Ala Arg Thr Val Leu Ser Asp Val Ile Ala
 1 5 10 15
 gaa acg cct gta aca gaa agc gct gca gcc gct ccc aat tta aat aat 96
 Glu Thr Pro Val Thr Glu Ser Ala Ala Ala Ala Pro Asn Leu Asn Asn
 20 25 30
 ttg tgc ttt gac ata att caa tcc tct tgg 126
 Leu Cys Phe Asp Ile Ile Gln Ser Ser Trp
 35 40

<210> 192
 <211> 42
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 192
 Met Ala Val Lys Phe Ala Ala Arg Thr Val Leu Ser Asp Val Ile Ala
 1 5 10 15
 Glu Thr Pro Val Thr Glu Ser Ala Ala Ala Ala Pro Asn Leu Asn Asn
 20 25 30
 Leu Cys Phe Asp Ile Ile Gln Ser Ser Trp
 35 40

<210> 193
 <211> 786
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1743 - cell wall-associated hydrolase

<220>

<221> CDS

<222> (1)... (786)

<400> 193

atg aat att aag aac aat ttc gta aaa gtt act gca gct gct gct tta	48
Met Asn Ile Lys Asn Asn Phe Val Lys Val Thr Ala Ala Ala Ala Leu	
1 5 10 15	
act ata acc ggt gtg gct gca gta aat gct gtt caa tca gat tca act	96
Thr Ile Thr Gly Val Ala Ala Val Asn Ala Val Gln Ser Asp Ser Thr	
20 25 30	
act gct aat gtt caa gct gcc aca att aaa gtt aca att aat tat gtt	144
Thr Ala Asn Val Gln Ala Ala Thr Ile Lys Val Thr Ile Asn Tyr Val	
35 40 45	
cca gga tat ggt gtt aac atc tgg gac aac tac aat ggc ggt cac ttc	192
Pro Gly Tyr Gly Val Asn Ile Trp Asp Asn Tyr Asn Gly Gly His Phe	
50 55 60	
acc ggc caa cgt gca caa cac ggt acc act tgg gaa gtg tta gag caa	240
Thr Gly Gln Arg Ala Gln His Gly Thr Thr Trp Glu Val Leu Glu Gln	
65 70 75 80	
aag ttt gat tca aag ggc cgt aat tgg tac aag att ggg gaa aat aaa	288
Lys Phe Asp Ser Lys Gly Arg Asn Trp Tyr Lys Ile Gly Glu Asn Lys	
85 90 95	
tgg att tta gca caa tat gct aca act gat gct agt gct gca tca act	336
Trp Ile Leu Ala Gln Tyr Ala Thr Thr Asp Ala Ser Ala Ala Ser Thr	
100 105 110	
aag aca gca aat gca gct acc aag aag acc act acc acc act gct gca	384
Lys Thr Ala Asn Ala Ala Thr Lys Lys Thr Thr Thr Thr Thr Ala Ala	
115 120 125	
gct aat aag acc aag aag gtt aag aag tca gtt caa gca act ggg gat	432
Ala Asn Lys Thr Lys Lys Val Lys Lys Ser Val Gln Ala Thr Gly Asp	
130 135 140	
gca tca tca gtt atc act tta gct tct gct caa gtt ggt aag cct tat	480
Ala Ser Ser Val Ile Thr Leu Ala Ser Ala Gln Val Gly Lys Pro Tyr	
145 150 155 160	
gtt tat ggt gct caa ggt aca gat agt ttt gac tgt tca ggt ctt act	528
Val Tyr Gly Ala Gln Gly Thr Asp Ser Phe Asp Cys Ser Gly Leu Thr	
165 170 175	
tca tat gtt tac tca aaa gca gct ggt gtt aat att ggt aga acc act	576
Ser Tyr Val Tyr Ser Lys Ala Ala Gly Val Asn Ile Gly Arg Thr Thr	
180 185 190	
tat gat caa gta aag caa ggt act acc gtt tca atg aat aac ctt caa	624
Tyr Asp Gln Val Lys Gln Gly Thr Thr Val Ser Met Asn Asn Leu Gln	
195 200 205	

```

cca ggt gat tta ctc ttc tgg ggt tcg gca agt gct cct tac cat gtg 672
Pro Gly Asp Leu Leu Phe Trp Gly Ser Ala Ser Ala Pro Tyr His Val
    210                215                220

ggt atc tat gtc ggt aac aat caa tat att cat gca gct act cct gga 720
Gly Ile Tyr Val Gly Asn Asn Gln Tyr Ile His Ala Ala Thr Pro Gly
225                230                235                240

caa ggt gta gtt aag caa act atc agc act tat ttc tac cca agt gtt 768
Gln Gly Val Val Lys Gln Thr Ile Ser Thr Tyr Phe Tyr Pro Ser Val
                245                250                255

gct aaa cgt att ttg aat 786
Ala Lys Arg Ile Leu Asn
                260

```

```

<210> 194
<211> 262
<212> PRT
<213> Lactobacillus acidophilus

```

```

<400> 194
Met Asn Ile Lys Asn Asn Phe Val Lys Val Thr Ala Ala Ala Ala Leu
 1                5                10                15
Thr Ile Thr Gly Val Ala Ala Val Asn Ala Val Gln Ser Asp Ser Thr
                20                25                30
Thr Ala Asn Val Gln Ala Ala Thr Ile Lys Val Thr Ile Asn Tyr Val
    35                40                45
Pro Gly Tyr Gly Val Asn Ile Trp Asp Asn Tyr Asn Gly Gly His Phe
 50                55                60
Thr Gly Gln Arg Ala Gln His Gly Thr Thr Trp Glu Val Leu Glu Gln
65                70                75                80
Lys Phe Asp Ser Lys Gly Arg Asn Trp Tyr Lys Ile Gly Glu Asn Lys
    85                90                95
Trp Ile Leu Ala Gln Tyr Ala Thr Thr Asp Ala Ser Ala Ala Ser Thr
    100                105                110
Lys Thr Ala Asn Ala Ala Thr Lys Lys Thr Thr Thr Thr Thr Ala Ala
    115                120                125
Ala Asn Lys Thr Lys Lys Val Lys Lys Ser Val Gln Ala Thr Gly Asp
    130                135                140
Ala Ser Ser Val Ile Thr Leu Ala Ser Ala Gln Val Gly Lys Pro Tyr
145                150                155                160
Val Tyr Gly Ala Gln Gly Thr Asp Ser Phe Asp Cys Ser Gly Leu Thr
    165                170                175
Ser Tyr Val Tyr Ser Lys Ala Ala Gly Val Asn Ile Gly Arg Thr Thr
    180                185                190
Tyr Asp Gln Val Lys Gln Gly Thr Thr Val Ser Met Asn Asn Leu Gln
    195                200                205
Pro Gly Asp Leu Leu Phe Trp Gly Ser Ala Ser Ala Pro Tyr His Val
    210                215                220
Gly Ile Tyr Val Gly Asn Asn Gln Tyr Ile His Ala Ala Thr Pro Gly
225                230                235                240
Gln Gly Val Val Lys Gln Thr Ile Ser Thr Tyr Phe Tyr Pro Ser Val
    245                250                255
Ala Lys Arg Ile Leu Asn
                260

```

<210> 195
 <211> 552
 <212> DNA
 <213> *Lactobacillus acidophilus*

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1744 - glycosidase

<220>
 <221> CDS
 <222> (1)...(552)

<400> 195
 ttg att ttc aaa cgt act ttg gtt aaa tac aca gca gct tta tca att 48
 Met Ile Phe Lys Arg Thr Leu Val Lys Tyr Thr Ala Ala Leu Ser Ile
 1 5 10 15
 ttc ttt aca ggt ctt tca gca gtt agc gtt cca gca act gtt cac gct 96
 Phe Phe Thr Gly Leu Ser Ala Val Ser Val Pro Ala Thr Val His Ala
 20 25 30
 gac gat gtt gaa aat acc act act gtt gac acc aac aac tca gct tca 144
 Asp Asp Val Glu Asn Thr Thr Thr Val Asp Thr Asn Asn Ser Ala Ser
 35 40 45
 tct att gaa acc agt aca cct gaa tca aat tca gta aag aag gtt tca 192
 Ser Ile Glu Thr Ser Thr Pro Glu Ser Asn Ser Val Lys Lys Val Ser
 50 55 60
 gct aca acc caa aag cgt aac gct att gtt aag ctt gct aag aag caa 240
 Ala Thr Thr Gln Lys Arg Asn Ala Ile Val Lys Leu Ala Lys Lys Gln
 65 70 75 80
 gtt ggt aag cct tac gtt tgg ggt gct act ggc cct tac gga ttc gac 288
 Val Gly Lys Pro Tyr Val Trp Gly Ala Thr Gly Pro Tyr Gly Phe Asp
 85 90 95
 tgc tca ggc tta act act tat gtt tac aag aat gca gct aac aag act 336
 Cys Ser Gly Leu Thr Thr Tyr Val Tyr Lys Asn Ala Ala Asn Lys Thr
 100 105 110
 tta cca aga act act tac ggt caa att act atc ggt aaa tca gta tca 384
 Leu Pro Arg Thr Thr Tyr Gly Gln Ile Thr Ile Gly Lys Ser Val Ser
 115 120 125
 gtt tca act aaa tct ctt aag aag ggt gac tta ttg ttc tgg ggt aac 432
 Val Ser Thr Lys Ser Leu Lys Lys Gly Asp Leu Leu Phe Trp Gly Asn
 130 135 140
 tca cac gta ggt atc tac att ggt aac ggt aag ttt gtt cac gct cca 480
 Ser His Val Gly Ile Tyr Ile Gly Asn Gly Lys Phe Val His Ala Pro
 145 150 155 160

gct cca ggt caa aat gtt aag act caa act tta gca tca ttc tac cca 528
 Ala Pro Gly Gln Asn Val Lys Thr Gln Thr Leu Ala Ser Phe Tyr Pro
 165 170 175

tca gct gct aag cgt gtt atc ggt 552
 Ser Ala Ala Lys Arg Val Ile Gly
 180

<210> 196

<211> 184

<212> PRT

<213> Lactobacillus acidophilus

<400> 196

Met Ile Phe Lys Arg Thr Leu Val Lys Tyr Thr Ala Ala Leu Ser Ile
 1 5 10 15
 Phe Phe Thr Gly Leu Ser Ala Val Ser Val Pro Ala Thr Val His Ala
 20 25 30
 Asp Asp Val Glu Asn Thr Thr Thr Val Asp Thr Asn Asn Ser Ala Ser
 35 40 45
 Ser Ile Glu Thr Ser Thr Pro Glu Ser Asn Ser Val Lys Lys Val Ser
 50 55 60
 Ala Thr Thr Gln Lys Arg Asn Ala Ile Val Lys Leu Ala Lys Lys Gln
 65 70 75 80
 Val Gly Lys Pro Tyr Val Trp Gly Ala Thr Gly Pro Tyr Gly Phe Asp
 85 90 95
 Cys Ser Gly Leu Thr Thr Tyr Val Tyr Lys Asn Ala Ala Asn Lys Thr
 100 105 110
 Leu Pro Arg Thr Thr Tyr Gly Gln Ile Thr Ile Gly Lys Ser Val Ser
 115 120 125
 Val Ser Thr Lys Ser Leu Lys Lys Gly Asp Leu Leu Phe Trp Gly Asn
 130 135 140
 Ser His Val Gly Ile Tyr Ile Gly Asn Gly Lys Phe Val His Ala Pro
 145 150 155 160
 Ala Pro Gly Gln Asn Val Lys Thr Gln Thr Leu Ala Ser Phe Tyr Pro
 165 170 175
 Ser Ala Ala Lys Arg Val Ile Gly
 180

<210> 197

<211> 447 .

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1745 - guanylate kinase

<220>

<221> CDS

<222> (1)...(447)

<400> 197

```

ttg aca cat acg acg cga ccg atg cga gct gga gaa aag caa ggt gtt 48
Met Thr His Thr Thr Arg Pro Met Arg Ala Gly Glu Lys Gln Gly Val
1 5 10 15

tca tat cat ttt gaa aca gat gaa act ttt aac cag ctc cat ttc ttt 96
Ser Tyr His Phe Glu Thr Asp Glu Thr Phe Asn Gln Leu His Phe Phe
20 25 30

gaa cat att act tat ggt tca tat caa tac ggc tca agt cgt gaa gca 144
Glu His Ile Thr Tyr Gly Ser Tyr Gln Tyr Gly Ser Ser Arg Glu Ala
35 40 45

tta aat ctc gct tgg aaa aag aac gac tta gtc tca tta att gtt gat 192
Leu Asn Leu Ala Trp Lys Lys Asn Asp Leu Val Ser Leu Ile Val Asp
50 55 60

atc aaa gga atc tat tct tac att aat cag ttg aaa gat aag gta tat 240
Ile Lys Gly Ile Tyr Ser Tyr Ile Asn Gln Leu Lys Asp Lys Val Tyr
65 70 75 80

ttt tta tac att act act tca act aaa gaa gaa tta aaa gag cgc ttg 288
Phe Leu Tyr Ile Thr Thr Ser Thr Lys Glu Glu Leu Lys Glu Arg Leu
85 90 95

tta aag cga gga gat gat cct gcc aaa atc aag gaa agg ctt agt ggc 336
Leu Lys Arg Gly Asp Asp Pro Ala Lys Ile Lys Glu Arg Leu Ser Gly
100 105 110

agt gag tta aac gca tta ccg gag gac tta aag cct tac gct cat gta 384
Ser Glu Leu Asn Ala Leu Pro Glu Asp Leu Lys Pro Tyr Ala His Val
115 120 125

tta gtt aat gat gat cta tct aag act aag aat gcg cta gat cag ctg 432
Leu Val Asn Asp Asp Leu Ser Lys Thr Lys Asn Ala Leu Asp Gln Leu
130 135 140

gta gca agc ttt cat 447
Val Ala Ser Phe His
145

```

<210> 198

<211> 149

<212> PRT

<213> Lactobacillus acidophilus

<400> 198

```

Met Thr His Thr Thr Arg Pro Met Arg Ala Gly Glu Lys Gln Gly Val
1 5 10 15
Ser Tyr His Phe Glu Thr Asp Glu Thr Phe Asn Gln Leu His Phe Phe
20 25 30
Glu His Ile Thr Tyr Gly Ser Tyr Gln Tyr Gly Ser Ser Arg Glu Ala
35 40 45
Leu Asn Leu Ala Trp Lys Lys Asn Asp Leu Val Ser Leu Ile Val Asp
50 55 60
Ile Lys Gly Ile Tyr Ser Tyr Ile Asn Gln Leu Lys Asp Lys Val Tyr

```

[illegible]

```
<210> 199
<211> 297
<212> DNA
<213> Lactobacillus acidophilus
```

```
<220>
<221> misc_feature
<222> (0)...(0)
<223> ORF 1746
```

<220>
<221> CDS
<222> (1) . . . (297)

<400>	199															
atg	aaa	aaa	gca	gat	gta	aaa	gtt	ggc	gcc	att	gtt	ggt	gct	aag	tca	48
Met	Lys	Lys	Ala	Asp	Val	Lys	Val	Gly	Ala	Ile	Val	Gly	Ala	Lys	Ser	
1				5					10					15		
gaa	gaa	gaa	ctt	aag	aag	ccg	ttc	caa	ggt	aaa	gta	gaa	aaa	att	tat	96
Glu	Glu	Glu	Leu	Lys	Lys	Pro	Phe	Gln	Gly	Lys	Val	Glu	Lys	Ile	Tyr	
			20					25					30			
gaa	aac	tct	gct	ctt	tta	gca	att	act	tca	tac	gat	cca	gtt	gat	acc	144
Glu	Asn	Ser	Ala	Leu	Leu	Ala	Ile	Thr	Ser	Tyr	Asp	Pro	Val	Asp	Thr	
		35					40					45				
acc	gcc	gtt	agt	gac	ctg	aac	aag	atc	gtt	gtt	aac	ttc	aag	aac		192
Thr	Ala	Val	Ser	Asp	Leu	Asn	Asn	Lys	Ile	Val	Val	Asn	Phe	Lys	Asn	
	50					55				60						
tta	aag	gct	gct	cgc	gcc	gct	aaa	aat	agt	aag	act	gct	tca	act	aac	240
Leu	Lys	Ala	Ala	Arg	Ala	Ala	Lys	Asn	Ser	Lys	Thr	Ala	Ser	Thr	Asn	
65					70					75					80	
aaa	gtt	aag	gtt	gaa	aag	atc	gct	aag	aag	aaa	gac	gat	tct	tca	aaa	288
Lys	Val	Lys	Val	Glu	Lys	Ile	Ala	Lys	Lys	Lys	Asp	Asp	Ser	Ser	Lys	
				85					90					95		
gaa	gaa	aaa														297
Glu	Glu	Lys														

<210> 200

<211> 99

<212> PRT

<213> *Lactobacillus acidophilus*

<400> 200

```

Met Lys Lys Ala Asp Val Lys Val Gly Ala Ile Val Gly Ala Lys Ser
 1          5          10          15
Glu Glu Glu Leu Lys Lys Pro Phe Gln Gly Lys Val Glu Lys Ile Tyr
      20          25          30
Glu Asn Ser Ala Leu Leu Ala Ile Thr Ser Tyr Asp Pro Val Asp Thr
      35          40          45
Thr Ala Val Ser Asp Leu Asn Asn Lys Ile Val Val Asn Phe Lys Asn
 50          55          60
Leu Lys Ala Ala Arg Ala Ala Lys Asn Ser Lys Thr Ala Ser Thr Asn
65          70          75          80
Lys Val Lys Val Glu Lys Ile Ala Lys Lys Lys Asp Asp Ser Ser Lys
      85          90          95
Glu Glu Lys

```

<210> 201

<211> 1509

<212> DNA

<213> *Lactobacillus acidophilus*

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1747

<220>

<221> CDS

<222> (1)...(1509)

<400> 201

```

atg aaa gaa aaa act aga act gtc ttg tat tgg ttc att ctt att cag      48
Met Lys Glu Lys Thr Arg Thr Val Leu Tyr Trp Phe Ile Leu Ile Gln
 1          5          10          15

cca ttt ctc gac ctt tat tgg ttc tac aat ggt aaa tta gcc aat att      96
Pro Phe Leu Asp Leu Tyr Trp Phe Tyr Asn Gly Lys Leu Ala Asn Ile
      20          25          30

ttg cca ttt act ctg cca aca att atc agg att tta gct gtt ttt gta      144
Leu Pro Phe Thr Leu Pro Thr Ile Ile Arg Ile Leu Ala Val Phe Val
      35          40          45

att ttt tgc atg ttt ttt agc caa aag caa aac tgg caa aaa tta ggc      192
Ile Phe Cys Met Phe Phe Ser Gln Lys Gln Asn Trp Gln Lys Leu Gly
      50          55          60

caa gaa aag tgg cta atc gtt tat ctg gct ctt ttg att att tac tcg      240
Gln Glu Lys Trp Leu Ile Val Tyr Leu Ala Leu Leu Ile Ile Tyr Ser

```

65	70	75	80	
ctc ttg cac tta atc cat gtc aga cat ttc aac agc gtt aat cca agc	288			
Leu Leu His Leu Ile His Val Arg His Phe Asn Ser Val Asn Pro Ser				
85	90	95		
gac tac aac tac tct act gtt agc gaa gta ttt tac tta att aga atg	336			
Asp Tyr Asn Tyr Ser Thr Val Ser Glu Val Phe Tyr Leu Ile Arg Met				
100	105	110		
ctt atg ccg cta atg gta att ttc ttt acc aaa gaa ttg aat ttt act	384			
Leu Met Pro Leu Met Val Ile Phe Phe Thr Lys Glu Leu Asn Phe Thr				
115	120	125		
cac aaa caa ttt aga cag gta att tca ggc att agc ggt cta ttc tcg	432			
His Lys Gln Phe Arg Gln Val Ile Ser Gly Ile Ser Gly Leu Phe Ser				
130	135	140		
ttc acc atc gtg att agt aac tta ttc gtc att tca ctt aga agt tac	480			
Phe Thr Ile Val Ile Ser Asn Leu Phe Val Ile Ser Leu Arg Ser Tyr				
145	150	155	160	
gaa acc ggc ttt att agt gcc aat atc ttt gaa tgg ttc att aac ccc	528			
Glu Thr Gly Phe Ile Ser Ala Asn Ile Phe Glu Trp Phe Ile Asn Pro				
165	170	175		
aac att ggc tat tcg cac atg gct tct aaa ggt ttc ttc aac ttt acg	576			
Asn Ile Gly Tyr Ser His Met Ala Ser Lys Gly Phe Phe Asn Phe Thr				
180	185	190		
aat atg gta tcg gca gtt ctt ttc atg ctc atg cct tta atg ctc tat	624			
Asn Met Val Ser Ala Val Leu Phe Met Leu Met Pro Leu Met Leu Tyr				
195	200	205		
ttc atg ttc agt cac ttc aac tgg agg att gtc aca cta aat att gtt	672			
Phe Met Phe Ser His Phe Asn Trp Arg Ile Val Thr Leu Asn Ile Val				
210	215	220		
caa gct tta gcc atg att gaa ctt gga acc aaa gtt gcc ttg atc ggc	720			
Gln Ala Leu Ala Met Ile Glu Leu Gly Thr Lys Val Ala Leu Ile Gly				
225	230	235	240	
tta atc ggt ggc att att atc ggt att ttg ctt tat gtc ttt cat cta	768			
Leu Ile Gly Gly Ile Ile Ile Gly Ile Leu Leu Tyr Val Phe His Leu				
245	250	255		
ttt att gtt aaa gat gtt caa aaa aat ggg aaa gct gtc ctc gtt gct	816			
Phe Ile Val Lys Asp Val Gln Lys Asn Gly Lys Ala Val Leu Val Ala				
260	265	270		
ctt tta atg gaa acc ggc aca att gcg atc att cct ttt ggc cca gca	864			
Leu Leu Met Glu Thr Gly Thr Ile Ala Ile Ile Pro Phe Gly Pro Ala				
275	280	285		
att cag cgc tac aat tac gaa aaa tat cta gct caa caa tcc gac aac	912			
Ile Gln Arg Tyr Asn Tyr Glu Lys Tyr Leu Ala Gln Gln Ser Asp Asn				
290	295	300		

```

agt tta act caa gct aaa caa gaa tta gct caa gga tta aag aag tat 960
Ser Leu Thr Gln Ala Lys Gln Glu Leu Ala Gln Gly Leu Lys Lys Tyr
305 310 315 320

cct act gga aaa aag cgc aaa gaa ttt tta act gac ttt atc gaa aag 1008
Pro Thr Gly Lys Lys Arg Lys Glu Phe Leu Thr Asp Phe Ile Glu Lys
325 330 335

cat tat caa gat tat gct tta aac aaa aaa ttt gtc act aag agc tac 1056
His Tyr Gln Asp Tyr Ala Leu Asn Lys Lys Phe Val Thr Lys Ser Tyr
340 345 350

cct tat aaa tat gat cca gaa ttc tgg ctt aag atc atg aat gag cca 1104
Pro Tyr Lys Tyr Asp Pro Glu Phe Trp Leu Lys Ile Met Asn Glu Pro
355 360 365

ggc act tct aga atg gaa aac cgt cac gtc gaa aag gcc atg ctg gat 1152
Gly Thr Ser Arg Met Glu Asn Arg His Val Glu Lys Ala Met Leu Asp
370 375 380

caa gta ctt aag act aac aac aat aaa tta gat aaa gtt ttc ggt att 1200
Gln Val Leu Lys Thr Asn Asn Asn Lys Leu Asp Lys Val Phe Gly Ile
385 390 395 400

tcc tat act cga gaa act aat atc ttt aac tta gag cgc gat ttc act 1248
Ser Tyr Thr Arg Glu Thr Asn Ile Phe Asn Leu Glu Arg Asp Phe Thr
405 410 415

agc cag gtc tat tca ctg ggg tgg cta ggc atg tta ctc ttc att gag 1296
Ser Gln Val Tyr Ser Leu Gly Trp Leu Gly Met Leu Leu Phe Ile Glu
420 425 430

cca tat ata gtt atc cta ctc tat gcc gca att aag tgg tta atg aat 1344
Pro Tyr Ile Val Ile Leu Leu Tyr Ala Ala Ile Lys Trp Leu Met Asn
435 440 445

aaa caa aaa cgt aca tat tta att agc tca atg ctt ttg tca att gct 1392
Lys Gln Lys Arg Thr Tyr Leu Ile Ser Ser Met Leu Leu Ser Ile Ala
450 455 460

ttc atg ctc ttt gca gca ttt tta tca ggc aat gtc atg gac ttc tta 1440
Phe Met Leu Phe Ala Ala Phe Leu Ser Gly Asn Val Met Asp Phe Leu
465 470 475 480

act gct agc ttt atc tta gct ttt gct gaa gga agt ttg ctt agc gaa 1488
Thr Ala Ser Phe Ile Leu Ala Phe Ala Glu Gly Ser Leu Leu Ser Glu
485 490 495

gtt act cga aaa aag acg gaa 1509
Val Thr Arg Lys Lys Thr Glu
500

```

<210> 202

<211> 503

<212> PRT

<213> Lactobacillus acidophilus

<400> 202

```

Met Lys Glu Lys Thr Arg Thr Val Leu Tyr Trp Phe Ile Leu Ile Gln
 1      5      10      15
Pro Phe Leu Asp Leu Tyr Trp Phe Tyr Asn Gly Lys Leu Ala Asn Ile
 20      25      30
Leu Pro Phe Thr Leu Pro Thr Ile Ile Arg Ile Leu Ala Val Phe Val
 35      40      45
Ile Phe Cys Met Phe Phe Ser Gln Lys Gln Asn Trp Gln Lys Leu Gly
 50      55      60
Gln Glu Lys Trp Leu Ile Val Tyr Leu Ala Leu Leu Ile Ile Tyr Ser
 65      70      75      80
Leu Leu His Leu Ile His Val Arg His Phe Asn Ser Val Asn Pro Ser
 85      90      95
Asp Tyr Asn Tyr Ser Thr Val Ser Glu Val Phe Tyr Leu Ile Arg Met
100      105      110
Leu Met Pro Leu Met Val Ile Phe Phe Thr Lys Glu Leu Asn Phe Thr
115      120      125
His Lys Gln Phe Arg Gln Val Ile Ser Gly Ile Ser Gly Leu Phe Ser
130      135      140
Phe Thr Ile Val Ile Ser Asn Leu Phe Val Ile Ser Leu Arg Ser Tyr
145      150      155      160
Glu Thr Gly Phe Ile Ser Ala Asn Ile Phe Glu Trp Phe Ile Asn Pro
165      170      175
Asn Ile Gly Tyr Ser His Met Ala Ser Lys Gly Phe Phe Asn Phe Thr
180      185      190
Asn Met Val Ser Ala Val Leu Phe Met Leu Met Pro Leu Met Leu Tyr
195      200      205
Phe Met Phe Ser His Phe Asn Trp Arg Ile Val Thr Leu Asn Ile Val
210      215      220
Gln Ala Leu Ala Met Ile Glu Leu Gly Thr Lys Val Ala Leu Ile Gly
225      230      235      240
Leu Ile Gly Gly Ile Ile Ile Gly Ile Leu Leu Tyr Val Phe His Leu
245      250      255
Phe Ile Val Lys Asp Val Gln Lys Asn Gly Lys Ala Val Leu Val Ala
260      265      270
Leu Leu Met Glu Thr Gly Thr Ile Ala Ile Ile Pro Phe Gly Pro Ala
275      280      285
Ile Gln Arg Tyr Asn Tyr Glu Lys Tyr Leu Ala Gln Gln Ser Asp Asn
290      295      300
Ser Leu Thr Gln Ala Lys Gln Glu Leu Ala Gln Gly Leu Lys Lys Tyr
305      310      315      320
Pro Thr Gly Lys Lys Arg Lys Glu Phe Leu Thr Asp Phe Ile Glu Lys
325      330      335
His Tyr Gln Asp Tyr Ala Leu Asn Lys Lys Phe Val Thr Lys Ser Tyr
340      345      350
Pro Tyr Lys Tyr Asp Pro Glu Phe Trp Leu Lys Ile Met Asn Glu Pro
355      360      365
Gly Thr Ser Arg Met Glu Asn Arg His Val Glu Lys Ala Met Leu Asp
370      375      380
Gln Val Leu Lys Thr Asn Asn Asn Lys Leu Asp Lys Val Phe Gly Ile
385      390      395      400
Ser Tyr Thr Arg Glu Thr Asn Ile Phe Asn Leu Glu Arg Asp Phe Thr
405      410      415
Ser Gln Val Tyr Ser Leu Gly Trp Leu Gly Met Leu Leu Phe Ile Glu
420      425      430

```

Pro Tyr Ile Val Ile Leu Leu Tyr Ala Ala Ile Lys Trp Leu Met Asn
 435 440 445
 Lys Gln Lys Arg Thr Tyr Leu Ile Ser Ser Met Leu Leu Ser Ile Ala
 450 455 460
 Phe Met Leu Phe Ala Ala Phe Leu Ser Gly Asn Val Met Asp Phe Leu
 465 470 475 480
 Thr Ala Ser Phe Ile Leu Ala Phe Ala Glu Gly Ser Leu Leu Ser Glu
 485 490 495
 Val Thr Arg Lys Lys Thr Glu
 500

<210> 203
 <211> 618
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1748

<220>
 <221> CDS
 <222> (1)...(618)

<400> 203
 atg ttt agc tgg aat att att ggg atc cta ata tgg gtc gct atc att 48
 Met Phe Ser Trp Asn Ile Ile Gly Ile Leu Ile Trp Val Ala Ile Ile
 1 5 10 15
 ctt tat tta gtc ttt atc atc caa aac att cgt aaa cgt cga att aag 96
 Leu Tyr Leu Val Phe Ile Ile Gln Asn Ile Arg Lys Arg Arg Ile Lys
 20 25 30
 atg att att aaa caa cat aaa cgc ttt agt tgg cct aac ttt tta ctt 144
 Met Ile Ile Lys Gln His Lys Arg Phe Ser Trp Pro Asn Phe Leu Leu
 35 40 45
 aat gca att gaa att gtc att tta tta gtt gct gct ggt tgg atg ttt 192
 Asn Ala Ile Glu Ile Val Ile Leu Leu Val Ala Ala Gly Trp Met Phe
 50 55 60
 aat cag acc ttt atg gat aat cca gat tta gaa gat gcc aat cgc att 240
 Asn Gln Thr Phe Met Asp Asn Pro Asp Leu Glu Asp Ala Asn Arg Ile
 65 70 75 80
 act tca acg gtt aaa tat gat ccg tta att atg aat act ggg act ggt 288
 Thr Ser Thr Val Lys Tyr Asp Pro Leu Ile Met Asn Thr Gly Thr Gly
 85 90 95
 aat tct agt tat gtg aca att aat tca gct aag aag aaa tat ggt tca 336
 Asn Ser Ser Tyr Val Thr Ile Asn Ser Ala Lys Lys Lys Tyr Gly Ser
 100 105 110
 cag act tat act ttt tat cga gca gga agt aaa ata act gcg tca agc 384

Gln Thr Tyr Thr Phe Tyr Arg Ala Gly Ser Lys Ile Thr Ala Ser Ser
 115 120 125

gat tat gcg tca att gca tat gga aac act tct tta gat gtt aat gct 432
 Asp Tyr Ala Ser Ile Ala Tyr Gly Asn Thr Ser Leu Asp Val Asn Ala
 130 135 140

gag aaa atc ccg tat gtt aaa aaa gaa ttg gcg aag atg gac aag aaa 480
 Glu Lys Ile Pro Tyr Val Lys Lys Glu Leu Ala Lys Met Asp Lys Lys
 145 150 155 160

tac caa cgt gct tat gtt gct gtt tat aca gct aaa tat aag aaa aat 528
 Tyr Gln Arg Ala Tyr Val Ala Val Tyr Thr Ala Lys Tyr Lys Lys Asn
 165 170 175

tgg caa aat gga ata ggg atg cat gca ggt cat tta gct acg cgc tat 576
 Trp Gln Asn Gly Ile Gly Met His Ala Gly His Leu Ala Thr Arg Tyr
 180 185 190

tac ttg att cgc att cca gat gca agt ttt att aaa cag aag 618
 Tyr Leu Ile Arg Ile Pro Asp Ala Ser Phe Ile Lys Gln Lys
 195 200 205

<210> 204

<211> 206

<212> PRT

<213> Lactobacillus acidophilus

<400> 204

Met Phe Ser Trp Asn Ile Ile Gly Ile Leu Ile Trp Val Ala Ile Ile
 1 5 10 15

Leu Tyr Leu Val Phe Ile Ile Gln Asn Ile Arg Lys Arg Arg Ile Lys
 20 25 30

Met Ile Ile Lys Gln His Lys Arg Phe Ser Trp Pro Asn Phe Leu Leu
 35 40 45

Asn Ala Ile Glu Ile Val Ile Leu Leu Val Ala Ala Gly Trp Met Phe
 50 55 60

Asn Gln Thr Phe Met Asp Asn Pro Asp Leu Glu Asp Ala Asn Arg Ile
 65 70 75 80

Thr Ser Thr Val Lys Tyr Asp Pro Leu Ile Met Asn Thr Gly Thr Gly
 85 90 95

Asn Ser Ser Tyr Val Thr Ile Asn Ser Ala Lys Lys Lys Tyr Gly Ser
 100 105 110

Gln Thr Tyr Thr Phe Tyr Arg Ala Gly Ser Lys Ile Thr Ala Ser Ser
 115 120 125

Asp Tyr Ala Ser Ile Ala Tyr Gly Asn Thr Ser Leu Asp Val Asn Ala
 130 135 140

Glu Lys Ile Pro Tyr Val Lys Lys Glu Leu Ala Lys Met Asp Lys Lys
 145 150 155 160

Tyr Gln Arg Ala Tyr Val Ala Val Tyr Thr Ala Lys Tyr Lys Lys Asn
 165 170 175

Trp Gln Asn Gly Ile Gly Met His Ala Gly His Leu Ala Thr Arg Tyr
 180 185 190

Tyr Leu Ile Arg Ile Pro Asp Ala Ser Phe Ile Lys Gln Lys
 195 200 205

<210> 205
 <211> 444
 <212> DNA
 <213> *Lactobacillus acidophilus*

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1749 - nrd1 ribonucleotide reductase

<220>
 <221> CDS
 <222> (1)...(444)

<400> 205
 atg gta gca ata gca ttt tat tca ata act ggg caa act gaa cgt ttt 48
 Met Val Ala Ile Ala Phe Tyr Ser Ile Thr Gly Gln Thr Glu Arg Phe
 1 5 10 15
 att gat aaa ata cag tta aaa gcc cat caa atc agc gat gcc aac cct 96
 Ile Asp Lys Ile Gln Leu Lys Ala His Gln Ile Ser Asp Ala Asn Pro
 20 25 30
 aag tat gac atg ggg caa aaa tat att tta att gtc cct tca tat cag 144
 Lys Tyr Asp Met Gly Gln Lys Tyr Ile Leu Ile Val Pro Ser Tyr Gln
 35 40 45
 gac ttt atg atg gat tcc gtt gtt gat ttt ttg acg tat aaa gat aat 192
 Asp Phe Met Met Asp Ser Val Val Asp Phe Leu Thr Tyr Lys Asp Asn
 50 55 60
 aag aaa aat atc att gga att ata ggt tgt ggc aat cga aac ttt aac 240
 Lys Lys Asn Ile Ile Gly Ile Ile Gly Cys Gly Asn Arg Asn Phe Asn
 65 70 75 80
 gac ctt ttt gct caa act gct aaa aag atc gca gca act tta aaa gta 288
 Asp Leu Phe Ala Gln Thr Ala Lys Lys Ile Ala Ala Thr Leu Lys Val
 85 90 95
 ccc att ctt tat ctg tta gaa ttt agt ggt act aat caa gat gtt aaa 336
 Pro Ile Leu Tyr Leu Leu Glu Phe Ser Gly Thr Asn Gln Asp Val Lys
 100 105 110
 aat gtc cgt aaa att gtt cat gat ctt tct gca gga cag agt acc aaa 384
 Asn Val Arg Lys Ile Val His Asp Leu Ser Ala Gly Gln Ser Thr Lys
 115 120 125
 gag gtt caa aag ccg aaa gaa tta cgt gga aat att agc ttt ttg agt 432
 Glu Val Gln Lys Pro Lys Glu Leu Arg Gly Asn Ile Ser Phe Leu Ser
 130 135 140
 gat tat aga gat 444
 Asp Tyr Arg Asp
 145

<210> 206
 <211> 148
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 206
 Met Val Ala Ile Ala Phe Tyr Ser Ile Thr Gly Gln Thr Glu Arg Phe
 1 5 10 15
 Ile Asp Lys Ile Gln Leu Lys Ala His Gln Ile Ser Asp Ala Asn Pro
 20 25 30
 Lys Tyr Asp Met Gly Gln Lys Tyr Ile Leu Ile Val Pro Ser Tyr Gln
 35 40 45
 Asp Phe Met Met Asp Ser Val Val Asp Phe Leu Thr Tyr Lys Asp Asn
 50 55 60
 Lys Lys Asn Ile Ile Gly Ile Ile Gly Cys Gly Asn Arg Asn Phe Asn
 65 70 75 80
 Asp Leu Phe Ala Gln Thr Ala Lys Lys Ile Ala Ala Thr Leu Lys Val
 85 90 95
 Pro Ile Leu Tyr Leu Leu Glu Phe Ser Gly Thr Asn Gln Asp Val Lys
 100 105 110
 Asn Val Arg Lys Ile Val His Asp Leu Ser Ala Gly Gln Ser Thr Lys
 115 120 125
 Glu Val Gln Lys Pro Lys Glu Leu Arg Gly Asn Ile Ser Phe Leu Ser
 130 135 140
 Asp Tyr Arg Asp
 145

<210> 207
 <211> 933
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1750 - ribonucleotide reductase

<220>
 <221> CDS
 <222> (1)...(933)

<400> 207
 atg aca aag aaa tat tac gaa gca ata aat tgg aat gac atg gag gat 48
 Met Thr Lys Lys Tyr Tyr Glu Ala Ile Asn Trp Asn Asp Met Glu Asp
 1 5 10 15
 aaa gta gat aaa tcc gct tgg gct cgg tta aat gat atc att tgg gag 96
 Lys Val Asp Lys Ser Ala Trp Ala Arg Leu Asn Asp Ile Ile Trp Glu
 20 25 30
 cca cgt cat gtt cca gta aaa gaa gac aaa aaa gaa ttt tta caa tta 144
 Pro Arg His Val Pro Val Lys Glu Asp Lys Lys Glu Phe Leu Gln Leu
 35 40 45

```

ccc agt cct gta aga tgt aca ctt ctt cat gtg ttt agc gct ctt tca 192
Pro Ser Pro Val Arg Cys Thr Leu Leu His Val Phe Ser Ala Leu Ser
      50                      55                      60

ttt tca tct ggt tta caa atg aaa agc ggt att gag caa att aag gta 240
Phe Ser Ser Gly Leu Gln Met Lys Ser Gly Ile Glu Gln Ile Lys Val
      65                      70                      75                      80

gac gca att acg cct gaa gaa gca gca gtc tta aat gca tta cag tat 288
Asp Ala Ile Thr      85      Glu Glu Ala Ala Val Leu Asn Ala Leu Gln Tyr
                                90                      95

ttg gaa tca att gct aat aag agt tac agc tat gtc tta cgt gaa ttg 336
Leu Glu Ser Ile Ala Asn Lys Ser Tyr Ser Tyr Val Leu Arg Glu Leu
      100                      105                      110

gct act cca gaa gaa gtt gat aat gca ttt gat tgg gct aac aat agt 384
Ala Thr Pro Glu Glu Val Asp Asn Ala Phe Asp Trp Ala Asn Asn Ser
      115                      120                      125

cct tat ttg caa aag aag att cac att ttg aat aaa att tat caa cgt 432
Pro Tyr Leu Gln Lys Lys Ile His Ile Leu Asn Lys Ile Tyr Gln Arg
      130                      135                      140

ggg gat gcc ttg caa aag aaa gct ggc aat gta att ttg gaa aca gct 480
Gly Asp Ala Leu Gln Lys Lys Ala Gly Asn Val Ile Leu Glu Thr Ala
      145                      150                      155                      160

ctt tat cat tca ggc ttt ttt gct cca ctt tac cta ttt ggg caa ggc 528
Leu Tyr His Ser Gly Phe Phe Ala Pro Leu Tyr Leu Phe Gly Gln Gly
      165                      170                      175

aag atg gtt aga act gct gaa att atc aaa tta gct cta cgc ggc aca 576
Lys Met Val Arg Thr Ala Glu Ile Ile Lys Leu Ala Leu Arg Gly Thr
      180                      185                      190

tca ttc agt ggt att tat cct ggt tat aag ttc cgt ctt ggc tat aaa 624
Ser Phe Ser Gly Ile Tyr Pro Gly Tyr Lys Phe Arg Leu Gly Tyr Lys
      195                      200                      205

aag tta ggc aaa acc gaa caa gag gac ctt aag cat tgg att gat aac 672
Lys Leu Gly Lys Thr Glu Gln Glu Asp Leu Lys His Trp Ile Asp Asn
      210                      215                      220

ttg tat gat gaa ctt gtg aaa aac gaa gaa aaa cac atc aga tta ctc 720
Leu Tyr Asp Glu Leu Val Lys Asn Glu Glu Lys His Ile Arg Leu Leu
      225                      230                      235                      240

tac aaa ggg aca ggt tgg act gaa gat gct tta cac tac atg tat tat 768
Tyr Lys Gly Thr Gly Trp Thr Glu Asp Ala Leu His Tyr Met Tyr Tyr
      245                      250                      255

agt gta aat aaa gct tac tta aac tta gga ttc cca ggg aaa tat cct 816
Ser Val Asn Lys Ala Tyr Leu Asn Leu Gly Phe Pro Gly Lys Tyr Pro
      260                      265                      270

```

gat aca tca gac aca atc aat cca gtt ctt gaa caa ggt gta att aaa 864
Asp Thr Ser Asp Thr Ile Asn Pro Val Leu Glu Gln Gly Val Ile Lys
275 280 285

agt gcg gta ttt gaa gat ttc ttc tac tac act aat gat cac agc tta 912
Ser Ala Val Phe Glu Asp Phe Phe Tyr Tyr Thr Asn Asp His Ser Leu
290 295 300

aat aaa ttc aaa gaa att aag 933
Asn Lys Phe Lys Glu Ile Lys
305 310

<210> 208

<211> 311

<212> PRT

<213> Lactobacillus acidophilus

<400> 208

Met Thr Lys Lys Tyr Tyr Glu Ala Ile Asn Trp Asn Asp Met Glu Asp
1 5 10 15
Lys Val Asp Lys Ser Ala Trp Ala Arg Leu Asn Asp Ile Ile Trp Glu
20 25 30
Pro Arg His Val Pro Val Lys Glu Asp Lys Lys Glu Phe Leu Gln Leu
35 40 45
Pro Ser Pro Val Arg Cys Thr Leu Leu His Val Phe Ser Ala Leu Ser
50 55 60
Phe Ser Ser Gly Leu Gln Met Lys Ser Gly Ile Glu Gln Ile Lys Val
65 70 75 80
Asp Ala Ile Thr Pro Glu Glu Ala Ala Val Leu Asn Ala Leu Gln Tyr
85 90 95
Leu Glu Ser Ile Ala Asn Lys Ser Tyr Ser Tyr Val Leu Arg Glu Leu
100 105 110
Ala Thr Pro Glu Glu Val Asp Asn Ala Phe Asp Trp Ala Asn Asn Ser
115 120 125
Pro Tyr Leu Gln Lys Lys Ile His Ile Leu Asn Lys Ile Tyr Gln Arg
130 135 140
Gly Asp Ala Leu Gln Lys Lys Ala Gly Asn Val Ile Leu Glu Thr Ala
145 150 155 160
Leu Tyr His Ser Gly Phe Phe Ala Pro Leu Tyr Leu Phe Gly Gln Gly
165 170 175
Lys Met Val Arg Thr Ala Glu Ile Ile Lys Leu Ala Leu Arg Gly Thr
180 185 190
Ser Phe Ser Gly Ile Tyr Pro Gly Tyr Lys Phe Arg Leu Gly Tyr Lys
195 200 205
Lys Leu Gly Lys Thr Glu Gln Glu Asp Leu Lys His Trp Ile Asp Asn
210 215 220
Leu Tyr Asp Glu Leu Val Lys Asn Glu Glu Lys His Ile Arg Leu Leu
225 230 235 240
Tyr Lys Gly Thr Gly Trp Thr Glu Asp Ala Leu His Tyr Met Tyr Tyr
245 250 255
Ser Val Asn Lys Ala Tyr Leu Asn Leu Gly Phe Pro Gly Lys Tyr Pro
260 265 270
Asp Thr Ser Asp Thr Ile Asn Pro Val Leu Glu Gln Gly Val Ile Lys
275 280 285
Ser Ala Val Phe Glu Asp Phe Phe Tyr Tyr Thr Asn Asp His Ser Leu
290 295 300

Asn Lys Phe Lys Glu Ile Lys
305 310

<210> 209
<211> 531
<212> DNA
<213> Lactobacillus acidophilus

<220>
<221> misc_feature
<222> (0)...(0)
<223> ORF 1751

<220>
<221> CDS
<222> (1)...(531)

<400> 209
ttg aag att aat tta aaa gat tta aat gat aaa att aaa aat caa gat 48
Met Lys Ile Asn Leu Lys Asp Leu Asn Asp Lys Ile Lys Asn Gln Asp
1 5 10 15
tac atc caa gat ctt gag aca gtt aaa tat gct gat ata agt aaa tct 96
Tyr Ile Gln Asp Leu Glu Thr Val Lys Tyr Ala Asp Ile Ser Lys Ser
20 25 30
aaa agc aaa atc aaa cca tat gca gaa aag atg att aaa gaa gtt ttg 144
Lys Ser Lys Ile Lys Pro Tyr Ala Glu Lys Met Ile Lys Glu Val Leu
35 40 45
gct gca tat aag cat gat tca ctg gta caa acc cag tta gca gtg att 192
Ala Ala Tyr Lys His Asp Ser Leu Val Gln Thr Gln Leu Ala Val Ile
50 55 60
ggg cag cgt cca gtt acc ttt gca tta gag acg aat att att aac ttg 240
Gly Gln Arg Pro Val Thr Phe Ala Leu Glu Thr Asn Ile Ile Asn Leu
65 70 75 80
cct tat gct aat tat aag aaa att gct aat ttc ttt gaa gaa ggt caa 288
Pro Tyr Ala Asn Tyr Lys Lys Ile Ala Asn Phe Phe Glu Glu Gly Gln
85 90 95
gaa tat ccg atc aat gtt tat ttt gag aca cgt tca gaa tat gtg aat 336
Glu Tyr Pro Ile Asn Val Tyr Phe Glu Thr Arg Ser Glu Tyr Val Asn
100 105 110
gta tct ggc ttt aga att gat caa ctt gct agc gaa gaa gaa gtt gaa 384
Val Ser Gly Phe Arg Ile Asp Gln Leu Ala Ser Glu Glu Glu Val Glu
115 120 125
aaa gat agc agt gca att gtt gat aag tta gtt gaa gca att att gaa 432
Lys Asp Ser Ser Ala Ile Val Asp Lys Leu Val Glu Ala Ile Ile Glu
130 135 140
aaa ttg acc gta gtc cgt gaa tat aaa aag cct gaa aaa act aaa act 480

Lys Leu Thr Val Val Arg Glu Tyr Lys Lys Pro Glu Lys Thr Lys Thr
 145 150 155 160
 gaa agt aag gaa aag acg aca act act aaa aag aaa acg aca act aag 528
 Glu Ser Lys Glu Lys Thr Thr Thr Thr Lys Lys Lys Thr Thr Thr Lys
 165 170 175
 aag 531
 Lys

<210> 210
 <211> 177
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 210
 Met Lys Ile Asn Leu Lys Asp Leu Asn Asp Lys Ile Lys Asn Gln Asp
 1 5 10 15
 Tyr Ile Gln Asp Leu Glu Thr Val Lys Tyr Ala Asp Ile Ser Lys Ser
 20 25 30
 Lys Ser Lys Ile Lys Pro Tyr Ala Glu Lys Met Ile Lys Glu Val Leu
 35 40 45
 Ala Ala Tyr Lys His Asp Ser Leu Val Gln Thr Gln Leu Ala Val Ile
 50 55 60
 Gly Gln Arg Pro Val Thr Phe Ala Leu Glu Thr Asn Ile Ile Asn Leu
 65 70 75 80
 Pro Tyr Ala Asn Tyr Lys Lys Ile Ala Asn Phe Phe Glu Glu Gly Gln
 85 90 95
 Glu Tyr Pro Ile Asn Val Tyr Phe Glu Thr Arg Ser Glu Tyr Val Asn
 100 105 110
 Val Ser Gly Phe Arg Ile Asp Gln Leu Ala Ser Glu Glu Val Glu
 115 120 125
 Lys Asp Ser Ser Ala Ile Val Asp Lys Leu Val Glu Ala Ile Ile Glu
 130 135 140
 Lys Leu Thr Val Val Arg Glu Tyr Lys Lys Pro Glu Lys Thr Lys Thr
 145 150 155 160
 Glu Ser Lys Glu Lys Thr Thr Thr Thr Lys Lys Lys Thr Thr Thr Lys
 165 170 175
 Lys

<210> 211
 <211> 720
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1752

<220>
 <221> CDS

<222> (1)...(720)

<400> 211

atg aac aac atg aaa cac aaa aaa act aat tac aaa tat tta tat ata	48
Met Asn Asn Met Lys His Lys Lys Thr Asn Tyr Lys Tyr Leu Tyr Ile	
1 5 10 15	
att att cca aca gct tta atc ctc gtt atg ggc tta gct tat atc cta	96
Ile Ile Pro Thr Ala Leu Ile Leu Val Met Gly Leu Ala Tyr Ile Leu	
20 25 30	
gtt aaa aat aaa att gat aat gaa ttt aac tgg att tca atg aaa gaa	144
Val Lys Asn Lys Ile Asp Asn Glu Phe Asn Trp Ile Ser Met Lys Glu	
35 40 45	
gaa caa aag tta aat gtg ccc att gaa aat caa atg cca gat tta cct	192
Glu Gln Lys Leu Asn Val Pro Ile Glu Asn Gln Met Pro Asp Leu Pro	
50 55 60	
aac ggc tgt gaa gta act agt tta tca atg cta atg aat tat tat ggc	240
Asn Gly Cys Glu Val Thr Ser Leu Ser Met Leu Met Asn Tyr Tyr Gly	
65 70 75 80	
att aga gta act aaa aat gaa tta gct caa aat atc cag cat gtc agt	288
Ile Arg Val Thr Lys Asn Glu Leu Ala Gln Asn Ile Gln His Val Ser	
85 90 95	
tcc ttt acc aat aat ggt aaa tat aga ggc aat cca aat caa gga ttt	336
Ser Phe Thr Asn Asn Gly Lys Tyr Arg Gly Asn Pro Asn Gln Gly Phe	
100 105 110	
gtt ggt tat atg tcc att gaa aat gca gga tgg tgt gtt tat aat ggg	384
Val Gly Tyr Met Ser Ile Glu Asn Ala Gly Trp Cys Val Tyr Asn Gly	
115 120 125	
ccg ctt tat aac gtt gca cgt aaa tat act aac cgt att caa aat gca	432
Pro Leu Tyr Asn Val Ala Arg Lys Tyr Thr Asn Arg Ile Gln Asn Ala	
130 135 140	
aca ggg agc gat ttt tta agt ata tta aag ctc gta tca gat ggt cat	480
Thr Gly Ser Asp Phe Leu Ser Ile Leu Lys Leu Val Ser Asp Gly His	
145 150 155 160	
ccg gtt ttg att att act acc act act ttt aat cgt gtt aat aat atg	528
Pro Val Leu Ile Ile Thr Thr Thr Thr Phe Asn Arg Val Asn Asn Met	
165 170 175	
caa act tgg gaa act aac acc gga aaa gta aat gta act cca tct tct	576
Gln Thr Trp Glu Thr Asn Thr Gly Lys Val Asn Val Thr Pro Ser Ser	
180 185 190	
cat gcc tgc gta att act ggt tat gac aag aaa aaa agg att gtt tat	624
His Ala Cys Val Ile Thr Gly Tyr Asp Lys Lys Lys Arg Ile Val Tyr	
195 200 205	
tta aac aat cct tat ggt att aaa aat caa gct gtc aat tgg aat aat	672
Leu Asn Asn Pro Tyr Gly Ile Lys Asn Gln Ala Val Asn Trp Asn Asn	

210	215	220	
ctt gaa aat agc tat aat caa caa ggc aaa caa gca tta tac att aag	720		
Leu Glu Asn Ser Tyr Asn Gln Gln Gly Lys Gln Ala Leu Tyr Ile Lys			
225	230	235	240

<210> 212

<211> 240

<212> PRT

<213> Lactobacillus acidophilus

<400> 212

Met Asn Asn Met Lys His Lys Lys Thr Asn Tyr Lys Tyr Leu Tyr Ile	
1 5 10 15	
Ile Ile Pro Thr Ala Leu Ile Leu Val Met Gly Leu Ala Tyr Ile Leu	
20 25 30	
Val Lys Asn Lys Ile Asp Asn Glu Phe Asn Trp Ile Ser Met Lys Glu	
35 40 45	
Glu Gln Lys Leu Asn Val Pro Ile Glu Asn Gln Met Pro Asp Leu Pro	
50 55 60	
Asn Gly Cys Glu Val Thr Ser Leu Ser Met Leu Met Asn Tyr Tyr Gly	
65 70 75 80	
Ile Arg Val Thr Lys Asn Glu Leu Ala Gln Asn Ile Gln His Val Ser	
85 90 95	
Ser Phe Thr Asn Asn Gly Lys Tyr Arg Gly Asn Pro Asn Gln Gly Phe	
100 105 110	
Val Gly Tyr Met Ser Ile Glu Asn Ala Gly Trp Cys Val Tyr Asn Gly	
115 120 125	
Pro Leu Tyr Asn Val Ala Arg Lys Tyr Thr Asn Arg Ile Gln Asn Ala	
130 135 140	
Thr Gly Ser Asp Phe Leu Ser Ile Leu Lys Leu Val Ser Asp Gly His	
145 150 155 160	
Pro Val Leu Ile Ile Thr Thr Thr Thr Phe Asn Arg Val Asn Asn Met	
165 170 175	
Gln Thr Trp Glu Thr Asn Thr Gly Lys Val Asn Val Thr Pro Ser Ser	
180 185 190	
His Ala Cys Val Ile Thr Gly Tyr Asp Lys Lys Lys Arg Ile Val Tyr	
195 200 205	
Leu Asn Asn Pro Tyr Gly Ile Lys Asn Gln Ala Val Asn Trp Asn Asn	
210 215 220	
Leu Glu Asn Ser Tyr Asn Gln Gln Gly Lys Gln Ala Leu Tyr Ile Lys	
225 230 235 240	

<210> 213

<211> 315

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1753

<220>

<221> CDS

<222> (1)...(315)

<400> 213

```

atg att gga gaa aaa atg agc gat aaa gaa aag gaa att tat aac gct 48
Met Ile Gly Glu Lys Met Ser Asp Lys Glu Lys Glu Ile Tyr Asn Ala
  1             5             10             15

tta aaa aca gta ata gat cct gaa tta acc gta aac tta gta gat tta 96
Leu Lys Thr Val Ile Asp Pro Glu Leu Thr Val Asn Leu Val Asp Leu
          20             25             30

ggg ttc att tat gat att cag gtt gaa gat agg act gca ata atc aaa 144
Gly Phe Ile Tyr Asp Ile Gln Val Glu Asp Arg Thr Ala Ile Ile Lys
          35             40             45

atg act tta aca att atg ggt tgt ccg cta act gag ctt ttg aat aaa 192
Met Thr Leu Thr Ile Met Gly Cys Pro Leu Thr Glu Leu Leu Asn Lys
          50             55             60

gag atc act acc gca gtc act ttt gtt cct caa atc gaa aag tgc aaa 240
Glu Ile Thr Thr Ala Val Thr Phe Val Pro Gln Ile Glu Lys Cys Lys
          65             70             75             80

atc aac tta gtt tgg tat cct caa tgg act cca gat aag atg agc cgt 288
Ile Asn Leu Val Trp Tyr Pro Gln Trp Thr Pro Asp Lys Met Ser Arg
          85             90             95

gca gct aga ctc atc tta gga ata cat 315
Ala Ala Arg Leu Ile Leu Gly Ile His
          100             105

```

<210> 214

<211> 105

<212> PRT

<213> Lactobacillus acidophilus

<400> 214

```

Met Ile Gly Glu Lys Met Ser Asp Lys Glu Lys Glu Ile Tyr Asn Ala
  1             5             10             15
Leu Lys Thr Val Ile Asp Pro Glu Leu Thr Val Asn Leu Val Asp Leu
          20             25             30
Gly Phe Ile Tyr Asp Ile Gln Val Glu Asp Arg Thr Ala Ile Ile Lys
          35             40             45
Met Thr Leu Thr Ile Met Gly Cys Pro Leu Thr Glu Leu Leu Asn Lys
          50             55             60
Glu Ile Thr Thr Ala Val Thr Phe Val Pro Gln Ile Glu Lys Cys Lys
          65             70             75             80
Ile Asn Leu Val Trp Tyr Pro Gln Trp Thr Pro Asp Lys Met Ser Arg
          85             90             95
Ala Ala Arg Leu Ile Leu Gly Ile His
          100             105

```

<210> 215

<211> 294
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1754

<220>
 <221> CDS
 <222> (1)...(294)

<400> 215
 atg gtg aag gcg cac gtt gaa tgc gat acg att atc atg gac gat atg 48
 Met Val Lys Ala His Val Glu Cys Asp Thr Ile Ile Met Asp Asp Met
 1 5 10 15
 tct tct tct gat acc att cct aca aat tca att gaa aac tct aat gtt 96
 Ser Ser Ser Asp Thr Ile Pro Thr Asn Ser Ile Glu Asn Ser Asn Val
 20 25 30
 gct atg gaa cat gag gca act gta tca aaa att tct gaa gaa gag ctg 144
 Ala Met Glu His Glu Ala Thr Val Ser Lys Ile Ser Glu Glu Glu Leu
 35 40 45
 tat tat ttg caa agc cgt ggg att cca gaa aga aaa gcc act gaa atg 192
 Tyr Tyr Leu Gln Ser Arg Gly Ile Pro Glu Arg Lys Ala Thr Glu Met
 50 55 60
 atc att atg gga ttt gtt gaa ccg ttt act aag caa tta cca atg gaa 240
 Ile Ile Met Gly Phe Val Glu Pro Phe Thr Lys Gln Leu Pro Met Glu
 65 70 75 80
 tat gca gtt gag tta aat cgt tta att agt ttc caa atg gag gga gca 288
 Tyr Ala Val Glu Leu Asn Arg Leu Ile Ser Phe Gln Met Glu Gly Ala
 85 90 95
 att gga 294
 Ile Gly

<210> 216
 <211> 98
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 216
 Met Val Lys Ala His Val Glu Cys Asp Thr Ile Ile Met Asp Asp Met
 1 5 10 15
 Ser Ser Ser Asp Thr Ile Pro Thr Asn Ser Ile Glu Asn Ser Asn Val
 20 25 30
 Ala Met Glu His Glu Ala Thr Val Ser Lys Ile Ser Glu Glu Glu Leu
 35 40 45
 Tyr Tyr Leu Gln Ser Arg Gly Ile Pro Glu Arg Lys Ala Thr Glu Met

```

      50      55      60
Ile Ile Met Gly Phe Val Glu Pro Phe Thr Lys Gln Leu Pro Met Glu
65      70      75      80
Tyr Ala Val Glu Leu Asn Arg Leu Ile Ser Phe Gln Met Glu Gly Ala
      85      90      95
Ile Gly

```

```

<210> 217
<211> 228
<212> DNA
<213> Lactobacillus acidophilus

```

```

<220>
<221> misc_feature
<222> (0)...(0)
<223> ORF 1755 - abs transporter

```

```

<220>
<221> CDS
<222> (1)...(228)

```

```

<400> 217
atg gcc gtt tta gaa att aaa gat ttg cat gtt gaa gta aaa gat aaa      48
Met Ala Val Leu Glu Ile Lys Asp Leu His Val Glu Val Lys Asp Lys
  1          5          10          15

gaa gaa aat aca cag aaa aaa atc tta aaa ggt ata aat tta act ctt      96
Glu Glu Asn Thr Gln Lys Lys Ile Leu Lys Gly Ile Asn Leu Thr Leu
          20          25          30

aaa act gga gaa att cac gca att atg gga ccc aat ggg acg ggt aag      144
Lys Thr Gly Glu Ile His Ala Ile Met Gly Pro Asn Gly Thr Gly Lys
          35          40          45

tct act tta tca gag acg att atg ggc aat cct aaa tat cat gtt ata      192
Ser Thr Leu Ser Glu Thr Ile Met Gly Asn Pro Lys Tyr His Val Ile
          50          55          60

caa ggc aaa ctt ctt tta aat ggt gaa ggc gca cgt      228
Gln Gly Lys Leu Leu Leu Asn Gly Glu Gly Ala Arg
  65          70          75

```

```

<210> 218
<211> 76
<212> PRT
<213> Lactobacillus acidophilus

```

```

<400> 218
Met Ala Val Leu Glu Ile Lys Asp Leu His Val Glu Val Lys Asp Lys
  1          5          10          15
Glu Glu Asn Thr Gln Lys Lys Ile Leu Lys Gly Ile Asn Leu Thr Leu
          20          25          30
Lys Thr Gly Glu Ile His Ala Ile Met Gly Pro Asn Gly Thr Gly Lys

```

```

          35          40          45
Ser Thr Leu Ser Glu Thr Ile Met Gly Asn Pro Lys Tyr His Val Ile
      50          55          60
Gln Gly Lys Leu Leu Leu Asn Gly Glu Gly Ala Arg
65          70          75

```

<210> 219
 <211> 156
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1756

<220>
 <221> CDS
 <222> (1)...(156)

```

<400> 219
gtg gca agt acg gga agt act gat gtt gga cat act gat gtg aac agt   48
Met Ala Ser Thr Gly Ser Thr Asp Val Gly His Thr Asp Val Asn Ser
  1          5          10          15

tta atg tcc aca tat gct tta tgc atg tgc ctt gag ttt ttg tca atg   96
Leu Met Ser Thr Tyr Ala Leu Cys Met Cys Leu Glu Phe Leu Ser Met
      20          25          30

aat att gat aaa gat atg aag aac caa aca gta ata tat att gct gtt   144
Asn Ile Asp Lys Asp Met Lys Asn Gln Thr Val Ile Tyr Ile Ala Val
      35          40          45

tgg ttc ttt ttt   156
Trp Phe Phe Phe
      50

```

<210> 220
 <211> 52
 <212> PRT
 <213> Lactobacillus acidophilus

```

<400> 220
Met Ala Ser Thr Gly Ser Thr Asp Val Gly His Thr Asp Val Asn Ser
  1          5          10          15
Leu Met Ser Thr Tyr Ala Leu Cys Met Cys Leu Glu Phe Leu Ser Met
      20          25          30
Asn Ile Asp Lys Asp Met Lys Asn Gln Thr Val Ile Tyr Ile Ala Val
      35          40          45
Trp Phe Phe Phe
      50

```

<210> 221

<211> 483
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1757

<220>
 <221> CDS
 <222> (1)...(483)

<400> 221
 atg cca ttt tgg tta gaa gtt gta att aat gtt gcg ttt tct tat cta 48
 Met Pro Phe Trp Leu Glu Val Val Ile Asn Val Ala Phe Ser Tyr Leu
 1 5 10 15
 gct tca gtt ggc ttt gct cta aca att aat gtg ccg cat cgt gcc tta 96
 Ala Ser Val Gly Phe Ala Leu Thr Ile Asn Val Pro His Arg Ala Leu
 20 25 30
 aat ttg tcc gga att agt ggg aca gtt ggc tgg atg gct tat tgg ttt 144
 Asn Leu Ser Gly Ile Ser Gly Thr Val Gly Trp Met Ala Tyr Trp Phe
 35 40 45
 tgt ttt cgt tta ggt gct ggt cga atg gca tct aat tta atc ggt gca 192
 Cys Phe Arg Leu Gly Ala Gly Arg Met Ala Ser Asn Leu Ile Gly Ala
 50 55 60
 ttt ttg att gga att ttg ggt tta gtt ttt gcc aga ata aaa aag tgt 240
 Phe Leu Ile Gly Ile Leu Gly Leu Val Phe Ala Arg Ile Lys Lys Cys
 65 70 75 80
 ccc gta aca gtg ttt aat att cca gct ttg gtt cca ttg gtg cca ggg 288
 Pro Val Thr Val Phe Asn Ile Pro Ala Leu Val Pro Leu Val Pro Gly
 85 90 95
 atg cct gcg tat cag gca gtt cga gcg ttt gta gtt gga gat tat att 336
 Met Pro Ala Tyr Gln Ala Val Arg Ala Phe Val Val Gly Asp Tyr Ile
 100 105 110
 caa ggt cag gaa cta att ttg cgt gta gca att gtt aca ggc gca att 384
 Gln Gly Gln Glu Leu Ile Leu Arg Val Ala Ile Val Thr Gly Ala Ile
 115 120 125
 ggc tta ggc ttc tta ctt tca acc atg tgt aca gaa gct ttt tat aag 432
 Gly Leu Gly Phe Leu Leu Ser Thr Met Cys Thr Glu Ala Phe Tyr Lys
 130 135 140
 ata aga tat cgt cat ttt aga aac aca gga ctg tac ttt aag cgg aaa 480
 Ile Arg Tyr Arg His Phe Arg Asn Thr Gly Leu Tyr Phe Lys Arg Lys
 145 150 155 160
 aaa 483
 Lys

<210> 222
 <211> 161
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 222
 Met Pro Phe Trp Leu Glu Val Val Ile Asn Val Ala Phe Ser Tyr Leu
 1 5 10 15
 Ala Ser Val Gly Phe Ala Leu Thr Ile Asn Val Pro His Arg Ala Leu
 20 25 30
 Asn Leu Ser Gly Ile Ser Gly Thr Val Gly Trp Met Ala Tyr Trp Phe
 35 40 45
 Cys Phe Arg Leu Gly Ala Gly Arg Met Ala Ser Asn Leu Ile Gly Ala
 50 55 60
 Phe Leu Ile Gly Ile Leu Gly Leu Val Phe Ala Arg Ile Lys Lys Cys
 65 70 75 80
 Pro Val Thr Val Phe Asn Ile Pro Ala Leu Val Pro Leu Val Pro Gly
 85 90 95
 Met Pro Ala Tyr Gln Ala Val Arg Ala Phe Val Val Gly Asp Tyr Ile
 100 105 110
 Gln Gly Gln Glu Leu Ile Leu Arg Val Ala Ile Val Thr Gly Ala Ile
 115 120 125
 Gly Leu Gly Phe Leu Leu Ser Thr Met Cys Thr Glu Ala Phe Tyr Lys
 130 135 140
 Ile Arg Tyr Arg His Phe Arg Asn Thr Gly Leu Tyr Phe Lys Arg Lys
 145 150 155 160
 Lys

<210> 223
 <211> 768
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1758

<220>
 <221> CDS
 <222> (1)...(768)

<400> 223
 atg tct gat aag cgg gat gct cga ttt tat caa gag gta tta gac att 48
 Met Ser Asp Lys Arg Asp Ala Arg Phe Tyr Gln Glu Val Leu Asp Ile
 1 5 10 15
 tgt tta act gca ggt cgt ctg atg att gaa ggc gga agc gaa atg tat 96
 Cys Leu Thr Ala Gly Arg Leu Met Ile Glu Gly Gly Ser Glu Met Tyr
 20 25 30

cga gtt gaa gat acc atg ctc aga att gct aga aac gcg gat att aat	144
Arg Val Glu Asp Thr Met Leu Arg Ile Ala Arg Asn Ala Asp Ile Asn	
35 40 45	
gat cca cgc gtt ttt gcg aca ccg act tgt gta ttt atg agc ctt gat	192
Asp Pro Arg Val Phe Ala Thr Pro Thr Cys Val Phe Met Ser Leu Asp	
50 55 60	
ggg gga aaa tta tct cag atg aag caa att cgt gat cga aat atc aat	240
Gly Gly Lys Leu Ser Gln Met Lys Gln Ile Arg Asp Arg Asn Ile Asn	
65 70 75 80	
tta gag ttg gtt gat cgc gta aat gaa tta tca aga gaa ttt gct act	288
Leu Glu Leu Val Asp Arg Val Asn Glu Leu Ser Arg Glu Phe Ala Thr	
85 90 95	
aaa aaa att gat tta tca gaa ttg aaa aat cgc att att gag gtt gct	336
Lys Lys Ile Asp Leu Ser Glu Leu Lys Asn Arg Ile Ile Glu Val Ala	
100 105 110	
aat gca cca tca ttt cca atg tgg atg cag ata att ggt gcg gcc gta	384
Asn Ala Pro Ser Phe Pro Met Trp Met Gln Ile Ile Gly Ala Ala Val	
115 120 125	
ctt agt gcc acc ttg atg gtt tta ttt atg gat gat tat gat tgg gta	432
Leu Ser Ala Thr Leu Met Val Leu Phe Met Asp Asp Tyr Asp Trp Val	
130 135 140	
gat ttt ccc ggt gca gct ctt gta gga gca att ggc ttt tgg gca tat	480
Asp Phe Pro Gly Ala Ala Leu Val Gly Ala Ile Gly Phe Trp Ala Tyr	
145 150 155 160	
tat gaa ttt aaa aag tat act aaa gtt cga ttt ttg tcg gaa tta atc	528
Tyr Glu Phe Lys Lys Tyr Thr Lys Val Arg Phe Leu Ser Glu Leu Ile	
165 170 175	
gct gca atg ata atg ggg gtc ttg gca ctt ggc tta aat tat ctt tat	576
Ala Ala Met Ile Met Gly Val Leu Ala Leu Gly Leu Asn Tyr Leu Tyr	
180 185 190	
cca aaa atg att atc gat aat att cta att ggt gca ttg atg act ttg	624
Pro Lys Met Ile Ile Asp Asn Ile Leu Ile Gly Ala Leu Met Thr Leu	
195 200 205	
gtg ccg ggg tta gcg atg acg aat gct ttg cgc gac ctt ttt atg ggg	672
Val Pro Gly Leu Ala Met Thr Asn Ala Leu Arg Asp Leu Phe Met Gly	
210 215 220	
gat ctg ctg tct ggc atc gtt aga atg tgt gag gcc att tta agt gca	720
Asp Leu Leu Ser Gly Ile Val Arg Met Cys Glu Ala Ile Leu Ser Ala	
225 230 235 240	
tta gct tta ggt ggt ggc gtc ggt ctg gtt ttg aag ttt gtg gga gga	768
Leu Ala Leu Gly Gly Gly Val Gly Leu Val Leu Lys Phe Val Gly Gly	
245 250 255	

<210> 224
 <211> 256
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 224
 Met Ser Asp Lys Arg Asp Ala Arg Phe Tyr Gln Glu Val Leu Asp Ile
 1 5 10 15
 Cys Leu Thr Ala Gly Arg Leu Met Ile Glu Gly Gly Ser Glu Met Tyr
 20 25 30
 Arg Val Glu Asp Thr Met Leu Arg Ile Ala Arg Asn Ala Asp Ile Asn
 35 40 45
 Asp Pro Arg Val Phe Ala Thr Pro Thr Cys Val Phe Met Ser Leu Asp
 50 55 60
 Gly Gly Lys Leu Ser Gln Met Lys Gln Ile Arg Asp Arg Asn Ile Asn
 65 70 75 80
 Leu Glu Leu Val Asp Arg Val Asn Glu Leu Ser Arg Glu Phe Ala Thr
 85 90 95
 Lys Lys Ile Asp Leu Ser Glu Leu Lys Asn Arg Ile Ile Glu Val Ala
 100 105 110
 Asn Ala Pro Ser Phe Pro Met Trp Met Gln Ile Ile Gly Ala Ala Val
 115 120 125
 Leu Ser Ala Thr Leu Met Val Leu Phe Met Asp Asp Tyr Asp Trp Val
 130 135 140
 Asp Phe Pro Gly Ala Ala Leu Val Gly Ala Ile Gly Phe Trp Ala Tyr
 145 150 155 160
 Tyr Glu Phe Lys Lys Tyr Thr Lys Val Arg Phe Leu Ser Glu Leu Ile
 165 170 175
 Ala Ala Met Ile Met Gly Val Leu Ala Leu Gly Leu Asn Tyr Leu Tyr
 180 185 190
 Pro Lys Met Ile Ile Asp Asn Ile Leu Ile Gly Ala Leu Met Thr Leu
 195 200 205
 Val Pro Gly Leu Ala Met Thr Asn Ala Leu Arg Asp Leu Phe Met Gly
 210 215 220
 Asp Leu Leu Ser Gly Ile Val Arg Met Cys Glu Ala Ile Leu Ser Ala
 225 230 235 240
 Leu Ala Leu Gly Gly Gly Val Gly Leu Val Leu Lys Phe Val Gly Gly
 245 250 255

<210> 225
 <211> 1539
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1759 ATPase component of ABC transporter

<220>
 <221> CDS
 <222> (1)...(1539)

<400> 225

atg agt tta tta act gtt aaa gat tta ggt cag agt ttt att gat aag	48
Met Ser Leu Leu Thr Val Lys Asp Leu Gly Gln Ser Phe Ile Asp Lys	
1 5 10 15	
acc tta tat gaa gat gct aac ttt gtg tta aac aaa gaa gac cac atg	96
Thr Leu Tyr Glu Asp Ala Asn Phe Val Leu Asn Lys Glu Asp His Met	
20 25 30	
gga gtt acc gga caa aac ggt gtc ggc aaa tct act tta att aag att	144
Gly Val Thr Gly Gln Asn Gly Val Gly Lys Ser Thr Leu Ile Lys Ile	
35 40 45	
ttg act ggt gag atc ttg cct gat aat ggt caa gta aaa tgg caa aac	192
Leu Thr Gly Glu Ile Leu Pro Asp Asn Gly Gln Val Lys Trp Gln Asn	
50 55 60	
aaa att gat gtg ggt tat tta gat cag tat gct aaa tta gca cca ggt	240
Lys Ile Asp Val Gly Tyr Leu Asp Gln Tyr Ala Lys Leu Ala Pro Gly	
65 70 75 80	
gtg act atc cgc gga ttt tta cgt aca gcc ttt gat gat tta ttc caa	288
Val Thr Ile Arg Gly Phe Leu Arg Thr Ala Phe Asp Asp Leu Phe Gln	
85 90 95	
aaa gaa aaa gaa tta aat gag ctt tac act aaa tac gct gaa act agt	336
Lys Glu Lys Glu Leu Asn Glu Leu Tyr Thr Lys Tyr Ala Glu Thr Ser	
100 105 110	
gat gaa gat cta ctt gaa aaa gcg ggc aag gtg caa act tat cta gaa	384
Asp Glu Asp Leu Leu Glu Lys Ala Gly Lys Val Gln Thr Tyr Leu Glu	
115 120 125	
gaa aat aat ttc tac gat att gat act gaa att gaa caa gtc gca tct	432
Glu Asn Asn Phe Tyr Asp Ile Asp Thr Glu Ile Glu Gln Val Ala Ser	
130 135 140	
ggg ttg ggc tta gct gac tta ggc tat gac cat gac gtt tca aaa tta	480
Gly Leu Gly Leu Ala Asp Leu Gly Tyr Asp His Asp Val Ser Lys Leu	
145 150 155 160	
tca ggt ggt caa cgc tca aag att att ttg ggt aaa tta tta tta caa	528
Ser Gly Gly Gln Arg Ser Lys Ile Ile Leu Gly Lys Leu Leu Leu Gln	
165 170 175	
aat cca gat gtt tta gta tta gac gag cca acc aac tac ctt gat gtg	576
Asn Pro Asp Val Leu Val Leu Asp Glu Pro Thr Asn Tyr Leu Asp Val	
180 185 190	
tca cat att gat tgg cta gtt gat tat ttg aat aat ttt gaa ggt gcc	624
Ser His Ile Asp Trp Leu Val Asp Tyr Leu Asn Asn Phe Glu Gly Ala	
195 200 205	
ttt atc gtt gtc agt cac gat tac gat ttc tta ggt aga atc act aac	672
Phe Ile Val Val Ser His Asp Tyr Asp Phe Leu Gly Arg Ile Thr Asn	
210 215 220	
tgt att atc gac atc gac ttt ggt acg att acg cgt tat acc ggt acc	720

Cys Ile Ile Asp Ile Asp Phe Gly Thr Ile Thr Arg Tyr Thr Gly Thr	
225 230 235 240	
tta aag caa gcg atg cgc caa aaa gct gct aac cgt gaa act tac ctt	768
Leu Lys Gln Ala Met Arg Gln Lys Ala Ala Asn Arg Glu Thr Tyr Leu	
245 250 255	
aaa gcc tat gct aac cag caa cgc aag att gct aag act gaa gca tat	816
Lys Ala Tyr Ala Asn Gln Gln Arg Lys Ile Ala Lys Thr Glu Ala Tyr	
260 265 270	
att cgt aag aat aaa gct ggt acg cgt gct aag agt gca aaa tcg cgt	864
Ile Arg Lys Asn Lys Ala Gly Thr Arg Ala Lys Ser Ala Lys Ser Arg	
275 280 285	
gaa aag caa tta gct aga atg gac gtt tta act ccg cct aaa aat aat	912
Glu Lys Gln Leu Ala Arg Met Asp Val Leu Thr Pro Pro Lys Asn Asn	
290 295 300	
cgt cgg gcc aag ttc gaa ttt cca tat gta gca act gct tcc aat ttg	960
Arg Arg Ala Lys Phe Gln Phe Pro Tyr Val Ala Thr Ala Ser Asn Leu	
305 310 315 320	
ctt ttg caa acg caa gac ttg gtt att ggt tat gat cag gct tta gtt	1008
Leu Leu Gln Thr Gln Asp Leu Val Ile Gly Tyr Asp Gln Ala Leu Val	
325 330 335	
aag tct gca ttt aac ttc tca gtt ggc ggt gat gaa aaa gta gca att	1056
Lys Ser Ala Phe Asn Phe Ser Val Gly Gly Asp Glu Lys Val Ala Ile	
340 345 350	
acc ggt ttc aac gga atc ggt aaa act acc ctt ctt aag act ctt tta	1104
Thr Gly Phe Asn Gly Ile Gly Lys Thr Thr Leu Leu Lys Thr Leu Leu	
355 360 365	
ggt caa tta aag ccg atc tat ggt tca tat gac ttg tca gtt act gct	1152
Gly Gln Leu Lys Pro Ile Tyr Gly Ser Tyr Asp Leu Ser Val Thr Ala	
370 375 380	
aag ctt gct tat ttt aag cag gat tta aca tgg cct aac aac aat atg	1200
Lys Leu Ala Tyr Phe Lys Gln Asp Leu Thr Trp Pro Asn Asn Asn Met	
385 390 395 400	
aca ccg cta caa tac ttg caa gaa gaa ttt gaa cgt aaa aag cca aag	1248
Thr Pro Leu Gln Tyr Leu Gln Glu Glu Phe Glu Arg Lys Lys Pro Lys	
405 410 415	
gaa ttg cgt caa gcc tta gct aga atg gga tta act gcg caa caa gca	1296
Glu Leu Arg Gln Ala Leu Ala Arg Met Gly Leu Thr Ala Gln Gln Ala	
420 425 430	
atg agt ccg tta aag gag ctt tcc ggt ggg gaa cag gaa aaa gta aaa	1344
Met Ser Pro Leu Lys Glu Leu Ser Gly Gly Glu Gln Glu Lys Val Lys	
435 440 445	
tta gct aaa atg cag ttt gag cca gct aac ttg ctc ttt ctt gat gaa	1392
Leu Ala Lys Met Gln Phe Glu Pro Ala Asn Leu Leu Phe Leu Asp Glu	

450	455	460	
cct act aac cac ttg gat aac gat act aag gat gca ttg cgc aag gcg			1440
Pro Thr Asn His Leu Asp Asn Asp Thr Lys Asp Ala Leu Arg Lys Ala			
465	470	475	480
att atc aat ttc tca ggt gga gta att att gta agt cac gaa cgc gac			1488
Ile Ile Asn Phe Ser Gly Gly Val Ile Ile Val Ser His Glu Arg Asp			
	485	490	495
ttc ttc cgt ggt gac tgg att gat aaa aca atc gat att gaa aca atg			1536
Phe Phe Arg Gly Asp Trp Ile Asp Lys Thr Ile Asp Ile Glu Thr Met			
	500	505	510
aat			1539
Asn			

<210> 226

<211> 513

<212> PRT

<213> Lactobacillus acidophilus

<400> 226

Met Ser Leu Leu Thr Val Lys Asp Leu Gly Gln Ser Phe Ile Asp Lys			
1	5	10	15
Thr Leu Tyr Glu Asp Ala Asn Phe Val Leu Asn Lys Glu Asp His Met			
	20	25	30
Gly Val Thr Gly Gln Asn Gly Val Gly Lys Ser Thr Leu Ile Lys Ile			
	35	40	45
Leu Thr Gly Glu Ile Leu Pro Asp Asn Gly Gln Val Lys Trp Gln Asn			
	50	55	60
Lys Ile Asp Val Gly Tyr Leu Asp Gln Tyr Ala Lys Leu Ala Pro Gly			
65	70	75	80
Val Thr Ile Arg Gly Phe Leu Arg Thr Ala Phe Asp Asp Leu Phe Gln			
	85	90	95
Lys Glu Lys Glu Leu Asn Glu Leu Tyr Thr Lys Tyr Ala Glu Thr Ser			
	100	105	110
Asp Glu Asp Leu Leu Glu Lys Ala Gly Lys Val Gln Thr Tyr Leu Glu			
	115	120	125
Glu Asn Asn Phe Tyr Asp Ile Asp Thr Glu Ile Glu Gln Val Ala Ser			
	130	135	140
Gly Leu Gly Leu Ala Asp Leu Gly Tyr Asp His Asp Val Ser Lys Leu			
145	150	155	160
Ser Gly Gly Gln Arg Ser Lys Ile Ile Leu Gly Lys Leu Leu Leu Gln			
	165	170	175
Asn Pro Asp Val Leu Val Leu Asp Glu Pro Thr Asn Tyr Leu Asp Val			
	180	185	190
Ser His Ile Asp Trp Leu Val Asp Tyr Leu Asn Asn Phe Glu Gly Ala			
	195	200	205
Phe Ile Val Val Ser His Asp Tyr Asp Phe Leu Gly Arg Ile Thr Asn			
	210	215	220
Cys Ile Ile Asp Ile Asp Phe Gly Thr Ile Thr Arg Tyr Thr Gly Thr			
225	230	235	240
Leu Lys Gln Ala Met Arg Gln Lys Ala Ala Asn Arg Glu Thr Tyr Leu			
	245	250	255

Lys Ala Tyr Ala Asn Gln Gln Arg Lys Ile Ala Lys Thr Glu Ala Tyr
 260 265 270
 Ile Arg Lys Asn Lys Ala Gly Thr Arg Ala Lys Ser Ala Lys Ser Arg
 275 280 285
 Glu Lys Gln Leu Ala Arg Met Asp Val Leu Thr Pro Pro Lys Asn Asn
 290 295 300
 Arg Arg Ala Lys Phe Glu Phe Pro Tyr Val Ala Thr Ala Ser Asn Leu
 305 310 315 320
 Leu Leu Gln Thr Gln Asp Leu Val Ile Gly Tyr Asp Gln Ala Leu Val
 325 330 335
 Lys Ser Ala Phe Asn Phe Ser Val Gly Gly Asp Glu Lys Val Ala Ile
 340 345 350
 Thr Gly Phe Asn Gly Ile Gly Lys Thr Thr Leu Leu Lys Thr Leu Leu
 355 360 365
 Gly Gln Leu Lys Pro Ile Tyr Gly Ser Tyr Asp Leu Ser Val Thr Ala
 370 375 380
 Lys Leu Ala Tyr Phe Lys Gln Asp Leu Thr Trp Pro Asn Asn Asn Met
 385 390 395 400
 Thr Pro Leu Gln Tyr Leu Gln Glu Glu Phe Glu Arg Lys Lys Pro Lys
 405 410 415
 Glu Leu Arg Gln Ala Leu Ala Arg Met Gly Leu Thr Ala Gln Gln Ala
 420 425 430
 Met Ser Pro Leu Lys Glu Leu Ser Gly Gly Glu Gln Glu Lys Val Lys
 435 440 445
 Leu Ala Lys Met Gln Phe Glu Pro Ala Asn Leu Leu Phe Leu Asp Glu
 450 455 460
 Pro Thr Asn His Leu Asp Asn Asp Thr Lys Asp Ala Leu Arg Lys Ala
 465 470 475 480
 Ile Ile Asn Phe Ser Gly Gly Val Ile Ile Val Ser His Glu Arg Asp
 485 490 495
 Phe Phe Arg Gly Asp Trp Ile Asp Lys Thr Ile Asp Ile Glu Thr Met
 500 505 510
 Asn

<210> 227
 <211> 372
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1760

<220>
 <221> CDS
 <222> (1)...(372)

<400> 227
 atg caa aaa aaa gaa tct ata ttt ccg gtt gtc tat ggc gta att tct 48
 Met Gln Lys Lys Glu Ser Ile Phe Pro Val Val Tyr Gly Val Ile Ser
 1 5 10 15
 gcc att att tcc ttt att gca gcc atg ttt att tgc tta cgt agt ttt 96

Ala Ile Ile Ser Phe Ile Ala Ala Met Phe Ile Cys Leu Arg Ser Phe
 20 25 30

aga ttg aac tta caa gta tcg att atc gtt gca ggt att ttt gca att 144
 Arg Leu Asn Leu Gln Val Ser Ile Ile Val Ala Gly Ile Phe Ala Ile
 35 40 45

ttc ttc ttc ggc ctg tct tat ttt aga gga cat gca tca gtc gaa att 192
 Phe Phe Phe Gly Leu Ser Tyr Phe Arg Gly His Ala Ser Val Glu Ile
 50 55 60

aag cga att gtt tat aaa tat aag ctg aca gat caa gaa tta gcc aaa 240
 Lys Arg Ile Val Tyr Lys Tyr Lys Leu Thr Asp Gln Glu Leu Ala Lys
 65 70 75 80

att aca ggg atg aaa gct agc gat ttc cca att tat cat gat cgc ttg 288
 Ile Thr Gly Met Lys Ala Ser Asp Phe Pro Ile Tyr His Asp Arg Leu
 85 90 95

caa tta att tta cct aaa aga tat tgg cca cgg gtt ctt gat gca ctc 336
 Gln Leu Ile Leu Pro Lys Arg Tyr Trp Pro Arg Val Leu Asp Ala Leu
 100 105 110

caa aaa tac gaa aaa gag cgt gag tcg gca ggg gag 372
 Gln Lys Tyr Glu Lys Glu Arg Glu Ser Ala Gly Glu
 115 120

<210> 228

<211> 124

<212> PRT

<213> Lactobacillus acidophilus

<400> 228

Met Gln Lys Lys Glu Ser Ile Phe Pro Val Val Tyr Gly Val Ile Ser
 1 5 10 15

Ala Ile Ile Ser Phe Ile Ala Ala Met Phe Ile Cys Leu Arg Ser Phe
 20 25 30

Arg Leu Asn Leu Gln Val Ser Ile Val Ala Gly Ile Phe Ala Ile
 35 40 45

Phe Phe Phe Gly Leu Ser Tyr Phe Arg Gly His Ala Ser Val Glu Ile
 50 55 60

Lys Arg Ile Val Tyr Lys Tyr Lys Leu Thr Asp Gln Glu Leu Ala Lys
 65 70 75 80

Ile Thr Gly Met Lys Ala Ser Asp Phe Pro Ile Tyr His Asp Arg Leu
 85 90 95

Gln Leu Ile Leu Pro Lys Arg Tyr Trp Pro Arg Val Leu Asp Ala Leu
 100 105 110

Gln Lys Tyr Glu Lys Glu Arg Glu Ser Ala Gly Glu
 115 120

<210> 229

<211> 219

<212> DNA

<213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1761

<220>
 <221> CDS
 <222> (1)...(219)

<400> 229
 atg aaa ata aaa aag att aat ttt aaa ata aat gat tta aaa atc gaa 48
 Met Lys Ile Lys Lys Ile Asn Phe Lys Ile Asn Asp Leu Lys Ile Glu
 1 5 10 15
 tta gtt aaa cca caa att gaa cac gca aca gat ctt tat caa gct att 96
 Leu Val Lys Pro Gln Ile Glu His Ala Thr Asp Leu Tyr Gln Ala Ile
 20 25 30
 aaa cat gat caa aaa agc cta agc aaa tgg tta cct tgg gct tat gac 144
 Lys His Asp Gln Lys Ser Leu Ser Lys Trp Leu Pro Trp Ala Tyr Asp
 35 40 45
 att aat tca att caa gct gag gct aat ttt att aaa cag att cag aaa 192
 Ile Asn Ser Ile Gln Ala Glu Ala Asn Phe Ile Lys Gln Ile Gln Lys
 50 55 60
 aaa gaa gaa att att gct cta act att 219
 Lys Glu Glu Ile Ile Ala Leu Thr Ile
 65 70

<210> 230
 <211> 73
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 230
 Met Lys Ile Lys Lys Ile Asn Phe Lys Ile Asn Asp Leu Lys Ile Glu
 1 5 10 15
 Leu Val Lys Pro Gln Ile Glu His Ala Thr Asp Leu Tyr Gln Ala Ile
 20 25 30
 Lys His Asp Gln Lys Ser Leu Ser Lys Trp Leu Pro Trp Ala Tyr Asp
 35 40 45
 Ile Asn Ser Ile Gln Ala Glu Ala Asn Phe Ile Lys Gln Ile Gln Lys
 50 55 60
 Lys Glu Glu Ile Ile Ala Leu Thr Ile
 65 70

<210> 231
 <211> 1272
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature

<222> (0)...(0)

<223> ORF 1762

<220>

<221> CDS

<222> (1)...(1272)

<400> 231

atg gat cca aat tcc aaa cgt aga gaa gat tat cgc aaa cat tca tca	48
Met Asp Pro Asn Ser Lys Arg Arg Glu Asp Tyr Arg Lys His Ser Ser	
1 5 10 15	
tta aat ctt cat cgc aat cat gct ttg gca gca gat tct tca tct ttt	96
Leu Asn Leu His Arg Asn His Ala Leu Ala Ala Asp Ser Ser Ser Phe	
20 25 30	
aaa gcc ggt aac atg ttt gct cgt ttt att ggg gtg atc gcg tta tta	144
Lys Ala Gly Asn Met Phe Ala Arg Phe Ile Gly Val Ile Ala Leu Leu	
35 40 45	
acc gtt tgt ttc ggt gtg gca tgg gct gct cat atg tat ttc aca att	192
Thr Val Cys Phe Gly Val Ala Trp Ala Ala His Met Tyr Phe Thr Ile	
50 55 60	
cat agt gca gtt gat ggt aaa aat aat ggt aat gtt gcg aca tcc gct	240
His Ser Ala Val Asp Gly Lys Asn Asn Gly Asn Val Ala Thr Ser Ala	
65 70 75 80	
aaa att tcg act aga caa cca gtt tca gta ttg att ttg gga gtc gat	288
Lys Ile Ser Thr Arg Gln Pro Val Ser Val Leu Ile Leu Gly Val Asp	
85 90 95	
caa gga att gaa ggc cgt cat gac cga ggt aac tct gat act tta att	336
Gln Gly Ile Glu Gly Arg His Asp Arg Gly Asn Ser Asp Thr Leu Ile	
100 105 110	
tta gca aca gct aat ccg caa aaa aat aag gca acg atg aca tct att	384
Leu Ala Thr Ala Asn Pro Gln Lys Asn Lys Ala Thr Met Thr Ser Ile	
115 120 125	
cca cgt gat aca ttg gct gat att aaa ggt gat cca ggt gac aaa tac	432
Pro Arg Asp Thr Leu Ala Asp Ile Lys Gly Asp Pro Gly Asp Lys Tyr	
130 135 140	
ttc atg ttt agg gtt aac tca gct tat gaa atc ggt ggt agt gaa gca	480
Phe Met Phe Arg Val Asn Ser Ala Tyr Glu Ile Gly Gly Ser Glu Ala	
145 150 155 160	
agt atg aaa act gtc tca aat atg tta aac gta ccg ata aac tat tat	528
Ser Met Lys Thr Val Ser Asn Met Leu Asn Val Pro Ile Asn Tyr Tyr	
165 170 175	
tta gaa gtt aac atg aag gcg ctg cgc agt tta gtt aac gca gtg ggc	576
Leu Glu Val Asn Met Lys Ala Leu Arg Ser Leu Val Asn Ala Val Gly	
180 185 190	

ggc gtt gat gta aat gtg cct ttc gat ttc tca tat gat tgg tgt gac	624
Gly Val Asp Val Asn Val Pro Phe Asp Phe Ser Tyr Asp Trp Cys Asp	
195 200 205	
ttc cac aag ggt aag caa cac ttg aat ggt cgg cac gca gtt gct tat	672
Phe His Lys Gly Lys Gln His Leu Asn Gly Arg His Ala Val Ala Tyr	
210 215 220	
gtc cga atg aga aaa gaa gat ccg cga ggt gac tat ggt aga caa ctc	720
Val Arg Met Arg Lys Glu Asp Pro Arg Gly Asp Tyr Gly Arg Gln Leu	
225 230 235 240	
cgt cag cgt caa gta att gaa gca att gct cat aag gct atg tca gtt	768
Arg Gln Arg Gln Val Ile Glu Ala Ile Ala His Lys Ala Met Ser Val	
245 250 255	
aat aca att agt aac tat cgt aaa tta att gat att ttt aac aaa tat	816
Asn Thr Ile Ser Asn Tyr Arg Lys Leu Ile Asp Ile Phe Asn Lys Tyr	
260 265 270	
gtc aag act aac tta act ttt aac gat atg ctc agt tta gct ctt aac	864
Val Lys Thr Asn Leu Thr Phe Asn Asp Met Leu Ser Leu Ala Leu Asn	
275 280 285	
tac cgt ggt tgt atg ggt aat tta gat agt ggc tat att caa ggt cat	912
Tyr Arg Gly Cys Met Gly Asn Leu Asp Ser Gly Tyr Ile Gln Gly His	
290 295 300	
gat gct tgg att gac ggt tcg tca att caa gta gcc cca act gca gaa	960
Asp Ala Trp Ile Asp Gly Ser Ser Ile Gln Val Ala Pro Thr Ala Glu	
305 310 315 320	
tta caa aaa att tca aat aag ctc aga aag aat ctg aat tta ccg gct	1008
Leu Gln Lys Ile Ser Asn Lys Leu Arg Lys Asn Leu Asn Leu Pro Ala	
325 330 335	
gaa aca ctt gat aat gaa gaa act cgt caa aat gat ttg aat gat caa	1056
Glu Thr Leu Asp Asn Glu Glu Thr Arg Gln Asn Asp Leu Asn Asp Gln	
340 345 350	
aat aac cat gta aaa tgg gat gat cct cag gca ttt act act tat cgt	1104
Asn Asn His Val Lys Trp Asp Asp Pro Gln Ala Phe Thr Thr Tyr Arg	
355 360 365	
att tat gag caa aat gca gat aag cca gcg ggc ggt tca aat tca ggc	1152
Ile Tyr Glu Gln Asn Ala Asp Lys Pro Ala Gly Gly Ser Asn Ser Gly	
370 375 380	
tat ggt gaa aat aaa gat acc aat tca ggt agt tca acc act tcc tct	1200
Tyr Gly Glu Asn Lys Asp Thr Asn Ser Gly Ser Ser Thr Thr Ser Ser	
385 390 395 400	
agt atg tcg agt tca tcg gac tca tta ggt agc tca tct tcg tct agt	1248
Ser Met Ser Ser Ser Asp Ser Leu Gly Ser Ser Ser Ser Ser Ser	
405 410 415	
agt aag act tgg aaa ttt cat tgg	1272

Ser Lys Thr Trp Lys Phe His Trp
420

<210> 232

<211> 424

<212> PRT

<213> Lactobacillus acidophilus

<400> 232

Met Asp Pro Asn Ser Lys Arg Arg Glu Asp Tyr Arg Lys His Ser Ser
1 5 10 15
Leu Asn Leu His Arg Asn His Ala Leu Ala Ala Asp Ser Ser Ser Phe
20 25 30
Lys Ala Gly Asn Met Phe Ala Arg Phe Ile Gly Val Ile Ala Leu Leu
35 40 45
Thr Val Cys Phe Gly Val Ala Trp Ala Ala His Met Tyr Phe Thr Ile
50 55 60
His Ser Ala Val Asp Gly Lys Asn Asn Gly Asn Val Ala Thr Ser Ala
65 70 75 80
Lys Ile Ser Thr Arg Gln Pro Val Ser Val Leu Ile Leu Gly Val Asp
85 90 95
Gln Gly Ile Glu Gly Arg His Asp Arg Gly Asn Ser Asp Thr Leu Ile
100 105 110
Leu Ala Thr Ala Asn Pro Gln Lys Asn Lys Ala Thr Met Thr Ser Ile
115 120 125
Pro Arg Asp Thr Leu Ala Asp Ile Lys Gly Asp Pro Gly Asp Lys Tyr
130 135 140
Phe Met Phe Arg Val Asn Ser Ala Tyr Glu Ile Gly Gly Ser Glu Ala
145 150 155 160
Ser Met Lys Thr Val Ser Asn Met Leu Asn Val Pro Ile Asn Tyr Tyr
165 170 175
Leu Glu Val Asn Met Lys Ala Leu Arg Ser Leu Val Asn Ala Val Gly
180 185 190
Gly Val Asp Val Asn Val Pro Phe Asp Phe Ser Tyr Asp Trp Cys Asp
195 200 205
Phe His Lys Gly Lys Gln His Leu Asn Gly Arg His Ala Val Ala Tyr
210 215 220
Val Arg Met Arg Lys Glu Asp Pro Arg Gly Asp Tyr Gly Arg Gln Leu
225 230 235 240
Arg Gln Arg Gln Val Ile Glu Ala Ile Ala His Lys Ala Met Ser Val
245 250 255
Asn Thr Ile Ser Asn Tyr Arg Lys Leu Ile Asp Ile Phe Asn Lys Tyr
260 265 270
Val Lys Thr Asn Leu Thr Phe Asn Asp Met Leu Ser Leu Ala Leu Asn
275 280 285
Tyr Arg Gly Cys Met Gly Asn Leu Asp Ser Gly Tyr Ile Gln Gly His
290 295 300
Asp Ala Trp Ile Asp Gly Ser Ser Ile Gln Val Ala Pro Thr Ala Glu
305 310 315 320
Leu Gln Lys Ile Ser Asn Lys Leu Arg Lys Asn Leu Asn Leu Pro Ala
325 330 335
Glu Thr Leu Asp Asn Glu Glu Thr Arg Gln Asn Asp Leu Asn Asp Gln
340 345 350
Asn Asn His Val Lys Trp Asp Asp Pro Gln Ala Phe Thr Thr Tyr Arg
355 360 365
Ile Tyr Glu Gln Asn Ala Asp Lys Pro Ala Gly Gly Ser Asn Ser Gly

```

      370      375      380
Tyr Gly Glu Asn Lys Asp Thr Asn Ser Gly Ser Ser Thr Thr Ser Ser
385      390      395      400
Ser Met Ser Ser Ser Asp Ser Leu Gly Ser Ser Ser Ser Ser Ser
      405      410      415
Ser Lys Thr Trp Lys Phe His Trp
      420

```

```

<210> 233
<211> 1614
<212> DNA
<213> Lactobacillus acidophilus

```

```

<220>
<221> misc_feature
<222> (0)...(0)
<223> ORF 1917 - polysaccharide transporter

```

```

<220>
<221> CDS
<222> (1)...(1614)

```

```

<400> 233
ttg aat aaa aaa atc ctg tcc ggt tca ttt tgg cta tca ttt ggt agt 48
Met Asn Lys Lys Ile Leu Ser Gly Ser Phe Trp Leu Ser Phe Gly Ser
1 5 10 15

atc gtc tct aga att cta gga gtt gtt tat tta att cca tgg ctt atc 96
Ile Val Ser Arg Ile Leu Gly Val Val Tyr Leu Ile Pro Trp Leu Ile
20 25 30

atg ctt ggc agc tac cat aat cag cta aat gcg cag gcg tta ttc aat 144
Met Leu Gly Ser Tyr His Asn Gln Leu Asn Ala Gln Ala Leu Phe Asn
35 40 45

tca tct tat acg cca tat gcg ctt ttc tta tct att ggt act gcg ggc 192
Ser Ser Tyr Thr Pro Tyr Ala Leu Phe Leu Ser Ile Gly Thr Ala Gly
50 55 60

tta cct tca gtt att gcc cgg gaa gta tca caa tta aat tct cag aat 240
Leu Pro Ser Val Ile Ala Arg Glu Val Ser Gln Leu Asn Ser Gln Asn
65 70 75 80

aga tat aaa gac agc cta tat att aca aaa tta ggc tta att atc atg 288
Arg Tyr Lys Asp Ser Leu Tyr Ile Thr Lys Leu Gly Leu Ile Ile Met
85 90 95

ctt gta atg gga tta gca tgt ggt att ttg tta tac gct act gct cct 336
Leu Val Met Gly Leu Ala Cys Gly Ile Leu Leu Tyr Ala Thr Ala Pro
100 105 110

ata att gct aag aat agt cca gta gat tca gta gct agt gct act att 384
Ile Ile Ala Lys Asn Ser Pro Val Asp Ser Val Ala Ser Ala Thr Ile
115 120 125

```

tct atc cgc gta ttg gtt cca gct gta att att ttg cca tca atg agt	432
Ser Ile Arg Val Leu Val Pro Ala Val Ile Ile Leu Pro Ser Met Ser	
130 135 140	
atg gta aga gga tgg ttt cag ggg aac aac gat atg aag cca tac ggc	480
Met Val Arg Gly Trp Phe Gln Gly Asn Asn Asp Met Lys Pro Tyr Gly	
145 150 155 160	
att tcc caa tta tgg gaa caa ttt gcg cgc att cta ttt att ctt tta	528
Ile Ser Gln Leu Trp Glu Gln Phe Ala Arg Ile Leu Phe Ile Leu Leu	
165 170 175	
tct act tta tta gtg atc gaa gtt ttt cat cat aat tat gtg aca gca	576
Ser Thr Leu Leu Val Ile Glu Val Phe His His Asn Tyr Val Thr Ala	
180 185 190	
gtt tat ttt agt gta ttc ggt gca tgt gtg ggt gct att gcc agt tat	624
Val Tyr Phe Ser Val Phe Gly Ala Cys Val Gly Ala Ile Ala Ser Tyr	
195 200 205	
ttg tat ctt ttt gcg tat atg cgc aag aag tgg gga tac tat aag ggg	672
Leu Tyr Leu Phe Ala Tyr Met Arg Lys Lys Trp Gly Tyr Tyr Lys Gly	
210 215 220	
tta att gaa aaa agt aaa cca cgg gct tta aac aat gtt tat cga agc	720
Leu Ile Glu Lys Ser Lys Pro Arg Ala Leu Asn Asn Val Tyr Arg Ser	
225 230 235 240	
ttg ctt aat ctt tgg tat gca tca ata cca ttt gtt tta ctt ggt tca	768
Leu Leu Asn Leu Trp Tyr Ala Ser Ile Pro Phe Val Leu Leu Gly Ser	
245 250 255	
ttc att act gtt acg caa tta gtt gat caa ctt tta ttc aag cag att	816
Phe Ile Thr Val Thr Gln Leu Val Asp Gln Leu Leu Phe Lys Gln Ile	
260 265 270	
ttg att agt ttt aac cat atg agt agc caa tat gtg agc tat ttg tat	864
Leu Ile Ser Phe Asn His Met Ser Ser Gln Tyr Val Ser Tyr Leu Tyr	
275 280 285	
acc ata ttt tca gct aat cca agt aag atc acc aca gta ata att tct	912
Thr Ile Phe Ser Ala Asn Pro Ser Lys Ile Thr Thr Val Ile Ile Ser	
290 295 300	
ctt gct aca gca gtt tct gag act agt ttg cca ctt tta gct ggt ctt	960
Leu Ala Thr Ala Val Ser Glu Thr Ser Leu Pro Leu Leu Ala Gly Leu	
305 310 315 320	
aag tat aag tcc aag gat aat caa gga agc att aaa aag ctg ctt tta	1008
Lys Tyr Lys Ser Lys Asp Asn Gln Gly Ser Ile Lys Lys Leu Leu Leu	
325 330 335	
gag aac tat cgc ctt ctt ctt ttt gta tta ctt ccg tta gtg tca ctt	1056
Glu Asn Tyr Arg Leu Leu Leu Phe Val Leu Leu Pro Leu Val Ser Leu	
340 345 350	
gca gca ttt gct tct tcg cca att tat aca gta cta ttt tct cat gat	1104

Ala Ala Phe Ala Ser Ser Pro Ile Tyr Thr Val Leu Phe Ser His Asp
355 360 365

agt ttg ggt gct tat tat ttg gtg gaa aac att gta caa agt cta tta 1152
Ser Leu Gly Ala Tyr Tyr Leu Val Glu Asn Ile Val Gln Ser Leu Leu
370 375 380

gcc ggc ctt gtg atg aac tca tta act ttg ctt cta gca ctt aat atg 1200
Ala Gly Leu Val Met Asn Ser Leu Thr Leu Leu Ala Leu Asn Met
385 390 395 400

aac aaa ttg gct gtt ggt tat atg att tgg gga att att gtc aag att 1248
Asn Lys Leu Ala Val Gly Tyr Met Ile Trp Gly Ile Ile Val Lys Ile
405 410 415

gta tta cag gtt cct atg acg atg ttt atg agt gca gat ggt gca att 1296
Val Leu Gln Val Pro Met Thr Met Phe Met Ser Ala Asp Gly Ala Ile
420 425 430

ctt tca act gat att gcc ttc tta ctt gta atc gtg ctt agt tat cat 1344
Leu Ser Thr Asp Ile Ala Phe Leu Leu Val Ile Val Leu Ser Tyr His
435 440 445

aag ctt gat aaa aca tat gat gtt aac ttg cat agc ttg ctg ccg att 1392
Lys Leu Asp Lys Thr Tyr Asp Val Asn Leu His Ser Leu Leu Pro Ile
450 455 460

gtt gta gta aat gaa atc tac att atc tta tta ttt att tac caa ctt 1440
Val Val Val Asn Glu Ile Tyr Ile Ile Leu Leu Phe Ile Tyr Gln Leu
465 470 475 480

tta att gga tat cat ttc aat agt tta gga aga atg gga agc ttc atc 1488
Leu Ile Gly Tyr His Phe Asn Ser Leu Gly Arg Met Gly Ser Phe Ile
485 490 495

tat tta gca atc ttc ggt tta gta ttc cta gga att tat atc tta ctt 1536
Tyr Leu Ala Ile Phe Gly Leu Val Phe Leu Gly Ile Tyr Ile Leu Leu
500 505 510

gct aat gta atg ggg act agc gag aca att ttt ggc aaa aag atc ggt 1584
Ala Asn Val Met Gly Thr Ser Glu Thr Ile Phe Gly Lys Lys Ile Gly
515 520 525

tac cgc tat tat cgt tat aaa cat ttt gaa 1614
Tyr Arg Tyr Tyr Arg Tyr Lys His Phe Glu
530 535

<210> 234

<211> 538

<212> PRT

<213> Lactobacillus acidophilus

<400> 234

Met Asn Lys Lys Ile Leu Ser Gly Ser Phe Trp Leu Ser Phe Gly Ser
1 5 10 15
Ile Val Ser Arg Ile Leu Gly Val Val Tyr Leu Ile Pro Trp Leu Ile

- 427 -

Leu Ile Gly Tyr His Phe Asn Ser Leu Gly Arg Met Gly Ser Phe Ile
 485 490 495
 Tyr Leu Ala Ile Phe Gly Leu Val Phe Leu Gly Ile Tyr Ile Leu Leu
 500 505 510
 Ala Asn Val Met Gly Thr Ser Glu Thr Ile Phe Gly Lys Lys Ile Gly
 515 520 525
 Tyr Arg Tyr Tyr Arg Tyr Lys His Phe Glu
 530 535

<210> 235

<211> 813

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 123 - EpsV

<220>

<221> CDS

<222> (1)...(813)

<400> 235

atg tta caa gtg cct aag tta act atc att atg ccg gtt tac aac acg	48
Met Leu Gln Val Pro Lys Leu Thr Ile Met Pro Val Tyr Asn Thr	
1 5 10 15	
gca caa tat ctg cca cgc gct ttt gat gct tta ctt aag caa atc gac	96
Ala Gln Tyr Leu Pro Arg Ala Phe Asp Ala Leu Leu Lys Gln Ile Asp	
20 25 30	
aaa agc ttt aag ttg atc gtg gtt gat gat ggc tca act gat aat tca	144
Lys Ser Phe Lys Leu Ile Val Val Asp Asp Gly Ser Thr Asp Asn Ser	
35 40 45	
gtt gag gta gcc caa aac tat gcc tat cgc ttt cca tat ttt aaa tta	192
Val Glu Val Ala Gln Asn Tyr Ala Tyr Arg Phe Pro Tyr Phe Lys Leu	
50 55 60	
att aaa aag aaa aat ggc ggc cca tct gat gca cgt aat gtt ggt atg	240
Ile Lys Lys Lys Asn Gly Gly Pro Ser Asp Ala Arg Asn Val Gly Met	
65 70 75 80	
cag tat att gac acg cca tat gtc acc ttt cat gat ggt gat gac tgg	288
Gln Tyr Ile Asp Thr Pro Tyr Val Thr Phe His Asp Gly Asp Asp Trp	
85 90 95	
gtg gat cca ggc tat acg tct ttt ttt att cgc gct ttt gaa gaa cat	336
Val Asp Pro Gly Tyr Thr Ser Phe Phe Ile Arg Ala Phe Glu Glu His	
100 105 110	
cct gat gta aat ctt gtt tct tgt gga tat tgg atg gac tat cca gat	384
Pro Asp Val Asn Leu Val Ser Cys Gly Tyr Trp Met Asp Tyr Pro Asp	
115 120 125	

```

aaa aag tca cgt gtt gtt gga cga cct gaa ggc ggt ttt tta acg cgg 432
Lys Lys Ser Arg Val Val Gly Arg Pro Glu Gly Gly Phe Leu Thr Arg
130 135 140

ggt gaa act tat cta aaa tta acc aat gtt ttt ggt tcg cca atg aaa 480
Gly Glu Thr Tyr Leu Lys Leu Thr Asn Val Phe Gly Ser Pro Met Lys
145 150 155 160

ggc tat agt tgg aat aaa gct tat aag aca gca att att aaa aaa ttc 528
Gly Tyr Ser Trp Asn Lys Ala Tyr Lys Thr Ala Ile Ile Lys Lys Phe
165 170 175

cat tta caa ttt gat cgc gat att tca cta ctt gag gat caa att ttt 576
His Leu Gln Phe Asp Arg Asp Ile Ser Leu Leu Glu Asp Gln Ile Phe
180 185 190

aat gtg aaa tat att tct gta gct aaa gga gtt tat tat act cag cgt 624
Asn Val Lys Tyr Ile Ser Val Ala Lys Gly Val Tyr Tyr Thr Gln Arg
195 200 205

cct tac tac cat tat tgg caa aga aaa gga agt att att cat caa cct 672
Pro Tyr Tyr His Tyr Trp Gln Arg Lys Gly Ser Ile Ile His Gln Pro
210 215 220

aat gtt aaa aag gta gcc gat aat ttc cgt ggt aat tat cga gta tgg 720
Asn Val Lys Lys Val Ala Asp Asn Phe Arg Gly Asn Tyr Arg Val Trp
225 230 235 240

cgc aga att att aag acg atg ctt aaa gat cat gaa gat gag aag atg 768
Arg Arg Ile Ile Lys Thr Met Leu Lys Asp His Glu Asp Glu Lys Met
245 250 255

cgt aaa aaa tta gat cgt tca cct ctt cgt gat agc gat gtt caa 813
Arg Lys Lys Leu Asp Arg Ser Pro Leu Arg Asp Ser Asp Val Gln
260 265 270

```

<210> 236

<211> 271

<212> PRT

<213> Lactobacillus acidophilus

<400> 236

```

Met Leu Gln Val Pro Lys Leu Thr Ile Ile Met Pro Val Tyr Asn Thr
1 5 10 15
Ala Gln Tyr Leu Pro Arg Ala Phe Asp Ala Leu Leu Lys Gln Ile Asp
20 25 30
Lys Ser Phe Lys Leu Ile Val Val Asp Asp Gly Ser Thr Asp Asn Ser
35 40 45
Val Glu Val Ala Gln Asn Tyr Ala Tyr Arg Phe Pro Tyr Phe Lys Leu
50 55 60
Ile Lys Lys Lys Asn Gly Gly Pro Ser Asp Ala Arg Asn Val Gly Met
65 70 75 80
Gln Tyr Ile Asp Thr Pro Tyr Val Thr Phe His Asp Gly Asp Asp Trp
85 90 95

```

Val Asp Pro Gly Tyr Thr Ser Phe Phe Ile Arg Ala Phe Glu Glu His
 100 105 110
 Pro Asp Val Asn Leu Val Ser Cys Gly Tyr Trp Met Asp Tyr Pro Asp
 115 120 125
 Lys Lys Ser Arg Val Val Gly Arg Pro Glu Gly Gly Phe Leu Thr Arg
 130 135 140
 Gly Glu Thr Tyr Leu Lys Leu Thr Asn Val Phe Gly Ser Pro Met Lys
 145 150 155 160
 Gly Tyr Ser Trp Asn Lys Ala Tyr Lys Thr Ala Ile Ile Lys Lys Phe
 165 170 175
 His Leu Gln Phe Asp Arg Asp Ile Ser Leu Leu Glu Asp Gln Ile Phe
 180 185 190
 Asn Val Lys Tyr Ile Ser Val Ala Lys Gly Val Tyr Tyr Thr Gln Arg
 195 200 205
 Pro Tyr Tyr His Tyr Trp Gln Arg Lys Gly Ser Ile Ile His Gln Pro
 210 215 220
 Asn Val Lys Lys Val Ala Asp Asn Phe Arg Gly Asn Tyr Arg Val Trp
 225 230 235 240
 Arg Arg Ile Ile Lys Thr Met Leu Lys Asp His Glu Asp Glu Lys Met
 245 250 255
 Arg Lys Lys Leu Asp Arg Ser Pro Leu Arg Asp Ser Asp Val Gln
 260 265 270

<210> 237

<211> 1428

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 525 - EpsU

<220>

<221> CDS

<222> (1)...(1428)

<400> 237

ttg cgc aaa aca ttt tta aat att ttg tat aat gcg gtt tat cag atc 48
 Met Arg Lys Thr Phe Leu Asn Ile Leu Tyr Asn Ala Val Tyr Gln Ile
 1 5 10 15

ttt att gta tta gtt cct ctg att acc gtt cca tat cta tcc aga gtt 96
 Phe Ile Val Leu Val Pro Leu Ile Thr Val Pro Tyr Leu Ser Arg Val
 20 25 30

ttg gga cct aag aca tat ggt att tat agt agc gtt aat aac act gta 144
 Leu Gly Pro Lys Thr Tyr Gly Ile Tyr Ser Ser Val Asn Asn Thr Val
 35 40 45

cag ttt ttg atg att ttt tgt atc ctt tct gtg tct tat gtg ggg atg 192
 Gln Phe Leu Met Ile Phe Cys Ile Leu Ser Val Ser Tyr Val Gly Met
 50 55 60

cgg acg att tca aga acg cgt aca tac gga aca cag gaa gaa tta act 240

Arg Thr Ile Ser Arg Thr Arg Thr Tyr Gly Thr Gln Glu Glu Leu Thr	
65 70 75 80	
aga gca ttt tgg ggc ttg tgg tat ttt caa ggt att gct ggc gca att	288
Arg Ala Phe Trp Gly Leu Trp Tyr Phe Gln Gly Ile Ala Gly Ala Ile	
85 90 95	
acg att gta att act att tta gta act act att ttt cat att caa tac	336
Thr Ile Val Ile Thr Ile Leu Val Thr Thr Ile Phe His Ile Gln Tyr	
100 105 110	
tgg ttt tac ctt tta ctt atg gtg cca tac tta att tct gct cag gta	384
Trp Phe Tyr Leu Leu Leu Met Val Pro Tyr Leu Ile Ser Ala Gln Val	
115 120 125	
gat att tct tgg ttt ttc caa gga tta gcc gac ttt ggt aga gtt gtt	432
Asp Ile Ser Trp Phe Phe Gln Gly Leu Ala Asp Phe Gly Arg Val Val	
130 135 140	
tta aaa aat act gct gta aag ctg gtt agt gtt gtt tta att ttg cta	480
Leu Lys Asn Thr Ala Val Lys Leu Val Ser Val Val Leu Ile Leu Leu	
145 150 155 160	
tgg gta aaa tca cca gca gat ttg tgg aaa tat tta ctg att atg tct	528
Trp Val Lys Ser Pro Ala Asp Leu Trp Lys Tyr Leu Leu Ile Met Ser	
165 170 175	
gtt tct aca atg cta ggt tct ttt gtc ttt tgg ttt gat att cac cgt	576
Val Ser Thr Met Leu Gly Ser Phe Val Phe Trp Phe Asp Ile His Arg	
180 185 190	
tat gtg ggt cga cca gta gcg cat ttt tat aaa ttt aag aag aat gct	624
Tyr Val Gly Arg Pro Val Ala His Phe Tyr Lys Phe Lys Lys Asn Ala	
195 200 205	
att gcg att gga act tta atg att ccg caa atc gct acc caa att tat	672
Ile Ala Ile Gly Thr Leu Met Ile Pro Gln Ile Ala Thr Gln Ile Tyr	
210 215 220	
aca tca tta gat aag cca att ttg ggt ctt ttt tca agt tct acc caa	720
Thr Ser Leu Asp Lys Pro Ile Leu Gly Leu Phe Ser Ser Ser Thr Gln	
225 230 235 240	
gtt tct ttt tat gat aat tca cag cga att tct aat atg att tta gga	768
Val Ser Phe Tyr Asp Asn Ser Gln Arg Ile Ser Asn Met Ile Leu Gly	
245 250 255	
gta att act agc att tcc ttg gta atc atg cct aaa atg gcc agt gaa	816
Val Ile Thr Ser Ile Ser Leu Val Ile Met Pro Lys Met Ala Ser Glu	
260 265 270	
gat gaa gaa tca caa aag gtt gtg atg aaa aag tcg cta gaa gct aca	864
Asp Glu Glu Ser Gln Lys Val Val Met Lys Lys Ser Leu Glu Ala Thr	
275 280 285	
gtg atg cta gga act tta ttt gct gta att att atg gca aat act aaa	912
Val Met Leu Gly Thr Leu Phe Ala Val Ile Ile Met Ala Asn Thr Lys	

290	295	300	
caa ttc gta cca ttc ttt ttt ggc act aaa tat att ccg atg aca ccg			960
Gln Phe Val Pro Phe Phe Phe Gly Thr Lys Tyr Ile Pro Met Thr Pro			
305	310	315	320
ttg atg ttt tgg ttc act ttg act att atc atg att cca acc ggt ggt			1008
Leu Met Phe Trp Phe Thr Leu Thr Ile Ile Met Ile Pro Thr Gly Gly			
	325	330	335
gtt ttt gcc aat caa ttt gcc cta gcc aat aga cgt gat aag gat tat			1056
Val Phe Ala Asn Gln Phe Ala Leu Ala Asn Arg Arg Asp Lys Asp Tyr			
	340	345	350
gct ttt cct gta gtt att ggt gca att tta gaa att att tta agt tat			1104
Ala Phe Pro Val Val Ile Gly Ala Ile Leu Glu Ile Ile Leu Ser Tyr			
	355	360	365
gtt cta gat cgg ccg tat ggt gca gca ggt gcg atg att gca att tta			1152
Val Leu Asp Arg Pro Tyr Gly Ala Ala Gly Ala Met Ile Ala Ile Leu			
	370	375	380
att aca gaa gcc gta gta tta gtt cta cgt tta tgg gtt gtg cgt gac			1200
Ile Thr Glu Ala Val Val Leu Val Leu Arg Leu Trp Val Val Arg Asp			
	385	390	395
ggc tat agt ttt aca tat gtt ttt cac gat gtt cct aaa tat att tta			1248
Gly Tyr Ser Phe Thr Tyr Val Phe His Asp Val Pro Lys Tyr Ile Leu			
	405	410	415
att gca tta atc act ctt acc att ggg atg ttt atg cct aac ttt att			1296
Ile Ala Leu Ile Thr Leu Thr Ile Gly Met Phe Met Pro Asn Phe Ile			
	420	425	430
tca tcg gcc ttt ttc aat atg gca ttt aaa tca att gtg atg ttg cta			1344
Ser Ser Ala Phe Phe Asn Met Ala Phe Lys Ser Ile Val Met Leu Leu			
	435	440	445
gtt tat atg ctt ttg atg ttt gca tta aag ctc gac ttt aac gaa gac			1392
Val Tyr Met Leu Leu Met Phe Ala Leu Lys Leu Asp Phe Asn Glu Asp			
	450	455	460
att att aaa tta ttc aag aat ttc ttt aaa aga ggt			1428
Ile Ile Lys Leu Phe Lys Asn Phe Phe Lys Arg Gly			
	465	470	475

<210> 238

<211> 476

<212> PRT

<213> Lactobacillus acidophilus

<400> 238

Met Arg Lys Thr Phe Leu Asn Ile Leu Tyr Asn Ala Val Tyr Gln Ile			
1	5	10	15
Phe Ile Val Leu Val Pro Leu Ile Thr Val Pro Tyr Leu Ser Arg Val			
	20	25	30

Leu	Gly	Pro	Lys	Thr	Tyr	Gly	Ile	Tyr	Ser	Ser	Val	Asn	Asn	Thr	Val
		35					40					45			
Gln	Phe	Leu	Met	Ile	Phe	Cys	Ile	Leu	Ser	Val	Ser	Tyr	Val	Gly	Met
	50					55					60				
Arg	Thr	Ile	Ser	Arg	Thr	Arg	Thr	Tyr	Gly	Thr	Gln	Glu	Glu	Leu	Thr
65					70					75					80
Arg	Ala	Phe	Trp	Gly	Leu	Trp	Tyr	Phe	Gln	Gly	Ile	Ala	Gly	Ala	Ile
				85					90					95	
Thr	Ile	Val	Ile	Thr	Ile	Leu	Val	Thr	Thr	Ile	Phe	His	Ile	Gln	Tyr
			100					105					110		
Trp	Phe	Tyr	Leu	Leu	Leu	Met	Val	Pro	Tyr	Leu	Ile	Ser	Ala	Gln	Val
		115					120					125			
Asp	Ile	Ser	Trp	Phe	Phe	Gln	Gly	Leu	Ala	Asp	Phe	Gly	Arg	Val	Val
	130					135					140				
Leu	Lys	Asn	Thr	Ala	Val	Lys	Leu	Val	Ser	Val	Val	Leu	Ile	Leu	Leu
145					150					155					160
Trp	Val	Lys	Ser	Pro	Ala	Asp	Leu	Trp	Lys	Tyr	Leu	Leu	Ile	Met	Ser
			165						170					175	
Val	Ser	Thr	Met	Leu	Gly	Ser	Phe	Val	Phe	Trp	Phe	Asp	Ile	His	Arg
			180					185					190		
Tyr	Val	Gly	Arg	Pro	Val	Ala	His	Phe	Tyr	Lys	Phe	Lys	Lys	Asn	Ala
		195				200						205			
Ile	Ala	Ile	Gly	Thr	Leu	Met	Ile	Pro	Gln	Ile	Ala	Thr	Gln	Ile	Tyr
	210					215					220				
Thr	Ser	Leu	Asp	Lys	Pro	Ile	Leu	Gly	Leu	Phe	Ser	Ser	Ser	Thr	Gln
225					230					235					240
Val	Ser	Phe	Tyr	Asp	Asn	Ser	Gln	Arg	Ile	Ser	Asn	Met	Ile	Leu	Gly
				245					250					255	
Val	Ile	Thr	Ser	Ile	Ser	Leu	Val	Ile	Met	Pro	Lys	Met	Ala	Ser	Glu
		260						265					270		
Asp	Glu	Glu	Ser	Gln	Lys	Val	Val	Met	Lys	Lys	Ser	Leu	Glu	Ala	Thr
		275					280					285			
Val	Met	Leu	Gly	Thr	Leu	Phe	Ala	Val	Ile	Ile	Met	Ala	Asn	Thr	Lys
	290					295					300				
Gln	Phe	Val	Pro	Phe	Phe	Phe	Gly	Thr	Lys	Tyr	Ile	Pro	Met	Thr	Pro
305					310					315					320
Leu	Met	Phe	Trp	Phe	Thr	Leu	Thr	Ile	Ile	Met	Ile	Pro	Thr	Gly	Gly
				325					330					335	
Val	Phe	Ala	Asn	Gln	Phe	Ala	Leu	Ala	Asn	Arg	Arg	Asp	Lys	Asp	Tyr
			340					345					350		
Ala	Phe	Pro	Val	Val	Ile	Gly	Ala	Ile	Leu	Glu	Ile	Ile	Leu	Ser	Tyr
		355				360						365			
Val	Leu	Asp	Arg	Pro	Tyr	Gly	Ala	Ala	Gly	Ala	Met	Ile	Ala	Ile	Leu
	370					375					380				
Ile	Thr	Glu	Ala	Val	Val	Leu	Val	Leu	Arg	Leu	Trp	Val	Val	Arg	Asp
385					390					395					400
Gly	Tyr	Ser	Phe	Thr	Tyr	Val	Phe	His	Asp	Val	Pro	Lys	Tyr	Ile	Leu
				405					410					415	
Ile	Ala	Leu	Ile	Thr	Leu	Thr	Ile	Gly	Met	Phe	Met	Pro	Asn	Phe	Ile
			420					425					430		
Ser	Ser	Ala	Phe	Phe	Asn	Met	Ala	Phe	Lys	Ser	Ile	Val	Met	Leu	Leu
		435					440					445			
Val	Tyr	Met	Leu	Leu	Met	Phe	Ala	Leu	Lys	Leu	Asp	Phe	Asn	Glu	Asp
	450					455					460				
Ile	Ile	Lys	Leu	Phe	Lys	Asn	Phe	Phe	Lys	Arg	Gly				
465					470					475					

<210> 239
 <211> 1101
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 188 - EpsA

<220>
 <221> CDS
 <222> (1)...(1101)

<400> 239
 atg aag gat aac aga gaa aga gaa aat cac ccg agc ggt act cga gtg 48
 Met Lys Asp Asn Arg Glu Arg Glu Asn His Pro Ser Gly Thr Arg Val
 1 5 10 15
 caa agt cat aaa tat aaa aat cga cat att tgg gcg tgg gct aca ggg 96
 Gln Ser His Lys Tyr Lys Asn Arg His Ile Trp Ala Trp Ala Thr Gly
 20 25 30
 ata att tta tta gtt gca gtc att gcg gca gta aca tac ttt gca tct 144
 Ile Ile Leu Leu Val Ala Val Ile Ala Ala Val Thr Tyr Phe Ala Ser
 35 40 45
 gtt tat ttt aag gcg aag aat gca gtt gat aaa acc tat gat cca gct 192
 Val Tyr Phe Lys Ala Lys Asn Ala Val Asp Lys Thr Tyr Asp Pro Ala
 50 55 60
 aca gca gtg aaa act aca ggt gaa ttt aat ggc aaa aag cgt ttt gcg 240
 Thr Ala Val Lys Thr Thr Gly Glu Phe Asn Gly Lys Lys Arg Phe Ala
 65 70 75 80
 gtt cta tta atg gga aca gac aca ggg gct tta aat aga act gag aaa 288
 Val Leu Leu Met Gly Thr Asp Thr Gly Ala Leu Asn Arg Thr Glu Lys
 85 90 95
 cgc ggt aga act gat acc atg att tta gct gta gtt aac cct gct aaa 336
 Arg Gly Arg Thr Asp Thr Met Ile Leu Ala Val Val Asn Pro Ala Lys
 100 105 110
 aag cgt tat acg ttg gta tct att ccg cgt gat aca atg gcg cag atg 384
 Lys Arg Tyr Thr Leu Val Ser Ile Pro Arg Asp Thr Met Ala Gln Met
 115 120 125
 gtt ggc tcc agt agt ttt act act gaa aag atc aat gct gct tat gaa 432
 Val Gly Ser Ser Ser Phe Thr Thr Glu Lys Ile Asn Ala Ala Tyr Glu
 130 135 140
 att ggc gga gct cga atg tca atg gac agc gtt tct gct ttg att aat 480
 Ile Gly Gly Ala Arg Met Ser Met Asp Ser Val Ser Ala Leu Ile Asn
 145 150 155 160

gtg ccg att aag tat tat gcc gtt gtc aac atg ggt gga att atg aag	528
Val Pro Ile Lys Tyr Tyr Ala Val Val Asn Met Gly Gly Ile Met Lys	
165 170 175	
atg att cgc tat gtt ggc ggg atc aat att cga cca acg ctt agc ttt	576
Met Ile Arg Tyr Val Gly Gly Ile Asn Ile Arg Pro Thr Leu Ser Phe	
180 185 190	
gag tat ggc ggc tat gtc ttt aaa aag ggt aag tta acc cat atg ggt	624
Glu Tyr Gly Gly Tyr Val Phe Lys Lys Gly Lys Leu Thr His Met Gly	
195 200 205	
ggg gcc ggt gca ctg gct tac tca aga atg cgt tat gat gat ccg cgc	672
Gly Ala Gly Ala Leu Ala Tyr Ser Arg Met Arg Tyr Asp Asp Pro Arg	
210 215 220	
ggg gac tat ggt aga caa gag cgg caa aga caa gtt att aca acg cta	720
Gly Asp Tyr Gly Arg Gln Glu Arg Gln Arg Gln Val Ile Thr Thr Leu	
225 230 235 240	
att aaa aaa gct gtt tca gta agt tct tta act aat tta gat tca att	768
Ile Lys Lys Ala Val Ser Val Ser Ser Leu Thr Asn Leu Asp Ser Ile	
245 250 255	
ctg act tca gta tca agt aac gtt aga act aat ttg cca ttt agt gct	816
Leu Thr Ser Val Ser Ser Asn Val Arg Thr Asn Leu Pro Phe Ser Ala	
260 265 270	
ttg caa caa att gcg ctt aat tac cgt ggt tgt gct aat agt tca tca	864
Leu Gln Gln Ile Ala Leu Asn Tyr Arg Gly Cys Ala Asn Ser Ser Ser	
275 280 285	
agc gat tat ctt cat ggc tat aat gcg atg atc gat gat gcc gct tat	912
Ser Asp Tyr Leu His Gly Tyr Asn Ala Met Ile Asp Asp Ala Ala Tyr	
290 295 300	
caa gtt caa cca aca gaa gaa ttg cag cgg att tct gat tta gta cgt	960
Gln Val Gln Pro Thr Glu Glu Leu Gln Arg Ile Ser Asp Leu Val Arg	
305 310 315 320	
act gag tta ggc tta gag aaa gaa acc att aat aac aat gaa act tat	1008
Thr Glu Leu Gly Leu Glu Lys Glu Thr Ile Asn Asn Asn Glu Thr Tyr	
325 330 335	
caa aat aag cga aat gaa gaa aat ggt ttt agt ttt aag agt act aag	1056
Gln Asn Lys Arg Asn Glu Glu Asn Gly Phe Ser Phe Lys Ser Thr Lys	
340 345 350	
aat caa acc tac cat att tat gat tac acc gaa gaa ggt gat aat	1101
Asn Gln Thr Tyr His Ile Tyr Asp Tyr Thr Glu Glu Gly Asp Asn	
355 360 365	

<210> 240

<211> 367

<212> PRT

<213> Lactobacillus acidophilus

<400> 240

```

Met Lys Asp Asn Arg Glu Arg Glu Asn His Pro Ser Gly Thr Arg Val
 1          5          10          15
Gln Ser His Lys Tyr Lys Asn Arg His Ile Trp Ala Trp Ala Thr Gly
      20          25          30
Ile Ile Leu Leu Val Ala Val Ile Ala Ala Val Thr Tyr Phe Ala Ser
      35          40          45
Val Tyr Phe Lys Ala Lys Asn Ala Val Asp Lys Thr Tyr Asp Pro Ala
      50          55          60
Thr Ala Val Lys Thr Thr Gly Glu Phe Asn Gly Lys Lys Arg Phe Ala
      65          70          75          80
Val Leu Leu Met Gly Thr Asp Thr Gly Ala Leu Asn Arg Thr Glu Lys
      85          90          95
Arg Gly Arg Thr Asp Thr Met Ile Leu Ala Val Val Asn Pro Ala Lys
      100          105          110
Lys Arg Tyr Thr Leu Val Ser Ile Pro Arg Asp Thr Met Ala Gln Met
      115          120          125
Val Gly Ser Ser Ser Phe Thr Thr Glu Lys Ile Asn Ala Ala Tyr Glu
      130          135          140
Ile Gly Gly Ala Arg Met Ser Met Asp Ser Val Ser Ala Leu Ile Asn
      145          150          155          160
Val Pro Ile Lys Tyr Tyr Ala Val Val Asn Met Gly Gly Ile Met Lys
      165          170          175
Met Ile Arg Tyr Val Gly Gly Ile Asn Ile Arg Pro Thr Leu Ser Phe
      180          185          190
Glu Tyr Gly Gly Tyr Val Phe Lys Lys Gly Lys Leu Thr His Met Gly
      195          200          205
Gly Ala Gly Ala Leu Ala Tyr Ser Arg Met Arg Tyr Asp Asp Pro Arg
      210          215          220
Gly Asp Tyr Gly Arg Gln Glu Arg Gln Arg Gln Val Ile Thr Thr Leu
      225          230          235          240
Ile Lys Lys Ala Val Ser Val Ser Ser Leu Thr Asn Leu Asp Ser Ile
      245          250          255
Leu Thr Ser Val Ser Ser Asn Val Arg Thr Asn Leu Pro Phe Ser Ala
      260          265          270
Leu Gln Gln Ile Ala Leu Asn Tyr Arg Gly Cys Ala Asn Ser Ser Ser
      275          280          285
Ser Asp Tyr Leu His Gly Tyr Asn Ala Met Ile Asp Asp Ala Ala Tyr
      290          295          300
Gln Val Gln Pro Thr Glu Glu Leu Gln Arg Ile Ser Asp Leu Val Arg
      305          310          315          320
Thr Glu Leu Gly Leu Glu Lys Glu Thr Ile Asn Asn Asn Glu Thr Tyr
      325          330          335
Gln Asn Lys Arg Asn Glu Glu Asn Gly Phe Ser Phe Lys Ser Thr Lys
      340          345          350
Asn Gln Thr Tyr His Ile Tyr Asp Tyr Thr Glu Glu Gly Asp Asn
      355          360          365

```

<210> 241

<211> 738

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature
 <222> (0)...(0)
 <223> ORF 1015 - capsular polysaccharide biosynthesis
 protein J

<220>
 <221> CDS
 <222> (1)...(738)

<400> 241
 gtg cca att ttg aat aat caa ttt ggc aat tgg tgc ttt atg act ttc 48
 Met Pro Ile Leu Asn Asn Gln Phe Gly Asn Trp Cys Phe Met Thr Phe
 1 5 10 15
 ttc aaa gta aaa tca ttt aaa aat tgt act gca tta caa gtt cct aca 96
 Phe Lys Val Lys Ser Phe Lys Asn Cys Thr Ala Leu Gln Val Pro Thr
 20 25 30
 cct aaa gta gct aaa tgg tta aag aaa aat cat ttc aaa cag aag cta 144
 Pro Lys Val Ala Lys Trp Leu Lys Lys Asn His Phe Lys Gln Lys Leu
 35 40 45
 ttt att gtt tca aac ggt atc agc gaa aag ttt att caa aat ccg cac 192
 Phe Ile Val Ser Asn Gly Ile Ser Glu Lys Phe Ile Gln Asn Pro His
 50 55 60
 aaa gaa aaa gtt gga cac ccc ttc act att tta tgt atc gga aga ttt 240
 Lys Glu Lys Val Gly His Pro Phe Thr Ile Leu Cys Ile Gly Arg Phe
 65 70 75 80
 tca cac gaa aaa cga caa gaa act tta ttc aaa gca atg cag cta tcc 288
 Ser His Glu Lys Arg Gln Glu Thr Leu Phe Lys Ala Met Gln Leu Ser
 85 90 95
 aaa cat act tct gaa atc cgt ctt att ttt gct gga caa gga cct tta 336
 Lys His Thr Ser Glu Ile Arg Leu Ile Phe Ala Gly Gln Gly Pro Leu
 100 105 110
 gaa aag gaa tat gcc aaa tta gct aaa cag ctt cct aag aaa cct atc 384
 Glu Lys Glu Tyr Ala Lys Leu Ala Lys Gln Leu Pro Lys Lys Pro Ile
 115 120 125
 atg cgc tat ttt gct cca gca gat ttg aaa gaa att atg ttt cag acc 432
 Met Arg Tyr Phe Ala Pro Ala Asp Leu Lys Glu Ile Met Phe Gln Thr
 130 135 140
 gat ttg gtt gtg cac tgt gct gat gta gaa ata gag gga atg gct tgc 480
 Asp Leu Val Val His Cys Ala Asp Val Glu Ile Glu Gly Met Ala Cys
 145 150 155 160
 atg gaa gct ttt tct agt ggc tgt gta tct gta att gct gat agt tcg 528
 Met Glu Ala Phe Ser Ser Gly Cys Val Ser Val Ile Ala Asp Ser Ser
 165 170 175
 tta tct tct act gtt agc tat gct tta agc gaa aat aat cgt ttc tct 576
 Leu Ser Ser Thr Val Ser Tyr Ala Leu Ser Glu Asn Asn Arg Phe Ser

180	185	190	
gct gga gac agt aga gct ctt gct caa aaa att gat tac tgg ttc gag			624
Ala Gly Asp Ser Arg Ala Leu Ala Gln Lys Ile Asp Tyr Trp Phe Glu			
195	200	205	
cat ccc tca gaa tta ata aaa atg aga caa gaa tat cgc agt tac ggt			672
His Pro Ser Glu Leu Ile Lys Met Arg Gln Glu Tyr Arg Ser Tyr Gly			
210	215	220	
aaa aca tta aat gtt gca cgt tca gcc aaa ata gcc tta ggt aat tta			720
Lys Thr Leu Asn Val Ala Arg Ser Ala Lys Ile Ala Leu Gly Asn Leu			
225	230	235	240
gaa aat ctg acc tta aag			738
Glu Asn Leu Thr Leu Lys			
245			

<210> 242

<211> 246

<212> PRT

<213> Lactobacillus acidophilus

<400> 242

Met Pro Ile Leu Asn Asn Gln Phe Gly Asn Trp Cys Phe Met Thr Phe			
1	5	10	15
Phe Lys Val Lys Ser Phe Lys Asn Cys Thr Ala Leu Gln Val Pro Thr			
20	25	30	
Pro Lys Val Ala Lys Trp Leu Lys Lys Asn His Phe Lys Gln Lys Leu			
35	40	45	
Phe Ile Val Ser Asn Gly Ile Ser Glu Lys Phe Ile Gln Asn Pro His			
50	55	60	
Lys Glu Lys Val Gly His Pro Phe Thr Ile Leu Cys Ile Gly Arg Phe			
65	70	75	80
Ser His Glu Lys Arg Gln Glu Thr Leu Phe Lys Ala Met Gln Leu Ser			
85	90	95	
Lys His Thr Ser Glu Ile Arg Leu Ile Phe Ala Gly Gln Gly Pro Leu			
100	105	110	
Glu Lys Glu Tyr Ala Lys Leu Ala Lys Gln Leu Pro Lys Lys Pro Ile			
115	120	125	
Met Arg Tyr Phe Ala Pro Ala Asp Leu Lys Glu Ile Met Phe Gln Thr			
130	135	140	
Asp Leu Val Val His Cys Ala Asp Val Glu Ile Glu Gly Met Ala Cys			
145	150	155	160
Met Glu Ala Phe Ser Ser Gly Cys Val Ser Val Ile Ala Asp Ser Ser			
165	170	175	
Leu Ser Ser Thr Val Ser Tyr Ala Leu Ser Glu Asn Asn Arg Phe Ser			
180	185	190	
Ala Gly Asp Ser Arg Ala Leu Ala Gln Lys Ile Asp Tyr Trp Phe Glu			
195	200	205	
His Pro Ser Glu Leu Ile Lys Met Arg Gln Glu Tyr Arg Ser Tyr Gly			
210	215	220	
Lys Thr Leu Asn Val Ala Arg Ser Ala Lys Ile Ala Leu Gly Asn Leu			
225	230	235	240
Glu Asn Leu Thr Leu Lys			
245			

<210> 243
 <211> 1140
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1720 - Cap5P

<220>
 <221> CDS
 <222> (1)...(1140)

<400> 243
 atg aac aag att aaa gta atg act gtt ttt ggt acc cga cca gaa gca 48
 Met Asn Lys Ile Lys Val Met Thr Val Phe Gly Thr Arg Pro Glu Ala
 1 5 10 15
 atc aag atg gca cca ctt gtt tta aaa tta aag caa gat gaa cgt ttt 96
 Ile Lys Met Ala Pro Leu Val Leu Lys Leu Lys Gln Asp Glu Arg Phe
 20 25 30
 gaa gaa gtt acg gtt gtt tca gcg cag cac cgt gag atg ctt gat cag 144
 Glu Glu Val Thr Val Val Ser Ala Gln His Arg Glu Met Leu Asp Gln
 35 40 45
 gta ctc gat att ttt aaa att aag cca gac tat gac ttt aac atc atg 192
 Val Leu Asp Ile Phe Lys Ile Lys Pro Asp Tyr Asp Phe Asn Ile Met
 50 55 60
 cat aag aac cag act ttg gaa gaa att act tct aaa gtt atg att gat 240
 His Lys Asn Gln Thr Leu Glu Glu Ile Thr Ser Lys Val Met Ile Asp
 65 70 75 80
 ttg gct aaa gta att aaa aaa gaa aag cct gat att gtt tta gtt cat 288
 Leu Ala Lys Val Ile Lys Lys Glu Lys Pro Asp Ile Val Leu Val His
 85 90 95
 ggc gat act aca act agt ttt gcg gca gga ctt gcc acc ttt tat gaa 336
 Gly Asp Thr Thr Ser Phe Ala Ala Gly Leu Ala Thr Phe Tyr Glu
 100 105 110
 caa aca act ctg ggg cac gta gaa gcc ggt ctt cgt act tgg aat aaa 384
 Gln Thr Thr Leu Gly His Val Glu Ala Gly Leu Arg Thr Trp Asn Lys
 115 120 125
 tat tca ccg ttc cct gaa gag atg aat cgt caa atg act gat gac ttg 432
 Tyr Ser Pro Phe Pro Glu Glu Met Asn Arg Gln Met Thr Asp Asp Leu
 130 135 140
 gca gac tta tat ttt gct cca act gaa gtg tcc aag gct aac tta tta 480
 Ala Asp Leu Tyr Phe Ala Pro Thr Glu Val Ser Lys Ala Asn Leu Leu
 145 150 155 160

aaa gaa aac cat cca gca gat aat att ttt gtt aca ggt aat aca gct	528
Lys Glu Asn His Pro Ala Asp Asn Ile Phe Val Thr Gly Asn Thr Ala	
165 170 175	
atc gat gcg ctt cat gaa act gtt caa aaa gat tat cat cac gat gtt	576
Ile Asp Ala Leu His Glu Thr Val Gln Lys Asp Tyr His His Asp Val	
180 185 190	
tta gat gaa att aaa cca ggc aat aag gtt atc ttg gtg aca atg cat	624
Leu Asp Glu Ile Lys Pro Gly Asn Lys Val Ile Leu Val Thr Met His	
195 200 205	
aga cga gaa aat cag ggc gaa cct atg cgt cgc gta ttt aaa gtc atg	672
Arg Arg Glu Asn Gln Gly Glu Pro Met Arg Arg Val Phe Lys Val Met	
210 215 220	
cgt caa gta atc gat agc cat gat gat gta gaa att att tat ccg gtc	720
Arg Gln Val Ile Asp Ser His Asp Asp Val Glu Ile Ile Tyr Pro Val	
225 230 235 240	
cat tta tca cca aaa gta caa caa gta gca aat gaa gta ctc gga ggt	768
His Leu Ser Pro Lys Val Gln Gln Val Ala Asn Glu Val Leu Gly Gly	
245 250 255	
gat ccg cga atc cac ttg att gaa ccg ctt gat gtg gtt gat ttt cat	816
Asp Pro Arg Ile His Leu Ile Glu Pro Leu Asp Val Val Asp Phe His	
260 265 270	
aat tta gct aag cgg agc tac ttc att atg act gat tct ggt ggc gtt	864
Asn Leu Ala Lys Arg Ser Tyr Phe Ile Met Thr Asp Ser Gly Gly Val	
275 280 285	
caa gaa gaa gca cca agt ctt ggt aaa cca gta ctt gtg ctt aga gat	912
Gln Glu Glu Ala Pro Ser Leu Gly Lys Pro Val Leu Val Leu Arg Asp	
290 295 300	
act act gaa cgt cca gaa ggc gtt aag gct ggc acc ttg aaa tta gtg	960
Thr Thr Glu Arg Pro Glu Gly Val Lys Ala Gly Thr Leu Lys Leu Val	
305 310 315 320	
ggc acc gaa gta gat aag gta aga gaa agt atg ctt gaa ctg ctt gaa	1008
Gly Thr Glu Val Asp Lys Val Arg Glu Ser Met Leu Glu Leu Leu Glu	
325 330 335	
aat aaa gaa gca tat gac aag atg gct aat gcc aag aat cca tat gga	1056
Asn Lys Glu Ala Tyr Asp Lys Met Ala Asn Ala Lys Asn Pro Tyr Gly	
340 345 350	
gat ggt cat gcc agc gat cga atc atg aat gca att tat tac tac ttc	1104
Asp Gly His Ala Ser Asp Arg Ile Met Asn Ala Ile Tyr Tyr Tyr Phe	
355 360 365	
aat aga gat acc gca atc aaa ccg aat gat ttt aaa	1140
Asn Arg Asp Thr Ala Ile Lys Pro Asn Asp Phe Lys	
370 375 380	

<210> 244
 <211> 380
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 244
 Met Asn Lys Ile Lys Val Met Thr Val Phe Gly Thr Arg Pro Glu Ala
 1 5 10 15
 Ile Lys Met Ala Pro Leu Val Leu Lys Leu Lys Gln Asp Glu Arg Phe
 20 25 30
 Glu Glu Val Thr Val Val Ser Ala Gln His Arg Glu Met Leu Asp Gln
 35 40 45
 Val Leu Asp Ile Phe Lys Ile Lys Pro Asp Tyr Asp Phe Asn Ile Met
 50 55 60
 His Lys Asn Gln Thr Leu Glu Glu Ile Thr Ser Lys Val Met Ile Asp
 65 70 75 80
 Leu Ala Lys Val Ile Lys Lys Glu Lys Pro Asp Ile Val Leu Val His
 85 90 95
 Gly Asp Thr Thr Thr Ser Phe Ala Ala Gly Leu Ala Thr Phe Tyr Glu
 100 105 110
 Gln Thr Thr Leu Gly His Val Glu Ala Gly Leu Arg Thr Trp Asn Lys
 115 120 125
 Tyr Ser Pro Phe Pro Glu Glu Met Asn Arg Gln Met Thr Asp Asp Leu
 130 135 140
 Ala Asp Leu Tyr Phe Ala Pro Thr Glu Val Ser Lys Ala Asn Leu Leu
 145 150 155 160
 Lys Glu Asn His Pro Ala Asp Asn Ile Phe Val Thr Gly Asn Thr Ala
 165 170 175
 Ile Asp Ala Leu His Glu Thr Val Gln Lys Asp Tyr His His Asp Val
 180 185 190
 Leu Asp Glu Ile Lys Pro Gly Asn Lys Val Ile Leu Val Thr Met His
 195 200 205
 Arg Arg Glu Asn Gln Gly Glu Pro Met Arg Arg Val Phe Lys Val Met
 210 215 220
 Arg Gln Val Ile Asp Ser His Asp Asp Val Glu Ile Ile Tyr Pro Val
 225 230 235 240
 His Leu Ser Pro Lys Val Gln Gln Val Ala Asn Glu Val Leu Gly Gly
 245 250 255
 Asp Pro Arg Ile His Leu Ile Glu Pro Leu Asp Val Val Asp Phe His
 260 265 270
 Asn Leu Ala Lys Arg Ser Tyr Phe Ile Met Thr Asp Ser Gly Gly Val
 275 280 285
 Gln Glu Glu Ala Pro Ser Leu Gly Lys Pro Val Leu Val Leu Arg Asp
 290 295 300
 Thr Thr Glu Arg Pro Glu Gly Val Lys Ala Gly Thr Leu Lys Leu Val
 305 310 315 320
 Gly Thr Glu Val Asp Lys Val Arg Glu Ser Met Leu Glu Leu Leu Glu
 325 330 335
 Asn Lys Glu Ala Tyr Asp Lys Met Ala Asn Ala Lys Asn Pro Tyr Gly
 340 345 350
 Asp Gly His Ala Ser Asp Arg Ile Met Asn Ala Ile Tyr Tyr Tyr Phe
 355 360 365
 Asn Arg Asp Thr Ala Ile Lys Pro Asn Asp Phe Lys
 370 375 380

<210> 245
 <211> 1197
 <212> DNA
 <213> *Lactobacillus acidophilus*

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 620 - Cap5P

<220>
 <221> CDS
 <222> (1)...(1197)

<400> 245
 ttg atg caa gat agg gtt aaa tcg gtt ata gtt aag ttt agt tat cgg 48
 Met Met Gln Asp Arg Val Lys Ser Val Ile Val Lys Phe Ser Tyr Arg
 1 5 10 15
 agg aaa ctt atg aac aag att aaa gta atg act gtt ttt ggt acc cga 96
 Arg Lys Leu Met Asn Lys Ile Lys Val Met Thr Val Phe Gly Thr Arg
 20 25 30
 cca gaa gca atc aag atg gca cca ctt gtt tta aaa tta aag caa gat 144
 Pro Glu Ala Ile Lys Met Ala Pro Leu Val Leu Lys Leu Lys Gln Asp
 35 40 45
 gaa cgt ttt gaa gaa gtt acg gtt gtt tca gcg cag cac cgt gag atg 192
 Glu Arg Phe Glu Glu Val Thr Val Val Ser Ala Gln His Arg Glu Met
 50 55 60
 ctt gat cag gta ctc gat att ttt aaa att aag cca gac tat gac ttt 240
 Leu Asp Gln Val Leu Asp Ile Phe Lys Ile Lys Pro Asp Tyr Asp Phe
 65 70 75 80
 aac atc atg cat aaa aac cag act ttg gaa gaa att act tct aaa gtg 288
 Asn Ile Met His Lys Asn Gln Thr Leu Glu Glu Ile Thr Ser Lys Val
 85 90 95
 atg att gat ttg gct aaa gta att aag aaa gaa aag cct gat att gtt 336
 Met Ile Asp Leu Ala Lys Val Ile Lys Lys Glu Lys Pro Asp Ile Val
 100 105 110
 tta gtt cat ggc gat act aca act agt ttt gcg gca gga ctt gcc acc 384
 Leu Val His Gly Asp Thr Thr Thr Ser Phe Ala Ala Gly Leu Ala Thr
 115 120 125
 ttt tat gaa caa aca act ctg ggg cac gta gaa gcc ggt ctt cgt act 432
 Phe Tyr Glu Gln Thr Thr Leu Gly His Val Glu Ala Gly Leu Arg Thr
 130 135 140
 tgg aat aaa tat tca ccg ttc cct gaa gag atg aat cgt caa atg act 480
 Trp Asn Lys Tyr Ser Pro Phe Pro Glu Glu Met Asn Arg Gln Met Thr
 145 150 155 160
 gat gac ttg gca gac tta tat ttt gct cca act gaa gtg tcc aag gca 528

Asp Asp Leu Ala Asp Leu Tyr Phe Ala Pro Thr Glu Val Ser Lys Ala	
165 170 175	
aat tta tta aaa gaa aac cat cca gca gat aat att ttt gtt aca ggt	576
Asn Leu Leu Lys Glu Asn His Pro Ala Asp Asn Ile Phe Val Thr Gly	
180 185 190	
aat aca gct atc gat gcg ctt cat gaa act gtt caa aaa gat tat cat	624
Asn Thr Ala Ile Asp Ala Leu His Glu Thr Val Gln Lys Asp Tyr His	
195 200 205	
cac gat gtt tta gat gaa att aaa ccg gga aat aaa gtt atc ttg gtg	672
His Asp Val Leu Asp Glu Ile Lys Pro Gly Asn Lys Val Ile Leu Val	
210 215 220	
aca atg cat aga cga gaa aat cag gcc gaa cct atg cgt cgc gta ttt	720
Thr Met His Arg Arg Glu Asn Gln Gly Glu Pro Met Arg Arg Val Phe	
225 230 235 240	
aaa gtc atg cgt cag gta atc gat agc cat gat gat gta gaa att att	768
Lys Val Met Arg Gln Val Ile Asp Ser His Asp Asp Val Glu Ile Ile	
245 250 255	
tat cca gtc cat tta tca cca aaa gta caa caa gta gca aat gag gta	816
Tyr Pro Val His Leu Ser Pro Lys Val Gln Gln Val Ala Asn Glu Val	
260 265 270	
ctc gga ggt gat cca cgt att cac ttg att gaa ccg ctt gat gtg gtt	864
Leu Gly Gly Asp Pro Arg Ile His Leu Ile Glu Pro Leu Asp Val Val	
275 280 285	
gat ttt cat aat tta gct aag cgg agc tac ttc att atg act gat tct	912
Asp Phe His Asn Leu Ala Lys Arg Ser Tyr Phe Ile Met Thr Asp Ser	
290 295 300	
ggg ggc gtt caa gaa gaa gca cca agt ctt ggt aaa ccg gta ctt gtg	960
Gly Gly Val Gln Glu Glu Ala Pro Ser Leu Gly Lys Pro Val Leu Val	
305 310 315 320	
ctt aga gat act act gaa cgt cca gaa ggc gtt aag gct ggc acc ttg	1008
Leu Arg Asp Thr Thr Glu Arg Pro Glu Gly Val Lys Ala Gly Thr Leu	
325 330 335	
aaa tta gtg ggc acc gaa gta gat aag gta aga gaa agt atg ctt gaa	1056
Lys Leu Val Gly Thr Glu Val Asp Lys Val Arg Glu Ser Met Leu Glu	
340 345 350	
ctg ctt gaa aat aaa gaa gca tat gac aag atg gct aat gcc aag aat	1104
Leu Leu Glu Asn Lys Glu Ala Tyr Asp Lys Met Ala Asn Ala Lys Asn	
355 360 365	
cca tat gga gat ggt cat gcc agc gat cga atc atg aat gca att tat	1152
Pro Tyr Gly Asp Gly His Ala Ser Asp Arg Ile Met Asn Ala Ile Tyr	
370 375 380	
tac tac ttc aat aga gat acc gta atc aaa cct aaa gat ttt gaa	1197
Tyr Tyr Phe Asn Arg Asp Thr Val Ile Lys Pro Lys Asp Phe Glu	

385

390

395

<210> 246

<211> 399

<212> PRT

<213> Lactobacillus acidophilus

<400> 246

```

Met Met Gln Asp Arg Val Lys Ser Val Ile Val Lys Phe Ser Tyr Arg
 1           5           10           15
Arg Lys Leu Met Asn Lys Ile Lys Val Met Thr Val Phe Gly Thr Arg
      20           25           30
Pro Glu Ala Ile Lys Met Ala Pro Leu Val Leu Lys Leu Lys Gln Asp
      35           40           45
Glu Arg Phe Glu Glu Val Thr Val Val Ser Ala Gln His Arg Glu Met
 50           55           60
Leu Asp Gln Val Leu Asp Ile Phe Lys Ile Lys Pro Asp Tyr Asp Phe
 65           70           75           80
Asn Ile Met His Lys Asn Gln Thr Leu Glu Ile Thr Ser Lys Val
      85           90           95
Met Ile Asp Leu Ala Lys Val Ile Lys Lys Glu Lys Pro Asp Ile Val
      100           105           110
Leu Val His Gly Asp Thr Thr Thr Ser Phe Ala Ala Gly Leu Ala Thr
      115           120           125
Phe Tyr Glu Gln Thr Thr Leu Gly His Val Glu Ala Gly Leu Arg Thr
      130           135           140
Trp Asn Lys Tyr Ser Pro Phe Pro Glu Glu Met Asn Arg Gln Met Thr
      145           150           155           160
Asp Asp Leu Ala Asp Leu Tyr Phe Ala Pro Thr Glu Val Ser Lys Ala
      165           170           175
Asn Leu Leu Lys Glu Asn His Pro Ala Asp Asn Ile Phe Val Thr Gly
      180           185           190
Asn Thr Ala Ile Asp Ala Leu His Glu Thr Val Gln Lys Asp Tyr His
      195           200           205
His Asp Val Leu Asp Glu Ile Lys Pro Gly Asn Lys Val Ile Leu Val
      210           215           220
Thr Met His Arg Arg Glu Asn Gln Gly Glu Pro Met Arg Arg Val Phe
      225           230           235           240
Lys Val Met Arg Gln Val Ile Asp Ser His Asp Asp Val Glu Ile Ile
      245           250           255
Tyr Pro Val His Leu Ser Pro Lys Val Gln Gln Val Ala Asn Glu Val
      260           265           270
Leu Gly Gly Asp Pro Arg Ile His Leu Ile Glu Pro Leu Asp Val Val
      275           280           285
Asp Phe His Asn Leu Ala Lys Arg Ser Tyr Phe Ile Met Thr Asp Ser
      290           295           300
Gly Gly Val Gln Glu Glu Ala Pro Ser Leu Gly Lys Pro Val Leu Val
      305           310           315           320
Leu Arg Asp Thr Thr Glu Arg Pro Glu Gly Val Lys Ala Gly Thr Leu
      325           330           335
Lys Leu Val Gly Thr Glu Val Asp Lys Val Arg Glu Ser Met Leu Glu
      340           345           350
Leu Leu Glu Asn Lys Glu Ala Tyr Asp Lys Met Ala Asn Ala Lys Asn
      355           360           365
Pro Tyr Gly Asp Gly His Ala Ser Asp Arg Ile Met Asn Ala Ile Tyr

```

370 375 380
 Tyr Tyr Phe Asn Arg Asp Thr Val Ile Lys Pro Lys Asp Phe Glu
 385 390 395

<210> 247
 <211> 696
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 526 - CpsIVN

<220>
 <221> CDS
 <222> (1)...(696)

<400> 247
 atg att cca aaa atc atc cat tac gtt tgg gta ggt cat aat cca aag 48
 Met Ile Pro Lys Ile Ile His Tyr Val Trp Val Gly His Asn Pro Lys
 1 5 10 15

 tct aag ttg atc caa gag tgt att gcc act tgg aag gaa aaa tta cct 96
 Ser Lys Leu Ile Gln Glu Cys Ile Ala Thr Trp Lys Glu Lys Leu Pro
 20 25 30

 gat tat caa ttt att gag tgg aat gaa gat aat ttt gat atg cac gaa 144
 Asp Tyr Gln Phe Ile Glu Trp Asn Glu Asp Asn Phe Asp Met His Glu
 35 40 45

 aat aag tac att gag caa gct tat aag gca aaa aag tgg gct ttt gtt 192
 Asn Lys Tyr Ile Glu Gln Ala Tyr Lys Ala Lys Lys Trp Ala Phe Val
 50 55 60

 tca gat tat att cgt gct aaa gct atc tat gaa caa ggt ggg att tat 240
 Ser Asp Tyr Ile Arg Ala Lys Ala Ile Tyr Glu Gln Gly Gly Ile Tyr
 65 70 75 80

 tta gat aca gat gtg cgt gta att gct agt ctg acg cct ttg ctt gat 288
 Leu Asp Thr Asp Val Arg Val Ile Ala Ser Leu Thr Pro Leu Leu Asp
 85 90 95

 aac aag gcc ttt att ggc ttt gaa aac aac aat tat ctt tcg gct gca 336
 Asn Lys Ala Phe Ile Gly Phe Glu Asn Asn Asn Tyr Leu Ser Ala Ala
 100 105 110

 att ttt ggc gca gaa aaa ggg cat cca ttt atg cag gat atc ctt gat 384
 Ile Phe Gly Ala Glu Lys Gly His Pro Phe Met Gln Asp Ile Leu Asp
 115 120 125

 tat tat aaa gat cgt aat ttt gaa tat gat gta aat aat caa atg gca 432
 Tyr Tyr Lys Asp Arg Asn Phe Glu Tyr Asp Val Asn Asn Gln Met Ala
 130 135 140

```

ggc gta aat agt gtt tcc gtt act gat atg ctg att gat cgg tat ggt      480
Gly Val Asn Ser Val Ser Val Thr Asp Met Leu Ile Asp Arg Tyr Gly
145                               150                               155                               160

tta aag att ggt aac aag gaa cag gaa tta aag gaa ggt att cat gtt      528
Leu Lys Ile Gly Asn Lys Glu Gln Glu Leu Lys Glu Gly Ile His Val
165                               170                               175

tat cca gat ggc gtt tta tgt aat ccg tct gtt aac tca ctt tcg att      576
Tyr Pro Asp Gly Val Leu Cys Asn Pro Ser Val Asn Ser Leu Ser Ile
180                               185                               190

cac tta ttt acg gga act tgg atg aac gga aaa cat tca ttt aaa cat      624
His Leu Phe Thr Gly Thr Trp Met Asn Gly Lys His Ser Phe Lys His
195                               200                               205

aaa ctt gtc act ttc ctt aag cgt cat att aat aca cct aaa gag gca      672
Lys Leu Val Thr Phe Leu Lys Arg His Ile Asn Thr Pro Lys Glu Ala
210                               215                               220

ggg tta tat gcc aag tgg att cga
Gly Leu Tyr Ala Lys Trp Ile Arg
225                               230

```

<210> 248

<211> 232

<212> PRT

<213> Lactobacillus acidophilus

<400> 248

```

Met Ile Pro Lys Ile Ile His Tyr Val Trp Val Gly His Asn Pro Lys
1      5      10      15
Ser Lys Leu Ile Gln Glu Cys Ile Ala Thr Trp Lys Glu Lys Leu Pro
20     25     30
Asp Tyr Gln Phe Ile Glu Trp Asn Glu Asp Asn Phe Asp Met His Glu
35     40     45
Asn Lys Tyr Ile Glu Gln Ala Tyr Lys Ala Lys Lys Trp Ala Phe Val
50     55     60
Ser Asp Tyr Ile Arg Ala Lys Ala Ile Tyr Glu Gln Gly Gly Ile Tyr
65     70     75     80
Leu Asp Thr Asp Val Arg Val Ile Ala Ser Leu Thr Pro Leu Leu Asp
85     90     95
Asn Lys Ala Phe Ile Gly Phe Glu Asn Asn Tyr Leu Ser Ala Ala
100    105    110
Ile Phe Gly Ala Glu Lys Gly His Pro Phe Met Gln Asp Ile Leu Asp
115    120    125
Tyr Tyr Lys Asp Arg Asn Phe Glu Tyr Asp Val Asn Asn Gln Met Ala
130    135    140
Gly Val Asn Ser Val Ser Val Thr Asp Met Leu Ile Asp Arg Tyr Gly
145    150    155    160
Leu Lys Ile Gly Asn Lys Glu Gln Glu Leu Lys Glu Gly Ile His Val
165    170    175
Tyr Pro Asp Gly Val Leu Cys Asn Pro Ser Val Asn Ser Leu Ser Ile
180    185    190
His Leu Phe Thr Gly Thr Trp Met Asn Gly Lys His Ser Phe Lys His
195    200    205

```

Lys Leu Val Thr Phe Leu Lys Arg His Ile Asn Thr Pro Lys Glu Ala
 210 215 220
 Gly Leu Tyr Ala Lys Trp Ile Arg
 225 230

<210> 249
 <211> 1161
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 444 - lipopolysaccharide biosynthesis protein

<220>
 <221> CDS
 <222> (1)...(1161)

<400> 249
 atg aat att ggt ctt tat acc gat aca tat ttt ccc caa ata agt ggc 48
 Met Asn Ile Gly Leu Tyr Thr Asp Thr Tyr Phe Pro Gln Ile Ser Gly
 1 5 10 15
 gta gct act tct att agg acg cta aaa gat gcg ctt gaa aga cag ggg 96
 Val Ala Thr Ser Ile Arg Thr Leu Lys Asp Ala Leu Glu Arg Gln Gly
 20 25 30
 cat aat gta ttt att ttt aca act aca gat cca aat gta gaa aag ggc 144
 His Asn Val Phe Ile Phe Thr Thr Thr Asp Pro Asn Val Glu Lys Gly
 35 40 45
 act gtt gag cca aat gtt ttt cgt ttt agc agt ata cct ttt gtt tca 192
 Thr Val Glu Pro Asn Val Phe Arg Phe Ser Ser Ile Pro Phe Val Ser
 50 55 60
 ttc aca gat cgt aga att gca ttt aga ggc tta ttt gaa gca act aag 240
 Phe Thr Asp Arg Arg Ile Ala Phe Arg Gly Leu Phe Glu Ala Thr Lys
 65 70 75 80
 gta gct aag gaa gta aat ttg gat att gta cat aca caa act gaa ttt 288
 Val Ala Lys Glu Val Asn Leu Asp Ile Val His Thr Gln Thr Glu Phe
 85 90 95
 gct tta ggt aca att ggc aaa tat gta gcc cac caa tta gat att cct 336
 Ala Leu Gly Thr Ile Gly Lys Tyr Val Ala His Gln Leu Asp Ile Pro
 100 105 110
 gca att cat act tat cac aca atg tat gaa gat tat ttg cat tat att 384
 Ala Ile His Thr Tyr His Thr Met Tyr Glu Asp Tyr Leu His Tyr Ile
 115 120 125
 tta aat ggt cac tta ttg cga cca tat cat gtt aaa caa ttc gta aaa 432
 Leu Asn Gly His Leu Leu Arg Pro Tyr His Val Lys Gln Phe Val Lys
 130 135 140

agc tat tta aaa aat atg gat ggc tgt att gcc cca agt gga cgt gta	480
Ser Tyr Leu Lys Asn Met Asp Gly Cys Ile Ala Pro Ser Gly Arg Val	
145 150 155 160	
gaa gat ttg tta aag cga tat ggc gtg caa att cca att agg gta att	528
Glu Asp Leu Leu Lys Arg Tyr Gly Val Gln Ile Pro Ile Arg Val Ile	
165 170 175	
cct act gga gta gat ttg cag gga atg aat ggc gat gct gaa cgt gat	576
Pro Thr Gly Val Asp Leu Gln Gly Met Asn Gly Asp Ala Glu Arg Asp	
180 185 190	
gta cgt cag gaa tta gga atc gac aaa gat gct cct gta att tta act	624
Val Arg Gln Glu Leu Gly Ile Asp Lys Asp Ala Pro Val Ile Leu Thr	
195 200 205	
tta agt. aga att gca gca gaa aag aaa ata aat cat att ctt aat gtg	672
Leu Ser Arg Ile Ala Ala Glu Lys Lys Ile Asn His Ile Leu Asn Val	
210 215 220	
atg cca gca att gta gaa gaa ttt cca aat att aaa ttt gta att gcc	720
Met Pro Ala Ile Val Glu Glu Phe Pro Asn Ile Lys Phe Val Ile Ala	
225 230 235 240	
ggg gat gga cct gat gtt aaa gtg ctg aaa gaa caa gtt gaa cgt tta	768
Gly Asp Gly Pro Asp Val Lys Val Leu Lys Glu Gln Val Glu Arg Leu	
245 250 255	
act tta gaa gat tat gtt tta ttt gtc ggt aac gtt gat cat gga gat	816
Thr Leu Glu Asp Tyr Val Leu Phe Val Gly Asn Val Asp His Gly Asp	
260 265 270	
gta ggc aat tat tat cga atg gcc gat ctt ttt gtt tct gcc agt gac	864
Val Gly Asn Tyr Tyr Arg Met Ala Asp Leu Phe Val Ser Ala Ser Asp	
275 280 285	
act gaa acc caa ggt ctt act tat ata gaa gct ttg gct gca ggt aca	912
Thr Glu Thr Gln Gly Leu Thr Tyr Ile Glu Ala Leu Ala Ala Gly Thr	
290 295 300	
cca tgt gta gtt tac gac act gat tac act gaa aat att ttt gat aat	960
Pro Cys Val Val Tyr Asp Thr Asp Tyr Thr Glu Asn Ile Phe Asp Asn	
305 310 315 320	
gat gtc ttt gga cgt act ttt gtt aca cag aag gaa atg ttg caa gaa	1008
Asp Val Phe Gly Arg Thr Phe Val Thr Gln Lys Glu Met Leu Gln Glu	
325 330 335	
att att gaa tta ttg aaa aaa gga cac aat. aga att cca caa gat ctt	1056
Ile Ile Glu Leu Leu Lys Lys Gly His Asn Arg Ile Pro Gln Asp Leu	
340 345 350	
tta caa aat aaa ttg cag aag att tca tcg gag caa ttt gct aca aat	1104
Leu Gln Asn Lys Leu Gln Lys Ile Ser Ser Glu Gln Phe Ala Thr Asn	
355 360 365	

gtc cat gat ttt tat aaa tac gcg att gat cat tat caa cct aaa cat 1152
 Val His Asp Phe Tyr Lys Tyr Ala Ile Asp His Tyr Gln Pro Lys His
 370 375 380

gaa gaa ata 1161
 Glu Glu Ile
 385

<210> 250

<211> 387

<212> PRT

<213> *Lactobacillus acidophilus*

<400> 250

Met Asn Ile Gly Leu Tyr Thr Asp Thr Tyr Phe Pro Gln Ile Ser Gly
 1 5 10 15
 Val Ala Thr Ser Ile Arg Thr Leu Lys Asp Ala Leu Glu Arg Gln Gly
 20 25 30
 His Asn Val Phe Ile Phe Thr Thr Thr Asp Pro Asn Val Glu Lys Gly
 35 40 45
 Thr Val Glu Pro Asn Val Phe Arg Phe Ser Ser Ile Pro Phe Val Ser
 50 55 60
 Phe Thr Asp Arg Arg Ile Ala Phe Arg Gly Leu Phe Glu Ala Thr Lys
 65 70 75 80
 Val Ala Lys Glu Val Asn Leu Asp Ile Val His Thr Gln Thr Glu Phe
 85 90 95
 Ala Leu Gly Thr Ile Gly Lys Tyr Val Ala His Gln Leu Asp Ile Pro
 100 105 110
 Ala Ile His Thr Tyr His Thr Met Tyr Glu Asp Tyr Leu His Tyr Ile
 115 120 125
 Leu Asn Gly His Leu Leu Arg Pro Tyr His Val Lys Gln Phe Val Lys
 130 135 140
 Ser Tyr Leu Lys Asn Met Asp Gly Cys Ile Ala Pro Ser Gly Arg Val
 145 150 155 160
 Glu Asp Leu Leu Lys Arg Tyr Gly Val Gln Ile Pro Ile Arg Val Ile
 165 170 175
 Pro Thr Gly Val Asp Leu Gln Gly Met Asn Gly Asp Ala Glu Arg Asp
 180 185 190
 Val Arg Gln Glu Leu Gly Ile Asp Lys Asp Ala Pro Val Ile Leu Thr
 195 200 205
 Leu Ser Arg Ile Ala Ala Glu Lys Lys Ile Asn His Ile Leu Asn Val
 210 215 220
 Met Pro Ala Ile Val Glu Phe Pro Asn Ile Lys Phe Val Ile Ala
 225 230 235 240
 Gly Asp Gly Pro Asp Val Lys Val Leu Lys Glu Gln Val Glu Arg Leu
 245 250 255
 Thr Leu Glu Asp Tyr Val Leu Phe Val Gly Asn Val Asp His Gly Asp
 260 265 270
 Val Gly Asn Tyr Tyr Arg Met Ala Asp Leu Phe Val Ser Ala Ser Asp
 275 280 285
 Thr Glu Thr Gln Gly Leu Thr Tyr Ile Glu Ala Leu Ala Ala Gly Thr
 290 295 300
 Pro Cys Val Val Tyr Asp Thr Asp Tyr Thr Glu Asn Ile Phe Asp Asn
 305 310 315 320
 Asp Val Phe Gly Arg Thr Phe Val Thr Gln Lys Glu Met Leu Gln Glu
 325 330 335

Ile Ile Glu Leu Leu Lys Lys Gly His Asn Arg Ile Pro Gln Asp Leu
 340 345 350
 Leu Gln Asn Lys Leu Gln Lys Ile Ser Ser Glu Gln Phe Ala Thr Asn
 355 360 365
 Val His Asp Phe Tyr Lys Tyr Ala Ile Asp His Tyr Gln Pro Lys His
 370 375 380
 Glu Glu Ile
 385

<210> 251

<211> 468

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 105 - cellulose synthase

<220>

<221> CDS

<222> (1)...(468)

<400> 251

atg aat gat gta atg caa ata atc act ctt att tca att tgg ctg tcg	48
Met Asn Asp Val Met Gln Ile Ile Thr Leu Ile Ser Ile Trp Leu Ser	
1 5 10 15	
tta ctg atg tct att att act tta agt gga gca att gca ttt tgg ctt	96
Leu Leu Met Ser Ile Ile Thr Leu Ser Gly Ala Ile Ala Phe Trp Leu	
20 25 30	
aaa cat agt aag gtt ttg gtt aaa ata gtg cca cta aag cgg tat ccc	144
Lys His Ser Lys Val Leu Val Lys Ile Val Pro Leu Lys Arg Tyr Pro	
35 40 45	
aaa gta acg att gtt gtt cca gct cat aat gaa gaa ttg gta att gag	192
Lys Val Thr Ile Val Val Pro Ala His Asn Glu Glu Leu Val Ile Glu	
50 55 60	
aaa aca gct aca gcg att tta aat tta aat tat cct aag gat aaa ttg	240
Lys Thr Ala Thr Ala Ile Leu Asn Leu Asn Tyr Pro Lys Asp Lys Leu	
65 70 75 80	
gaa gta tta ttt tat gct gat aat tgt gaa gat aaa aca gct gat gtt	288
Glu Val Leu Phe Tyr Ala Asp Asn Cys Glu Asp Lys Thr Ala Asp Val	
85 90 95	
tta gat gaa gtt tta aaa aat aag cag tat tac aaa tgt aac gca cga	336
Leu Asp Glu Val Leu Lys Asn Lys Gln Tyr Tyr Lys Cys Asn Ala Arg	
100 105 110	
gtt att aga cga act ggt tct ggt ggt aaa gct ggt gtg ttg aat gat	384
Val Ile Arg Arg Thr Gly Ser Gly Gly Lys Ala Gly Val Leu Asn Asp	
115 120 125	

gct ttg aag att gct cat ggt gaa tat tta ggt gtt tat gat gca gat 432
 Ala Leu Lys Ile Ala His Gly Glu Tyr Leu Gly Val Tyr Asp Ala Asp
 130 135 140

gcg atg ccc aga aga gaa tgc att ata ctt tct agt 468
 Ala Met Pro Arg Arg Glu Cys Ile Ile Leu Ser Ser
 145 150 155

<210> 252

<211> 156

<212> PRT

<213> Lactobacillus acidophilus

<400> 252

Met Asn Asp Val Met Gln Ile Ile Thr Leu Ile Ser Ile Trp Leu Ser
 1 5 10 15
 Leu Leu Met Ser Ile Ile Thr Leu Ser Gly Ala Ile Ala Phe Trp Leu
 20 25 30
 Lys His Ser Lys Val Leu Val Lys Ile Val Pro Leu Lys Arg Tyr Pro
 35 40 45
 Lys Val Thr Ile Val Val Pro Ala His Asn Glu Glu Leu Val Ile Glu
 50 55 60
 Lys Thr Ala Thr Ala Ile Leu Asn Leu Asn Tyr Pro Lys Asp Lys Leu
 65 70 75 80
 Glu Val Leu Phe Tyr Ala Asp Asn Cys Glu Asp Lys Thr Ala Asp Val
 85 90 95
 Leu Asp Glu Val Leu Lys Asn Lys Gln Tyr Tyr Lys Cys Asn Ala Arg
 100 105 110
 Val Ile Arg Arg Thr Gly Ser Gly Gly Lys Ala Gly Val Leu Asn Asp
 115 120 125
 Ala Leu Lys Ile Ala His Gly Glu Tyr Leu Gly Val Tyr Asp Ala Asp
 130 135 140
 Ala Met Pro Arg Arg Glu Cys Ile Ile Leu Ser Ser
 145 150 155

<210> 253

<211> 1470

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 507 - sucrose phosphorylase

<220>

<221> CDS

<222> (1)...(1470)

<400> 253

ttg aac ctt ttt tat aag gaa ggt tta aaa atg aaa tta caa aat aag 48
 Met Asn Leu Phe Tyr Lys Glu Gly Leu Lys Met Lys Leu Gln Asn Lys
 1 5 10 15

gca ata ttg ata act tat cca gat agt tta ggt cat aat ttg aag gac	96
Ala Ile Leu Ile Thr Tyr Pro Asp Ser Leu Gly His Asn Leu Lys Asp	
20 25 30	
ttg gat cat gta atg gat cgc tat ttt aat aaa acg ata ggt ggt att	144
Leu Asp His Val Met Asp Arg Tyr Phe Asn Lys Thr Ile Gly Gly Ile	
35 40 45	
cat tta tta cca ttt ttc cct tca aac ggt gat cgc ggt ttt tct cct	192
His Leu Leu Pro Phe Phe Pro Ser Asn Gly Asp Arg Gly Phe Ser Pro	
50 55 60	
aca aga tat gat gta gtt gag cct aag ttt ggt tca tgg gaa gat gta	240
Thr Arg Tyr Asp Val Val Glu Pro Lys Phe Gly Ser Trp Glu Asp Val	
65 70 75 80	
gaa aag tta agt caa aag tat tat ttg atg ttt gac ttt atg att aat	288
Glu Lys Leu Ser Gln Lys Tyr Tyr Leu Met Phe Asp Phe Met Ile Asn	
85 90 95	
cat ctt tct aaa aaa tcc tca tat ttt gaa gat ttt gaa gcc aag cac	336
His Leu Ser Lys Lys Ser Ser Tyr Phe Glu Asp Phe Glu Ala Lys His	
100 105 110	
gat aaa agc aaa tat agc gat ctt ttc tta agt tgg gat aaa ttt tgg	384
Asp Lys Ser Lys Tyr Ser Asp Leu Phe Leu Ser Trp Asp Lys Phe Trp	
115 120 125	
cca aag ggc aga cca act aaa gaa gat ata gat tta att tat aaa cga	432
Pro Lys Gly Arg Pro Thr Lys Glu Asp Ile Asp Leu Ile Tyr Lys Arg	
130 135 140	
aaa gat aag gcc cca tat caa aat att aaa ttt gaa gat ggt act cat	480
Lys Asp Lys Ala Pro Tyr Gln Asn Ile Lys Phe Glu Asp Gly Thr His	
145 150 155 160	
gaa aag atg tgg aat act ttc ggc cca gat caa atg gat ttg gat gtt	528
Glu Lys Met Trp Asn Thr Phe Gly Pro Asp Gln Met Asp Leu Asp Val	
165 170 175	
aga acc aag aca aca caa gat ttt ata aag cat aat tta caa aat ctt	576
Arg Thr Lys Thr Thr Gln Asp Phe Ile Lys His Asn Leu Gln Asn Leu	
180 185 190	
tct aaa cat ggt gct agt ttg att cgt tta gat gca ttt gct tat gca	624
Ser Lys His Gly Ala Ser Leu Ile Arg Leu Asp Ala Phe Ala Tyr Ala	
195 200 205	
att aaa aag tta gat aca aat gac ttc ttt gta gaa ccg gaa att tgg	672
Ile Lys Lys Leu Asp Thr Asn Asp Phe Phe Val Glu Pro Glu Ile Trp	
210 215 220	
aat tta ctc gaa aag gta aat gat tat ctt aaa gat act cca act act	720
Asn Leu Leu Glu Lys Val Asn Asp Tyr Leu Lys Asp Thr Pro Thr Thr	
225 230 235 240	

att ctg cct gaa att cat gag cat tat acg atg cca ttt aag gtg gca	768
Ile Leu Pro Glu Ile His Glu His Tyr Thr Met Pro Phe Lys Val Ala	
245 250 255	
gaa cat gga tac ttt att tat gat ttt gct tta cca atg gta ttg ttg	816
Glu His Gly Tyr Phe Ile Tyr Asp Phe Ala Leu Pro Met Val Leu Leu	
260 265 270	
tat tca ctt tat agc ggt aat agt act caa ctt gct gct tgg cta aag	864
Tyr Ser Leu Tyr Ser Gly Asn Ser Thr Gln Leu Ala Ala Trp Leu Lys	
275 280 285	
aaa tgt ccg atg aag caa ttt act act tta gat acc cac gat gga tta	912
Lys Cys Pro Met Lys Gln Phe Thr Thr Leu Asp Thr His Asp Gly Leu	
290 295 300	
ggc gta gtt gac gca aag gat att ctt acg gac gat caa att agc tac	960
Gly Val Val Asp Ala Lys Asp Ile Leu Thr Asp Asp Gln Ile Ser Tyr	
305 310 315 320	
aca aca aac gaa ctt tat aaa att ggt gct aac gtc aag aag aaa tat	1008
Thr Thr Asn Glu Leu Tyr Lys Ile Gly Ala Asn Val Lys Lys Lys Tyr	
325 330 335	
tct agt gct gaa tat cat aat ttg gat att tat caa att aat act act	1056
Ser Ser Ala Glu Tyr His Asn Leu Asp Ile Tyr Gln Ile Asn Thr Thr	
340 345 350	
tat tat tct gca ttg ggt aat gat gat aaa aaa tat ttt att gca cgg	1104
Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys Lys Tyr Phe Ile Ala Arg	
355 360 365	
tta tta caa atc ttt gcc cct ggt att cca caa att tat tat gtt gga	1152
Leu Leu Gln Ile Phe Ala Pro Gly Ile Pro Gln Ile Tyr Tyr Val Gly	
370 375 380	
ttg tta gca gga gaa aat gat att caa tta tta gag aag aca aaa gaa	1200
Leu Leu Ala Gly Glu Asn Asp Ile Gln Leu Leu Glu Lys Thr Lys Glu	
385 390 395 400	
gga cgc gat att aat cgc cac tat tat gat ttg gat gag att gcg gaa	1248
Gly Arg Asp Ile Asn Arg His Tyr Tyr Asp Leu Asp Glu Ile Ala Glu	
405 410 415	
caa gtt caa aga cct gta gta aaa tct ttg att aag tta ttg gaa ttt	1296
Gln Val Gln Arg Pro Val Val Lys Ser Leu Ile Lys Leu Leu Glu Phe	
420 425 430	
cgt aat tct gta cct gca ttt gat ttg gaa ggt tca atc aaa gtt gaa	1344
Arg Asn Ser Val Pro Ala Phe Asp Leu Glu Gly Ser Ile Lys Val Glu	
435 440 445	
act cca agt gaa cat gaa att att gtc act aga tca aat aag gca gga	1392
Thr Pro Ser Glu His Glu Ile Ile Val Thr Arg Ser Asn Lys Ala Gly	
450 455 460	
aca gaa gta gct agt acg tac gta gac ttt aag aac tta gac tat caa	1440

Thr Glu Val Ala Ser Thr Tyr Val Asp Phe Lys Asn Leu Asp Tyr Gln
 465 470 475 480

ggt aaa tac aat gat cag gtc ttt aat ttt 1470
 Val Lys Tyr Asn Asp Gln Val Phe Asn Phe
 485 490

<210> 254

<211> 490

<212> PRT

<213> Lactobacillus acidophilus

<400> 254

Met Asn Leu Phe Tyr Lys Glu Gly Leu Lys Met Lys Leu Gln Asn Lys
 1 5 10 15
 Ala Ile Leu Ile Thr Tyr Pro Asp Ser Leu Gly His Asn Leu Lys Asp
 20 25 30
 Leu Asp His Val Met Asp Arg Tyr Phe Asn Lys Thr Ile Gly Gly Ile
 35 40 45
 His Leu Leu Pro Phe Phe Pro Ser Asn Gly Asp Arg Gly Phe Ser Pro
 50 55 60
 Thr Arg Tyr Asp Val Val Glu Pro Lys Phe Gly Ser Trp Glu Asp Val
 65 70 75 80
 Glu Lys Leu Ser Gln Lys Tyr Tyr Leu Met Phe Asp Phe Met Ile Asn
 85 90 95
 His Leu Ser Lys Lys Ser Ser Tyr Phe Glu Asp Phe Glu Ala Lys His
 100 105 110
 Asp Lys Ser Lys Tyr Ser Asp Leu Phe Leu Ser Trp Asp Lys Phe Trp
 115 120 125
 Pro Lys Gly Arg Pro Thr Lys Glu Asp Ile Asp Leu Ile Tyr Lys Arg
 130 135 140
 Lys Asp Lys Ala Pro Tyr Gln Asn Ile Lys Phe Glu Asp Gly Thr His
 145 150 155 160
 Glu Lys Met Trp Asn Thr Phe Gly Pro Asp Gln Met Asp Leu Asp Val
 165 170 175
 Arg Thr Lys Thr Thr Gln Asp Phe Ile Lys His Asn Leu Gln Asn Leu
 180 185 190
 Ser Lys His Gly Ala Ser Leu Ile Arg Leu Asp Ala Phe Ala Tyr Ala
 195 200 205
 Ile Lys Lys Leu Asp Thr Asn Asp Phe Phe Val Glu Pro Glu Ile Trp
 210 215 220
 Asn Leu Leu Glu Lys Val Asn Asp Tyr Leu Lys Asp Thr Pro Thr Thr
 225 230 235 240
 Ile Leu Pro Glu Ile His Glu His Tyr Thr Met Pro Phe Lys Val Ala
 245 250 255
 Glu His Gly Tyr Phe Ile Tyr Asp Phe Ala Leu Pro Met Val Leu Leu
 260 265 270
 Tyr Ser Leu Tyr Ser Gly Asn Ser Thr Gln Leu Ala Ala Trp Leu Lys
 275 280 285
 Lys Cys Pro Met Lys Gln Phe Thr Thr Leu Asp Thr His Asp Gly Leu
 290 295 300
 Gly Val Val Asp Ala Lys Asp Ile Leu Thr Asp Asp Gln Ile Ser Tyr
 305 310 315 320
 Thr Thr Asn Glu Leu Tyr Lys Ile Gly Ala Asn Val Lys Lys Lys Tyr
 325 330 335
 Ser Ser Ala Glu Tyr His Asn Leu Asp Ile Tyr Gln Ile Asn Thr Thr

```

          340          345          350
Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys Lys Tyr Phe Ile Ala Arg
          355          360          365
Leu Leu Gln Ile Phe Ala Pro Gly Ile Pro Gln Ile Tyr Tyr Val Gly
          370          375          380
Leu Leu Ala Gly Glu Asn Asp Ile Gln Leu Leu Glu Lys Thr Lys Glu
385          390          395          400
Gly Arg Asp Ile Asn Arg His Tyr Tyr Asp Leu Asp Glu Ile Ala Glu
          405          410          415
Gln Val Gln Arg Pro Val Val Lys Ser Leu Ile Lys Leu Leu Glu Phe
          420          425          430
Arg Asn Ser Val Pro Ala Phe Asp Leu Glu Gly Ser Ile Lys Val Glu
          435          440          445
Thr Pro Ser Glu His Glu Ile Ile Val Thr Arg Ser Asn Lys Ala Gly
450          455          460
Thr Glu Val Ala Ser Thr Tyr Val Asp Phe Lys Asn Leu Asp Tyr Gln
465          470          475          480
Val Lys Tyr Asn Asp Gln Val Phe Asn Phe
          485          490

```

<210> 255

<211> 1644

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1616 - Polysaccharide transporter

<220>

<221> CDS

<222> (1)...(1644)

<400> 255

```

atg gaa gaa gaa aat aac tta aat agc aaa gat aca caa aat acc ttt 48
Met Glu Glu Glu Asn Asn Leu Asn Ser Lys Asp Thr Gln Asn Thr Phe
1          5          10          15

```

```

cta aaa ggt tct gcg tgg atg act ttt ggc tca att gcc tca aga att 96
Leu Lys Gly Ser Ala Trp Met Thr Phe Gly Ser Ile Ala Ser Arg Ile
          20          25          30

```

```

ctg gga gct tta tat att att ccg tgg tat gcc tgg atg ggg caa tat 144
Leu Gly Ala Leu Tyr Ile Ile Pro Trp Tyr Ala Trp Met Gly Gln Tyr
          35          40          45

```

```

ggt aat atc gcc aat gcc tta act gca cga agt tat aat att tat act 192
Gly Asn Ile Ala Asn Ala Leu Thr Ala Arg Ser Tyr Asn Ile Tyr Thr
          50          55          60

```

```

att ttt atc tta att tcg act gca ggt att cct ggt gcg atc gct aaa 240
Ile Phe Ile Leu Ile Ser Thr Ala Gly Ile Pro Gly Ala Ile Ala Lys
65          70          75          80

```

cag gta gca aag tat aat gct tta aat gaa tat gga att ggg cgt agg	288
Gln Val Ala Lys Tyr Asn Ala Leu Asn Glu Tyr Gly Ile Gly Arg Arg	
85 90 95	
tta ttc cat aaa gga tta att ttg atg gcc att cta ggg gtg gtt tca	336
Leu Phe His Lys Gly Leu Ile Leu Met Ala Ile Leu Gly Val Val Ser	
100 105 110	
gct gca att atg tat ttt gct tgc ccg ctt ctt gct tca aat ggt agt	384
Ala Ala Ile Met Tyr Phe Ala Ser Pro Leu Leu Ala Ser Asn Gly Ser	
115 120 125	
caa agt gat ccg agg caa att gcg gtt atg cgg agc ttg tca tat gca	432
Gln Ser Asp Pro Arg Gln Ile Ala Val Met Arg Ser Leu Ser Tyr Ala	
130 135 140	
atc ttg att atc cct att tta agt att atg cgt gga tat ttt cag ggt	480
Ile Leu Ile Ile Pro Ile Leu Ser Ile Met Arg Gly Tyr Phe Gln Gly	
145 150 155 160	
tat gcg gat atg atg cct agt gca atg tgc cag ttt gta gaa caa ttt	528
Tyr Ala Asp Met Met Pro Ser Ala Met Ser Gln Phe Val Glu Gln Phe	
165 170 175	
gcc cgt gtc gtc tgg atg ctt ttg act gct ttt gta att atg caa gtc	576
Ala Arg Val Val Trp Met Leu Leu Thr Ala Phe Val Ile Met Gln Val	
180 185 190	
cag cat ggg tca tat gtt cat gca gtt att caa tca aat ttg gct gct	624
Gln His Gly Ser Tyr Val His Ala Val Ile Gln Ser Asn Leu Ala Ala	
195 200 205	
gca gtt gga gca gca ttt ggg att gga tta tta gtc tgg ttt ttg ttt	672
Ala Val Gly Ala Ala Phe Gly Ile Gly Leu Leu Val Trp Phe Leu Phe	
210 215 220	
tca cgt agg aaa caa ttg gat tat cta gta gct aat tcc aat aat cgg	720
Ser Arg Arg Lys Gln Leu Asp Tyr Leu Val Ala Asn Ser Asn Asn Arg	
225 230 235 240	
tta cgt gtg tcc act aca gaa tta ttt gcg gaa att att gaa cag gca	768
Leu Arg Val Ser Thr Thr Glu Leu Phe Ala Glu Ile Ile Glu Gln Ala	
245 250 255	
att ccc ttt atc att att gac tca ggg att aca ttg ttc tgc ttg gtt	816
Ile Pro Phe Ile Ile Ile Asp Ser Gly Ile Thr Leu Phe Ser Leu Val	
260 265 270	
gat caa tat act ttc cat cca atg att gct ggg ttg gtt cat gca agt	864
Asp Gln Tyr Thr Phe His Pro Met Ile Ala Gly Leu Val His Ala Ser	
275 280 285	
tca gat gcg atc gaa gat tgg tat gca cta ttt ggc tta aat gct aat	912
Ser Asp Ala Ile Glu Asp Trp Tyr Ala Leu Phe Gly Leu Asn Ala Asn	
290 295 300	
aaa tta att atg att atc gta tct tta gct agt gca atg gca gta aca	960

Lys	Leu	Ile	Met	Ile	Ile	Val	Ser	Leu	Ala	Ser	Ala	Met	Ala	Val	Thr	
305					310					315					320	
gca	att	cca	ctt	ttg	tca	gct	gct	cat	aca	aga	ggg	gac	tac	aag	agt	1008
Ala	Ile	Pro	Leu	Leu	Ser	Ala	Ala	His	Thr	Arg	Gly	Asp	Tyr	Lys	Ser	
			325						330					335		
att	tct	cgt	cag	att	gct	aat	acg	atg	gat	tta	ttc	ttg	ttc	gta	atg	1056
Ile	Ser	Arg	Gln	Ile	Ala	Asn	Thr	Met	Asp	Leu	Phe	Leu	Phe	Val	Met	
			340					345						350		
att	cca	gcg	gca	ttt	gga	atg	gct	gcc	att	agt	cga	ccg	att	tat	aca	1104
Ile	Pro	Ala	Ala	Phe	Gly	Met	Ala	Ala	Ile	Ser	Arg	Pro	Ile	Tyr	Thr	
		355					360					365				
gtt	ttt	tat	gga	cca	gat	caa	tta	ggg	agt	aat	gtt	tta	tac	ttg	tct	1152
Val	Phe	Tyr	Gly	Pro	Asp	Gln	Leu	Gly	Ser	Asn	Val	Leu	Tyr	Leu	Ser	
	370					375					380					
gct	ttt	act	gca	atc	agt	tta	ggg	ttg	ttt	act	gta	tta	atg	gca	att	1200
Ala	Phe	Thr	Ala	Ile	Ser	Leu	Gly	Leu	Phe	Thr	Val	Leu	Met	Ala	Ile	
385					390					395				400		
ttg	cag	gga	ctt	tca	gaa	aat	ggc	ctg	gca	att	aag	tat	tta	gtt	cta	1248
Leu	Gln	Gly	Leu	Ser	Glu	Asn	Gly	Leu	Ala	Ile	Lys	Tyr	Leu	Val	Leu	
			405					410						415		
ggg	tta	att	tta	aaa	gga	att	cta	cag	tat	ccg	atg	atc	ttc	ttg	ttt	1296
Gly	Leu	Ile	Leu	Lys	Gly	Ile	Leu	Gln	Tyr	Pro	Met	Ile	Phe	Leu	Phe	
			420					425					430			
aag	ata	tat	ggg	cca	ctt	gta	gca	act	aat	tta	gga	tta	ttg	gta	ata	1344
Lys	Ile	Tyr	Gly	Pro	Leu	Val	Ala	Thr	Asn	Leu	Gly	Leu	Leu	Val	Ile	
		435					440					445				
gtt	ctg	ttg	tcg	ctc	aaa	cac	tta	gaa	gtt	cag	tat	aac	ttt	aac	tta	1392
Val	Leu	Leu	Ser	Leu	Lys	His	Leu	Glu	Val	Gln	Tyr	Asn	Phe	Asn	Leu	
	450					455					460					
aat	cga	act	agt	cgg	aga	tta	gta	ggg	att	aca	gcc	ttt	tca	att	gga	1440
Asn	Arg	Thr	Ser	Arg	Arg	Leu	Val	Gly	Ile	Thr	Ala	Phe	Ser	Ile	Gly	
465					470					475					480	
atg	ttt	ata	att	gtt	aaa	ttg	gtt	gaa	atg	gga	tta	ggg	aaa	ttc	tta	1488
Met	Phe	Ile	Ile	Val	Lys	Leu	Val	Glu	Met	Gly	Leu	Gly	Lys	Phe	Leu	
				485				490						495		
agt	cct	gat	cga	aga	att	tca	gct	tta	att	tta	gta	att	gta	gca	gta	1536
Ser	Pro	Asp	Arg	Arg	Ile	Ser	Ala	Leu	Ile	Leu	Val	Ile	Val	Ala	Val	
			500					505					510			
agt	att	ggc	ata	ata	ttc	tat	ggc	ttt	gct	gca	ttg	aag	aca	gat	tta	1584
Ser	Ile	Gly	Ile	Ile	Phe	Tyr	Gly	Phe	Ala	Ala	Leu	Lys	Thr	Asp	Leu	
		515					520					525				
gct	caa	aag	att	atg	gga	agt	aaa	atc	gaa	agt	att	ttg	gtt	agg	tta	1632
Ala	Gln	Lys	Ile	Met	Gly	Ser	Lys	Ile	Glu	Ser	Ile	Leu	Val	Arg	Leu	

530

535

540

cgc atc cat gat
Arg Ile His Asp
545

1644

<210> 256

<211> 548

<212> PRT

<213> *Lactobacillus acidophilus*

<400> 256

Met	Glu	Glu	Glu	Asn	Asn	Leu	Asn	Ser	Lys	Asp	Thr	Gln	Asn	Thr	Phe
1				5					10				15		
Leu	Lys	Gly	Ser	Ala	Trp	Met	Thr	Phe	Gly	Ser	Ile	Ala	Ser	Arg	Ile
			20					25					30		
Leu	Gly	Ala	Leu	Tyr	Ile	Ile	Pro	Trp	Tyr	Ala	Trp	Met	Gly	Gln	Tyr
		35					40					45			
Gly	Asn	Ile	Ala	Asn	Ala	Leu	Thr	Ala	Arg	Ser	Tyr	Asn	Ile	Tyr	Thr
	50					55				60					
Ile	Phe	Ile	Leu	Ile	Ser	Thr	Ala	Gly	Ile	Pro	Gly	Ala	Ile	Ala	Lys
65				70					75						80
Gln	Val	Ala	Lys	Tyr	Asn	Ala	Leu	Asn	Glu	Tyr	Gly	Ile	Gly	Arg	Arg
			85					90					95		
Leu	Phe	His	Lys	Gly	Leu	Ile	Leu	Met	Ala	Ile	Leu	Gly	Val	Val	Ser
			100					105					110		
Ala	Ala	Ile	Met	Tyr	Phe	Ala	Ser	Pro	Leu	Leu	Ala	Ser	Asn	Gly	Ser
		115					120					125			
Gln	Ser	Asp	Pro	Arg	Gln	Ile	Ala	Val	Met	Arg	Ser	Leu	Ser	Tyr	Ala
	130				135					140					
Ile	Leu	Ile	Ile	Pro	Ile	Leu	Ser	Ile	Met	Arg	Gly	Tyr	Phe	Gln	Gly
145				150					155						160
Tyr	Ala	Asp	Met	Met	Pro	Ser	Ala	Met	Ser	Gln	Phe	Val	Glu	Gln	Phe
			165					170					175		
Ala	Arg	Val	Val	Trp	Met	Leu	Leu	Thr	Ala	Phe	Val	Ile	Met	Gln	Val
			180					185					190		
Gln	His	Gly	Ser	Tyr	Val	His	Ala	Val	Ile	Gln	Ser	Asn	Leu	Ala	Ala
	195					200						205			
Ala	Val	Gly	Ala	Ala	Phe	Gly	Ile	Gly	Leu	Leu	Val	Trp	Phe	Leu	Phe
	210					215					220				
Ser	Arg	Arg	Lys	Gln	Leu	Asp	Tyr	Leu	Val	Ala	Asn	Ser	Asn	Asn	Arg
225				230					235						240
Leu	Arg	Val	Ser	Thr	Thr	Glu	Leu	Phe	Ala	Glu	Ile	Ile	Glu	Gln	Ala
			245					250					255		
Ile	Pro	Phe	Ile	Ile	Ile	Asp	Ser	Gly	Ile	Thr	Leu	Phe	Ser	Leu	Val
		260						265					270		
Asp	Gln	Tyr	Thr	Phe	His	Pro	Met	Ile	Ala	Gly	Leu	Val	His	Ala	Ser
	275					280						285			
Ser	Asp	Ala	Ile	Glu	Asp	Trp	Tyr	Ala	Leu	Phe	Gly	Leu	Asn	Ala	Asn
	290					295					300				
Lys	Leu	Ile	Met	Ile	Ile	Val	Ser	Leu	Ala	Ser	Ala	Met	Ala	Val	Thr
305				310					315						320
Ala	Ile	Pro	Leu	Leu	Ser	Ala	Ala	His	Thr	Arg	Gly	Asp	Tyr	Lys	Ser
			325					330					335		
Ile	Ser	Arg	Gln	Ile	Ala	Asn	Thr	Met	Asp	Leu	Phe	Leu	Phe	Val	Met
			340					345					350		

```

Ile Pro Ala Ala Phe Gly Met Ala Ala Ile Ser Arg Pro Ile Tyr Thr
      355              360              365
Val Phe Tyr Gly Pro Asp Gln Leu Gly Ser Asn Val Leu Tyr Leu Ser
      370              375              380
Ala Phe Thr Ala Ile Ser Leu Gly Leu Phe Thr Val Leu Met Ala Ile
385              390              395              400
Leu Gln Gly Leu Ser Glu Asn Gly Leu Ala Ile Lys Tyr Leu Val Leu
      405              410              415
Gly Leu Ile Leu Lys Gly Ile Leu Gln Tyr Pro Met Ile Phe Leu Phe
      420              425              430
Lys Ile Tyr Gly Pro Leu Val Ala Thr Asn Leu Gly Leu Leu Val Ile
      435              440              445
Val Leu Leu Ser Leu Lys His Leu Glu Val Gln Tyr Asn Phe Asn Leu
      450              455              460
Asn Arg Thr Ser Arg Arg Leu Val Gly Ile Thr Ala Phe Ser Ile Gly
465              470              475              480
Met Phe Ile Ile Val Lys Leu Val Glu Met Gly Leu Gly Lys Phe Leu
      485              490              495
Ser Pro Asp Arg Arg Ile Ser Ala Leu Ile Leu Val Ile Val Ala Val
      500              505              510
Ser Ile Gly Ile Ile Phe Tyr Gly Phe Ala Ala Leu Lys Thr Asp Leu
      515              520              525
Ala Gln Lys Ile Met Gly Ser Lys Ile Glu Ser Ile Leu Val Arg Leu
      530              535              540
Arg Ile His Asp
545

```

<210> 257

<211> 1089

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 520 - LPS biosynthesis protein

<220>

<221> CDS

<222> (1)...(1089)

<400> 257

```

atg aag gtt ttg cat gta aat gct ggt ctt gaa aat ggt ggc ggg tta 48
Met Lys Val Leu His Val Asn Ala Gly Leu Glu Asn Gly Gly Gly Leu
  1              5              10              15

```

```

tcg cat att gta aat ttg ctt act gag gct aaa aga gaa aat aaa gat 96
Ser His Ile Val Asn Leu Leu Thr Glu Ala Lys Arg Glu Asn Lys Asp
      20              25              30

```

```

ttt gat tta tta act ttg gct gat ggt cca gtg gct gct gca gca aga 144
Phe Asp Leu Leu Thr Leu Ala Asp Gly Pro Val Ala Ala Ala Ala Arg
      35              40              45

```

```

gaa cat gga att aat act tat gta ctt gga gca aag agt cgc tac aat 192

```

Glu	His	Gly	Ile	Asn	Thr	Tyr	Val	Leu	Gly	Ala	Lys	Ser	Arg	Tyr	Asn		
50						55					60						
ttg	gca	agt	tta	aaa	aag	ttg	atc	aaa	ttt	att	aat	gat	gga	cat	tat	240	
Leu	Ala	Ser	Leu	Lys	Lys	Leu	Ile	Lys	Phe	Ile	Asn	Asp	Gly	His	Tyr	80	
65					70				75								
gac	ata	gtg	cat	aca	cat	ggc	gcc	cga	gct	aat	ctt	ttt	ctt	tct	tta	288	
Asp	Ile	Val	His	Thr	His	Gly	Ala	Arg	Ala	Asn	Leu	Phe	Leu	Ser	Leu	95	
				85				90									
att	cat	aag	aga	atc	tca	gct	gta	tgg	tgc	gtt	act	gtg	cac	tct	aac	336	
Ile	His	Lys	Arg	Ile	Ser	Ala	Val	Trp	Cys	Val	Thr	Val	His	Ser	Asn	110	
			100					105									
cca	tat	ctt	gat	ttt	gaa	gga	cgc	ggc	ttt	tta	ggc	aaa	gtt	ttc	act	384	
Pro	Tyr	Leu	Asp	Phe	Glu	Gly	Arg	Gly	Phe	Leu	Gly	Lys	Val	Phe	Thr	125	
		115					120										
aag	ttt	aat	tta	cgt	gca	tta	aaa	aaa	gcg	gac	tgt	ata	ttt	gca	gtc	432	
Lys	Phe	Asn	Leu	Arg	Ala	Leu	Lys	Lys	Ala	Asp	Cys	Ile	Phe	Ala	Val	140	
	130					135											
act	aag	cgt	ttt	gcc	aat	ctg	tta	gtt	aat	caa	aca	caa	cta	gat	aaa	480	
Thr	Lys	Arg	Phe	Ala	Asn	Leu	Leu	Val	Asn	Gln	Thr	Gln	Leu	Asp	Lys	160	
					150					155							
aat	aaa	gta	cat	gtg	att	tat	aat	ggg	atc	ttt	ttc	cac	aat	gat	agt	528	
Asn	Lys	Val	His	Val	Ile	Tyr	Asn	Gly	Ile	Phe	Phe	His	Asn	Asp	Ser	175	
				165				170									
gaa	atc	cct	gct	aaa	tat	gag	cat	act	tac	ttt	aat	gta	att	aac	gta	576	
Glu	Ile	Pro	Ala	Lys	Tyr	Glu	His	Thr	Tyr	Phe	Asn	Val	Ile	Asn	Val	190	
			180					185									
gct	cgt	aca	gaa	aaa	gtg	aaa	ggg	caa	gaa	ttg	tta	ctt	aaa	gca	gtt	624	
Ala	Arg	Thr	Glu	Lys	Val	Lys	Gly	Gln	Glu	Leu	Leu	Leu	Lys	Ala	Val	205	
		195					200										
aaa	aag	ctc	aac	gat	caa	cat	atc	cgt	tta	cat	att	gca	gga	gac	ggc	672	
Lys	Lys	Leu	Asn	Asp	Gln	His	Ile	Arg	Leu	His	Ile	Ala	Gly	Asp	Gly	220	
		210				215											
agt	caa	ctt	gaa	cca	ctt	aaa	gct	ctt	act	cgc	cag	cta	aat	atg	gca	720	
Ser	Gln	Leu	Glu	Pro	Leu	Lys	Ala	Leu	Thr	Arg	Gln	Leu	Asn	Met	Ala	240	
					230					235							
ccc	caa	gta	act	ttt	cat	ggc	ttt	atg	act	cat	cat	cag	tta	agt	gga	768	
Pro	Gln	Val	Thr	Phe	His	Gly	Phe	Met	Thr	His	His	Gln	Leu	Ser	Gly	255	
				245					250								
ctt	tat	aaa	aga	att	gat	ctg	gct	gtt	tta	aca	tca	tat	tca	gaa	agt	816	
Leu	Tyr	Lys	Arg	Ile	Asp	Leu	Ala	Val	Leu	Thr	Ser	Tyr	Ser	Glu	Ser	270	
			260					265									
ttt	ccc	ctt	gtt	tta	tta	gaa	gca	acc	gat	aat	tta	att	cct	atc	tta	864	
Phe	Pro	Leu	Val	Leu	Leu	Glu	Ala	Thr	Asp	Asn	Leu	Ile	Pro	Ile	Leu		

275	280	285	
tct act gat gtt ggt gac atc cat aag atg att cca gga cct aaa tat			912
Ser Thr Asp Val Gly Asp Ile His Lys Met Ile Pro Gly Pro Lys Tyr			
290	295	300	
ggt ttt att gct aaa act ggt gat att gat tca att gcc aag cag ctt			960
Gly Phe Ile Ala Lys Thr Gly Asp Ile Asp Ser Ile Ala Lys Gln Leu			
305	310	315	320
gaa tta gct gtc aat aag act aca aag cag cta cgt gaa atg gcc tat			1008
Glu Leu Ala Val Asn Lys Thr Thr Lys Gln Leu Arg Glu Met Ala Tyr			
325	330	335	
aca gaa aaa cgc tat gct gaa gaa cac ttt tct gtg aag aat caa cta			1056
Thr Glu Lys Arg Tyr Ala Glu Glu His Phe Ser Val Lys Asn Gln Leu			
340	345	350	
gca gat att gaa aaa gtt tat agt act tta atc			1089
Ala Asp Ile Glu Lys Val Tyr Ser Thr Leu Ile			
355	360		

<210> 258

<211> 363

<212> PRT

<213> Lactobacillus acidophilus

<400> 258

Met Lys Val Leu His Val Asn Ala Gly Leu Glu Asn Gly Gly Gly Leu	
1 5 10 15	
Ser His Ile Val Asn Leu Leu Thr Glu Ala Lys Arg Glu Asn Lys Asp	
20 25 30	
Phe Asp Leu Leu Thr Leu Ala Asp Gly Pro Val Ala Ala Ala Arg	
35 40 45	
Glu His Gly Ile Asn Thr Tyr Val Leu Gly Ala Lys Ser Arg Tyr Asn	
50 55 60	
Leu Ala Ser Leu Lys Lys Leu Ile Lys Phe Ile Asn Asp Gly His Tyr	
65 70 75 80	
Asp Ile Val His Thr His Gly Ala Arg Ala Asn Leu Phe Leu Ser Leu	
85 90 95	
Ile His Lys Arg Ile Ser Ala Val Trp Cys Val Thr Val His Ser Asn	
100 105 110	
Pro Tyr Leu Asp Phe Glu Gly Arg Gly Phe Leu Gly Lys Val Phe Thr	
115 120 125	
Lys Phe Asn Leu Arg Ala Leu Lys Lys Ala Asp Cys Ile Phe Ala Val	
130 135 140	
Thr Lys Arg Phe Ala Asn Leu Leu Val Asn Gln Thr Gln Leu Asp Lys	
145 150 155 160	
Asn Lys Val His Val Ile Tyr Asn Gly Ile Phe Phe His Asn Asp Ser	
165 170 175	
Glu Ile Pro Ala Lys Tyr Glu His Thr Tyr Phe Asn Val Ile Asn Val	
180 185 190	
Ala Arg Thr Glu Lys Val Lys Gly Gln Glu Leu Leu Leu Lys Ala Val	
195 200 205	
Lys Lys Leu Asn Asp Gln His Ile Arg Leu His Ile Ala Gly Asp Gly	
210 215 220	

```

Ser Gln Leu Glu Pro Leu Lys Ala Leu Thr Arg Gln Leu Asn Met Ala
225                230                235                240
Pro Gln Val Thr Phe His Gly Phe Met Thr His His Gln Leu Ser Gly
                245                250                255
Leu Tyr Lys Arg Ile Asp Leu Ala Val Leu Thr Ser Tyr Ser Glu Ser
                260                265                270
Phe Pro Leu Val Leu Leu Glu Ala Thr Asp Asn Leu Ile Pro Ile Leu
                275                280                285
Ser Thr Asp Val Gly Asp Ile His Lys Met Ile Pro Gly Pro Lys Tyr
                290                295                300
Gly Phe Ile Ala Lys Thr Gly Asp Ile Asp Ser Ile Ala Lys Gln Leu
305                310                315                320
Glu Leu Ala Val Asn Lys Thr Thr Lys Gln Leu Arg Glu Met Ala Tyr
                325                330                335
Thr Glu Lys Arg Tyr Ala Glu Glu His Phe Ser Val Lys Asn Gln Leu
                340                345                350
Ala Asp Ile Glu Lys Val Tyr Ser Thr Leu Ile
                355                360

```

<210> 259

<211> 1668

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1872 - oligo-1,6-glucosidase

<220>

<221> CDS

<222> (1)...(1668)

<400> 259.

```

gtg gag gaa aaa att atg tca cat tgg tac gat cat gca att att tat      48
Met Glu Glu Lys Ile Met Ser His Trp Tyr Asp His Ala Ile Ile Tyr
 1                5                10                15

caa att tat cct aag tct ttt caa gat agc aat gac gat ggt att ggc      96
Gln Ile Tyr Pro Lys Ser Phe Gln Asp Ser Asn Asp Asp Gly Ile Gly
                20                25                30

gat ctt aat ggt att cgt aaa aga att ccc tat tta caa aat tta gga     144
Asp Leu Asn Gly Ile Arg Lys Arg Ile Pro Tyr Leu Gln Asn Leu Gly
                35                40                45

gtt aat gca gtt tgg ctt aat cct gtt ttt gtt tcg cca caa gtg gat     192
Val Asn Ala Val Trp Leu Asn Pro Val Phe Val Ser Pro Gln Val Asp
                50                55                60

aac ggt tat gat gtc tca aat tat ttt gcg att gat tct cac atg gga     240
Asn Gly Tyr Asp Val Ser Asn Tyr Phe Ala Ile Asp Ser His Met Gly
        65                70                75                80

acg atg gaa gat atg gag aat tta att aaa gat ctg cat aaa gct gga     288

```

Thr	Met	Glu	Asp	Met	Glu	Asn	Leu	Ile	Lys	Asp	Leu	His	Lys	Ala	Gly		
				85					90					95			
att	cat	atc	att	atg	gat	ttt	gtc	tta	aat	cat	act	tca	gat	caa	cat	336	
Ile	His	Ile	Ile	Met	Asp	Phe	Val	Leu	Asn	His	Thr	Ser	Asp	Gln	His		
			100					105					110				
cca	tgg	ttc	caa	gat	gct	att	aag	aat	ccg	gat	agt	tta	tat	cgt	gat	384	
Pro	Trp	Phe	Gln	Asp	Ala	Ile	Lys	Asn	Pro	Asp	Ser	Leu	Tyr	Arg	Asp		
		115					120					125					
tac	tac	att	ttt	gct	ggc	cat	gat	aat	aaa	caa	cct	aat	aat	tgg	gga	432	
Tyr	Tyr	Ile	Phe	Ala	Gly	His	Asp	Asn	Lys	Gln	Pro	Asn	Asn	Trp	Gly		
	130					135					140						
tct	ttc	ttt	gga	gga	agc	gtc	tgg	gaa	cct	gat	ccg	gca	ggc	act	ggc	480	
Ser	Phe	Phe	Gly	Gly	Ser	Val	Trp	Glu	Pro	Asp	Pro	Ala	Gly	Thr	Gly		
145					150				155					160			
cag	tca	tat	ttt	cac	tta	ttt	gat	aaa	cgg	atg	cca	gat	ctt	aac	tgg	528	
Gln	Ser	Tyr	Phe	His	Leu	Phe	Asp	Lys	Arg	Met	Pro	Asp	Leu	Asn	Trp		
			165					170						175			
aaa	aac	cct	gaa	gtt	cga	cat	gct	atg	ctt	gaa	ata	gct	gaa	ttt	tgg	576	
Lys	Asn	Pro	Glu	Val	Arg	His	Ala	Met	Leu	Glu	Ile	Ala	Glu	Phe	Trp		
		180					185						190				
tta	aag	aag	gga	ata	gac	ggc	tta	aga	ctt	gat	gca	ttt	att	cat	att	624	
Leu	Lys	Lys	Gly	Ile	Asp	Gly	Leu	Arg	Leu	Asp	Ala	Phe	Ile	His	Ile		
		195				200						205					
ggc	aag	gca	gac	tta	aga	caa	aat	tat	cca	gct	atg	gat	gat	aaa	ccg	672	
Gly	Lys	Ala	Asp	Leu	Arg	Gln	Asn	Tyr	Pro	Ala	Met	Asp	Asp	Lys	Pro		
	210					215					220						
gtt	att	gca	gag	ccg	ttt	ttt	gct	aat	ttg	cca	caa	gtg	caa	gaa	tgg	720	
Val	Ile	Ala	Glu	Pro	Phe	Phe	Ala	Asn	Leu	Pro	Gln	Val	Gln	Glu	Trp		
225					230				235					240			
atg	aga	cca	ttt	tgt	gaa	caa	att	aaa	gaa	gat	tat	cca	gat	gca	ctt	768	
Met	Arg	Pro	Phe	Cys	Glu	Gln	Ile	Lys	Glu	Asp	Tyr	Pro	Asp	Ala	Leu		
			245					250						255			
tta	ctt	ggc	gaa	gca	gct	agt	gct	agc	gtt	aac	tta	gca	gtt	gat	tat	816	
Leu	Leu	Gly	Glu	Ala	Ala	Ser	Ala	Ser	Val	Asn	Leu	Ala	Val	Asp	Tyr		
		260				265							270				
acg	aat	aaa	cgt	aat	cat	tta	atg	gat	tgc	gtg	att	aca	ttt	cgt	tat	864	
Thr	Asn	Lys	Arg	Asn	His	Leu	Met	Asp	Cys	Val	Ile	Thr	Phe	Arg	Tyr		
		275				280						285					
ttt	aca	gaa	gat	gat	tcc	aaa	atc	gat	aag	agt	tat	tcc	gca	caa	tat	912	
Phe	Thr	Glu	Asp	Asp	Ser	Lys	Ile	Asp	Lys	Ser	Tyr	Ser	Ala	Gln	Tyr		
	290					295					300						
cag	cct	aag	gag	ctt	gat	tta	aca	gct	ttt	aaa	caa	aat	cag	gtg	gtt	960	
Gln	Pro	Lys	Glu	Leu	Asp	Leu	Thr	Ala	Phe	Lys	Gln	Asn	Gln	Val	Val		

305	310	315	320	
tgg caa caa acg tta gct gat ata tca caa ccc acg ctt tat tgg aat				1008
Trp Gln Gln Thr	Leu Ala Asp Ile	Ser Gln Pro Thr	Leu Tyr Trp Asn	
	325	330	335	
aat cac gat atg gca aga ctt gct act aga att gcg aag act tca act				1056
Asn His Asp Met	Ala Arg Leu Ala	Thr Arg Ile Ala	Lys Thr Ser Thr	
	340	345	350	
caa gca aag agc tta gca atg ttg atg tat ctg caa cgc ggt att ccg				1104
Gln Ala Lys Ser	Leu Ala Met Leu	Met Tyr Leu Gln	Arg Gly Ile Pro	
	355	360	365	
att att tat tat ggt gaa gaa tta ggg ctt aag aat tta cac ttt act				1152
Ile Ile Tyr Tyr	Gly Glu Leu Gly	Leu Lys Asn Leu	His Phe Thr	
	370	375	380	
agt gtt gat caa ttt gaa gat caa act gtt gct cca tgg ata aaa gag				1200
Ser Val Asp Gln	Phe Glu Asp Gln	Thr Val Ala Pro	Trp Ile Lys Glu	
	385	390	395	400
gca caa aaa gct gga ata agt aga gat gcc gca ttt gct atg gtt agc				1248
Ala Gln Lys Ala	Gly Ile Ser Arg	Asp Ala Ala Phe	Ala Met Val Ser	
	405	410	415	
gat acc cat aaa tta ccg gct cgt ggt cca atg cca tgg aac gat aca				1296
Asp Thr His Lys	Leu Pro Ala Arg	Gly Pro Met Pro	Trp Asn Asp Thr	
	420	425	430	
gaa aat aat ggt ttt act agt gct aaa cct tgg ctc aat gga att agt				1344
Glu Asn Asn Gly	Phe Thr Ser Ala	Lys Pro Trp Leu	Asn Gly Ile Ser	
	435	440	445	
caa gat gat gta aca gtt gca aat gaa gtc aac tct gat aac agc atg				1392
Gln Asp Asp Val	Thr Val Ala Asn	Glu Val Asn Ser	Asp Asn Ser Met	
	450	455	460	
ttt act ttt tat aaa aat atg ctg aat ctg aaa aaa gaa aaa cta ttc				1440
Phe Thr Phe Tyr	Lys Asn Met Leu	Asn Leu Lys Lys	Glu Lys Leu Phe	
	465	470	475	480
caa gac gga act tac tat atg atc tca act ggt aag gac agt tac gtt				1488
Gln Asp Gly Thr	Tyr Tyr Met Ile	Ser Thr Gly Lys	Asp Ser Tyr Val	
	485	490	495	
tat caa cgt gat ttg ggc aat gag agt gcg att gta gct gtt tcg tta				1536
Tyr Gln Arg Asp	Leu Gly Asn Glu	Ser Ala Ile Val	Ala Val Ser Leu	
	500	505	510	
agt aat aaa aag att tca atc gat ctt ccg gaa gag tat att aaa gaa				1584
Ser Asn Lys Lys	Ile Ser Ile Asp	Leu Pro Glu Glu	Tyr Ile Lys Glu	
	515	520	525	
cta tta aag gct ggg gaa tat caa tta act aat gga aaa tta act tta				1632
Leu Leu Lys Ala	Gly Glu Tyr Gln	Leu Thr Asn Gly	Lys Leu Thr Leu	
	530	535	540	

atg cct tac gcg ggt gtt gtt ttg aaa aag gag aat
 Met Pro Tyr Ala Gly Val Val Leu Lys Lys Glu Asn
 545 550 555

1668

<210> 260

<211> 556

<212> PRT

<213> Lactobacillus acidophilus

<400> 260

Met Glu Glu Lys Ile Met Ser His Trp Tyr Asp His Ala Ile Ile Tyr
 1 5 10 15
 Gln Ile Tyr Pro Lys Ser Phe Gln Asp Ser Asn Asp Asp Gly Ile Gly
 20 25 30
 Asp Leu Asn Gly Ile Arg Lys Arg Ile Pro Tyr Leu Gln Asn Leu Gly
 35 40 45
 Val Asn Ala Val Trp Leu Asn Pro Val Phe Val Ser Pro Gln Val Asp
 50 55 60
 Asn Gly Tyr Asp Val Ser Asn Tyr Phe Ala Ile Asp Ser His Met Gly
 65 70 75 80
 Thr Met Glu Asp Met Glu Asn Leu Ile Lys Asp Leu His Lys Ala Gly
 85 90 95
 Ile His Ile Ile Met Asp Phe Val Leu Asn His Thr Ser Asp Gln His
 100 105 110
 Pro Trp Phe Gln Asp Ala Ile Lys Asn Pro Asp Ser Leu Tyr Arg Asp
 115 120 125
 Tyr Tyr Ile Phe Ala Gly His Asp Asn Lys Gln Pro Asn Asn Trp Gly
 130 135 140
 Ser Phe Phe Gly Gly Ser Val Trp Glu Pro Asp Pro Ala Gly Thr Gly
 145 150 155 160
 Gln Ser Tyr Phe His Leu Phe Asp Lys Arg Met Pro Asp Leu Asn Trp
 165 170 175
 Lys Asn Pro Glu Val Arg His Ala Met Leu Glu Ile Ala Glu Phe Trp
 180 185 190
 Leu Lys Lys Gly Ile Asp Gly Leu Arg Leu Asp Ala Phe Ile His Ile
 195 200 205
 Gly Lys Ala Asp Leu Arg Gln Asn Tyr Pro Ala Met Asp Asp Lys Pro
 210 215 220
 Val Ile Ala Glu Pro Phe Phe Ala Asn Leu Pro Gln Val Gln Glu Trp
 225 230 235 240
 Met Arg Pro Phe Cys Glu Gln Ile Lys Glu Asp Tyr Pro Asp Ala Leu
 245 250 255
 Leu Leu Gly Glu Ala Ala Ser Ala Ser Val Asn Leu Ala Val Asp Tyr
 260 265 270
 Thr Asn Lys Arg Asn His Leu Met Asp Cys Val Ile Thr Phe Arg Tyr
 275 280 285
 Phe Thr Glu Asp Asp Ser Lys Ile Asp Lys Ser Tyr Ser Ala Gln Tyr
 290 295 300
 Gln Pro Lys Glu Leu Asp Leu Thr Ala Phe Lys Gln Asn Gln Val Val
 305 310 315 320
 Trp Gln Gln Thr Leu Ala Asp Ile Ser Gln Pro Thr Leu Tyr Trp Asn
 325 330 335
 Asn His Asp Met Ala Arg Leu Ala Thr Arg Ile Ala Lys Thr Ser Thr
 340 345 350
 Gln Ala Lys Ser Leu Ala Met Leu Met Tyr Leu Gln Arg Gly Ile Pro

```

      355      360      365
Ile Ile Tyr Tyr Gly Glu Glu Leu Gly Leu Lys Asn Leu His Phe Thr
      370      375      380
Ser Val Asp Gln Phe Glu Asp Gln Thr Val Ala Pro Trp Ile Lys Glu
385      390      395      400
Ala Gln Lys Ala Gly Ile Ser Arg Asp Ala Ala Phe Ala Met Val Ser
      405      410      415
Asp Thr His Lys Leu Pro Ala Arg Gly Pro Met Pro Trp Asn Asp Thr
      420      425      430
Glu Asn Asn Gly Phe Thr Ser Ala Lys Pro Trp Leu Asn Gly Ile Ser
      435      440      445
Gln Asp Asp Val Thr Val Ala Asn Glu Val Asn Ser Asp Asn Ser Met
      450      455      460
Phe Thr Phe Tyr Lys Asn Met Leu Asn Leu Lys Lys Glu Lys Leu Phe
465      470      475      480
Gln Asp Gly Thr Tyr Tyr Met Ile Ser Thr Gly Lys Asp Ser Tyr Val
      485      490      495
Tyr Gln Arg Asp Leu Gly Asn Glu Ser Ala Ile Val Ala Val Ser Leu
      500      505      510
Ser Asn Lys Lys Ile Ser Ile Asp Leu Pro Glu Glu Tyr Ile Lys Glu
      515      520      525
Leu Leu Lys Ala Gly Glu Tyr Gln Leu Thr Asn Gly Lys Leu Thr Leu
      530      535      540
Met Pro Tyr Ala Gly Val Val Leu Lys Lys Glu Asn
545      550      555

```

<210> 261

<211> 2277

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1365 - Alpha-glucosidase

<220>

<221> CDS

<222> (1)...(2277)

<400> 261

```

atg aaa tat ttg aat gga aat tgg cta gtg aga gat ggc ttt gca atc   48
Met Lys Tyr Leu Asn Gly Asn Trp Leu Val Arg Asp Gly Phe Ala Ile
  1           5           10           15

```

```

gat tat ggt caa agt att tac gat agt gaa att aaa gat gat aaa tta   96
Asp Tyr Gly Gln Ser Ile Tyr Asp Ser Glu Ile Lys Asp Asp Lys Leu
      20           25           30

```

```

act tta tgg gtg cct ttt aaa gtg att acc aat ccg ggg atg acg ctg   144
Thr Leu Trp Val Pro Phe Lys Val Ile Thr Asn Pro Gly Met Thr Leu
      35           40           45

```

```

gat gat ggg atg ctt acc tta gag att acc tca cca aga gaa aat att   192
Asp Asp Gly Met Leu Thr Leu Glu Ile Thr Ser Pro Arg Glu Asn Ile

```

50	55	60	
att cgc act aag att att aat ttt aaa ggc gcc att gat aac ggt cct			240
Ile Arg Thr Lys Ile Ile Asn Phe Lys Gly Ala Ile Asp Asn Gly Pro			
65	70	75	80
aaa ttt gat tta aac gta gat tcc aaa ttt aag ccg aat att ttt gaa			288
Lys Phe Asp Leu Asn Val Asp Ser Lys Phe Lys Pro Asn Ile Phe Glu			
	85	90	95
gat agt gaa aaa ttt act att gaa tca ggt aat aca cgt ctt gaa att			336
Asp Ser Glu Lys Phe Thr Ile Glu Ser Gly Asn Thr Arg Leu Glu Ile			
	100	105	110
caa aaa ggt gat caa atc tta ttt acg tat ttc tat aaa aat gaa atg			384
Gln Lys Gly Asp Gln Ile Leu Phe Thr Tyr Phe Tyr Lys Asn Glu Met			
	115	120	125
cgt gct gaa ata ccg gca cgt tcc gtt gct aga att ttt gat cct aaa			432
Arg Ala Glu Ile Pro Ala Arg Ser Val Ala Arg Ile Phe Asp Pro Lys			
	130	135	140
ggg cac acc cat att tca aat tca ttt gta ctt gaa cca gac gaa aag			480
Gly His Thr His Ile Ser Asn Ser Phe Val Leu Glu Pro Asp Glu Lys			
	145	150	155
att tat ggg tta gga gaa aga ttt tcc aat ttt gtt aaa aat ggt caa			528
Ile Tyr Gly Leu Gly Glu Arg Phe Ser Asn Phe Val Lys Asn Gly Gln			
	165	170	175
gaa gtt gaa atg tgg aat gca gat ggc ggt aca gaa aca atc caa tcc			576
Glu Val Glu Met Trp Asn Ala Asp Gly Gly Thr Glu Thr Ile Gln Ser			
	180	185	190
tac aag aat att cca ttg tac tta tct aac aga aaa tat ggt ata ttt			624
Tyr Lys Asn Ile Pro Leu Tyr Leu Ser Asn Arg Lys Tyr Gly Ile Phe			
	195	200	205
gtt aat tca att gcc aag gtc tcc tat gaa gtt gct tct caa caa gtt			672
Val Asn Ser Ile Ala Lys Val Ser Tyr Glu Val Ala Ser Gln Gln Val			
	210	215	220
gac cgc gta gaa ttc tct gtt cca ggt caa gaa ctt gat tat ata ttt			720
Asp Arg Val Glu Phe Ser Val Pro Gly Gln Glu Leu Asp Tyr Ile Phe			
	225	230	235
att ggt gga atg gat aac aag gaa gta tta gat cac tac act gcc tta			768
Ile Gly Gly Met Asp Asn Lys Glu Val Leu Asp His Tyr Thr Ala Leu			
	245	250	255
aca ggt cgt cca cca ctt ctt cca gca tgg agc ttt ggt tta tgg ttg			816
Thr Gly Arg Pro Pro Leu Leu Pro Ala Trp Ser Phe Gly Leu Trp Leu			
	260	265	270
act aca tca ttt act act aaa tat gat gaa gag aca gtt atg agc ttt			864
Thr Thr Ser Phe Thr Thr Lys Tyr Asp Glu Glu Thr Val Met Ser Phe			
	275	280	285

att aat ggt atg ctt gat cgt cat att cca tta tct gtc ttt cac ttt	912
Ile Asn Gly Met Leu Asp Arg His Ile Pro Leu Ser Val Phe His Phe	
290 295 300	
gac tgt tgc tgg atg aag cca aca caa tgg tgt gac ttt gta tgg gat	960
Asp Cys Cys Trp Met Lys Pro Thr Gln Trp Cys Asp Phe Val Trp Asp	
305 310 315 320	
cca gat atc ttt cca gat cca gaa ggt ctt ttg aag aag atc cat gat	1008
Pro Asp Ile Phe Pro Asp Pro Glu Gly Leu Leu Lys Lys Ile His Asp	
325 330 335	
aaa ggt att aaa gtt tgt gtc tgg att aat ccg tat att gcc caa aaa	1056
Lys Gly Ile Lys Val Cys Val Trp Ile Asn Pro Tyr Ile Ala Gln Lys	
340 345 350	
tct cgt tta ttt gaa gaa ggg atg aag aat ggt tac ttc att aag aag	1104
Ser Arg Leu Phe Glu Glu Gly Met Lys Asn Gly Tyr Phe Ile Lys Lys	
355 360 365	
agt aat ggg gat gta tgg caa tgg gat aag tgg caa gct ggt atg gcc	1152
Ser Asn Gly Asp Val Trp Gln Trp Asp Lys Trp Gln Ala Gly Met Ala	
370 375 380	
att gtt gac ttt act aac cct gac gca gtt aag tgg tat caa ggc tat	1200
Ile Val Asp Phe Thr Asn Pro Asp Ala Val Lys Trp Tyr Gln Gly Tyr	
385 390 395 400	
ttg aaa gaa ctg ctt cat caa gga gtc gat gtc ttt aag acg gac ttt	1248
Leu Lys Glu Leu Leu His Gln Gly Val Asp Val Phe Lys Thr Asp Phe	
405 410 415	
ggt gac cga att cca agt gaa ggc gtt aaa ttc ttt gat ggt tca gat	1296
Gly Asp Arg Ile Pro Ser Glu Gly Val Lys Phe Phe Asp Gly Ser Asp	
420 425 430	
cct aag aaa atg cat aat tac tac aca ctt ttg tat aac aag atc gtt	1344
Pro Lys Lys Met His Asn Tyr Tyr Thr Leu Leu Tyr Asn Lys Ile Val	
435 440 445	
act gat gca att agt gaa gtt aaa gga aaa aaa gag gct ctt gtc ttt	1392
Thr Asp Ala Ile Ser Glu Val Lys Gly Lys Lys Glu Ala Leu Val Phe	
450 455 460	
gct aga agt gca act gta ggt agt caa tgt tac cca gtc cat tgg ggt	1440
Ala Arg Ser Ala Thr Val Gly Ser Gln Cys Tyr Pro Val His Trp Gly	
465 470 475 480	
ggt gac tca tct tcg aac tac tca tca atg gcg gaa act ctt aga agc	1488
Gly Asp Ser Ser Ser Asn Tyr Ser Ser Met Ala Glu Thr Leu Arg Ser	
485 490 495	
ggc ttg tcc ttt agt atg agt ggc ttt ggc tat tgg tcg cat gat att	1536
Gly Leu Ser Phe Ser Met Ser Gly Phe Gly Tyr Trp Ser His Asp Ile	
500 505 510	

tca ggg ttt gaa gca agt gct aca cca gac tta tat aaa cgc tgg agt	1584
Ser Gly Phe Glu Ala Ser Ala Thr Pro Asp Leu Tyr Lys Arg Trp Ser	
515 520 525	
caa ttt ggt tta cta agt tct cat tca aga tat cat ggt tca act act	1632
Gln Phe Gly Leu Leu Ser Ser His Ser Arg Tyr His Gly Ser Thr Thr	
530 535 540	
tat aaa gtt cca tgg tta tat ggt gat gaa gct gta gaa gta tca aag	1680
Tyr Lys Val Pro Trp Leu Tyr Gly Asp Glu Ala Val Glu Val Ser Lys	
545 550 555 560	
aaa ttt acc aat tta aaa tta cgg tta ttg ccg tat ctt ctt gca atg	1728
Lys Phe Thr Asn Leu Lys Leu Arg Leu Leu Pro Tyr Leu Leu Ala Met	
565 570 575	
tct aac gaa gct cat aaa cat ggt acg cca att ctt cgt cca atg att	1776
Ser Asn Glu Ala His Lys His Gly Thr Pro Ile Leu Arg Pro Met Ile	
580 585 590	
tta gaa ttc cct gat gat ccg gga tgc gaa gac ctt gat atg caa tat	1824
Leu Glu Phe Pro Asp Asp Pro Gly Cys Glu Asp Leu Asp Met Gln Tyr	
595 600 605	
atg ctt ggt ggt agt ctg ttg gtt gct cca att ttc aat gac caa gga	1872
Met Leu Gly Gly Ser Leu Leu Val Ala Pro Ile Phe Asn Asp Gln Gly	
610 615 620	
gaa gct tgt ttt tat gcc cca caa ggt caa ggt aaa tgg att agt tta	1920
Glu Ala Cys Phe Tyr Ala Pro Gln Gly Gln Gly Lys Trp Ile Ser Leu	
625 630 635 640	
cta act aat gaa agt tat gaa ggt gga cgc tgg tac aag caa aag ttt	1968
Leu Thr Asn Glu Ser Tyr Glu Gly Gly Arg Trp Tyr Lys Gln Lys Phe	
645 650 655	
aat gaa aag act ttg cca tta ctt gta aaa cct aat tca att att gtg	2016
Asn Glu Lys Thr Leu Pro Leu Leu Val Lys Pro Asn Ser Ile Ile Val	
660 665 670	
act ggc gaa cat gat gat cag acg atg tat gat tac act aag cac cca	2064
Thr Gly Glu His Asp Asp Gln Thr Met Tyr Asp Tyr Thr Lys His Pro	
675 680 685	
agt att cat tta ttt gaa atg caa gat ggc aaa gta tcg aca ata att	2112
Ser Ile His Leu Phe Glu Met Gln Asp Gly Lys Val Ser Thr Ile Ile	
690 695 700	
act gat aat tat ggt aaa aaa gta gcg acg gta act tct gaa aag tcg	2160
Thr Asp Asn Tyr Gly Lys Lys Val Ala Thr Val Thr Ser Glu Lys Ser	
705 710 715 720	
gct gat aag att gta gta act aca gaa aat att gaa aaa ttt gat tta	2208
Ala Asp Lys Ile Val Val Thr Thr Glu Asn Ile Glu Lys Phe Asp Leu	
725 730 735	
ata att cat cgt agt gat caa tac gcc gta att atg aaa gat aat caa	2256

Ile Ile His Arg Ser Asp Gln Tyr Ala Val Ile Met Lys Asp Asn Gln
 740 745 750

caa aaa gta gaa gtt gat cta
 Gln Lys Val Glu Val Asp Leu
 755

2277

<210> 262
 <211> 759
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 262
 Met Lys Tyr Leu Asn Gly Asn Trp Leu Val Arg Asp Gly Phe Ala Ile
 1 5 10 15
 Asp Tyr Gly Gln Ser Ile Tyr Asp Ser Glu Ile Lys Asp Asp Lys Leu
 20 25 30
 Thr Leu Trp Val Pro Phe Lys Val Ile Thr Asn Pro Gly Met Thr Leu
 35 40 45
 Asp Asp Gly Met Leu Thr Leu Glu Ile Thr Ser Pro Arg Glu Asn Ile
 50 55 60
 Ile Arg Thr Lys Ile Ile Asn Phe Lys Gly Ala Ile Asp Asn Gly Pro
 65 70 75 80
 Lys Phe Asp Leu Asn Val Asp Ser Lys Phe Lys Pro Asn Ile Phe Glu
 85 90 95
 Asp Ser Glu Lys Phe Thr Ile Glu Ser Gly Asn Thr Arg Leu Glu Ile
 100 105 110
 Gln Lys Gly Asp Gln Ile Leu Phe Thr Tyr Phe Tyr Lys Asn Glu Met
 115 120 125
 Arg Ala Glu Ile Pro Ala Arg Ser Val Ala Arg Ile Phe Asp Pro Lys
 130 135 140
 Gly His Thr His Ile Ser Asn Ser Phe Val Leu Glu Pro Asp Glu Lys
 145 150 155 160
 Ile Tyr Gly Leu Gly Glu Arg Phe Ser Asn Phe Val Lys Asn Gly Gln
 165 170 175
 Glu Val Glu Met Trp Asn Ala Asp Gly Gly Thr Glu Thr Ile Gln Ser
 180 185 190
 Tyr Lys Asn Ile Pro Leu Tyr Leu Ser Asn Arg Lys Tyr Gly Ile Phe
 195 200 205
 Val Asn Ser Ile Ala Lys Val Ser Tyr Glu Val Ala Ser Gln Gln Val
 210 215 220
 Asp Arg Val Glu Phe Ser Val Pro Gly Gln Glu Leu Asp Tyr Ile Phe
 225 230 235 240
 Ile Gly Gly Met Asp Asn Lys Glu Val Leu Asp His Tyr Thr Ala Leu
 245 250 255
 Thr Gly Arg Pro Pro Leu Leu Pro Ala Trp Ser Phe Gly Leu Trp Leu
 260 265 270
 Thr Thr Ser Phe Thr Thr Lys Tyr Asp Glu Glu Thr Val Met Ser Phe
 275 280 285
 Ile Asn Gly Met Leu Asp Arg His Ile Pro Leu Ser Val Phe His Phe
 290 295 300
 Asp Cys Cys Trp Met Lys Pro Thr Gln Trp Cys Asp Phe Val Trp Asp
 305 310 315 320
 Pro Asp Ile Phe Pro Asp Pro Glu Gly Leu Leu Lys Lys Ile His Asp
 325 330 335
 Lys Gly Ile Lys Val Cys Val Trp Ile Asn Pro Tyr Ile Ala Gln Lys

```

          340          345          350
Ser Arg Leu Phe Glu Glu Gly Met Lys Asn Gly Tyr Phe Ile Lys Lys
          355          360          365
Ser Asn Gly Asp Val Trp Gln Trp Asp Lys Trp Gln Ala Gly Met Ala
          370          375          380
Ile Val Asp Phe Thr Asn Pro Asp Ala Val Lys Trp Tyr Gln Gly Tyr
385          390          395          400
Leu Lys Glu Leu Leu His Gln Gly Val Asp Val Phe Lys Thr Asp Phe
          405          410          415
Gly Asp Arg Ile Pro Ser Glu Gly Val Lys Phe Phe Asp Gly Ser Asp
          420          425          430
Pro Lys Lys Met His Asn Tyr Tyr Thr Leu Leu Tyr Asn Lys Ile Val
          435          440          445
Thr Asp Ala Ile Ser Glu Val Lys Gly Lys Lys Glu Ala Leu Val Phe
          450          455          460
Ala Arg Ser Ala Thr Val Gly Ser Gln Cys Tyr Pro Val His Trp Gly
465          470          475          480
Gly Asp Ser Ser Ser Asn Tyr Ser Ser Met Ala Glu Thr Leu Arg Ser
          485          490          495
Gly Leu Ser Phe Ser Met Ser Gly Phe Gly Tyr Trp Ser His Asp Ile
          500          505          510
Ser Gly Phe Glu Ala Ser Ala Thr Pro Asp Leu Tyr Lys Arg Trp Ser
          515          520          525
Gln Phe Gly Leu Leu Ser Ser His Ser Arg Tyr His Gly Ser Thr Thr
          530          535          540
Tyr Lys Val Pro Trp Leu Tyr Gly Asp Glu Ala Val Glu Val Ser Lys
545          550          555          560
Lys Phe Thr Asn Leu Lys Leu Arg Leu Leu Pro Tyr Leu Leu Ala Met
          565          570          575
Ser Asn Glu Ala His Lys His Gly Thr Pro Ile Leu Arg Pro Met Ile
          580          585          590
Leu Glu Phe Pro Asp Asp Pro Gly Cys Glu Asp Leu Asp Met Gln Tyr
          595          600          605
Met Leu Gly Gly Ser Leu Leu Val Ala Pro Ile Phe Asn Asp Gln Gly
          610          615          620
Glu Ala Cys Phe Tyr Ala Pro Gln Gly Gln Gly Lys Trp Ile Ser Leu
625          630          635          640
Leu Thr Asn Glu Ser Tyr Glu Gly Gly Arg Trp Tyr Lys Gln Lys Phe
          645          650          655
Asn Glu Lys Thr Leu Pro Leu Leu Val Lys Pro Asn Ser Ile Ile Val
          660          665          670
Thr Gly Glu His Asp Asp Gln Thr Met Tyr Asp Tyr Thr Lys His Pro
          675          680          685
Ser Ile His Leu Phe Glu Met Gln Asp Gly Lys Val Ser Thr Ile Ile
          690          695          700
Thr Asp Asn Tyr Gly Lys Lys Val Ala Thr Val Thr Ser Glu Lys Ser
705          710          715          720
Ala Asp Lys Ile Val Val Thr Thr Glu Asn Ile Glu Lys Phe Asp Leu
          725          730          735
Ile Ile His Arg Ser Asp Gln Tyr Ala Val Ile Met Lys Asp Asn Gln
          740          745          750
Gln Lys Val Glu Val Asp Leu
          755

```

<210> 263

<211> 2301

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1812 - ALPHA-GLUCOSIDASE II

<220>

<221> CDS

<222> (1)...(2301)

<400> 263

atg gct aac aaa ctt aaa aat ttc atc caa gat ggg caa aaa gtt acc	48
Met Ala Asn Lys Leu Lys Asn Phe Ile Gln Asp Gly Gln Lys Val Thr	
1 5 10 15	
tta aat tat gaa gat ggg gaa ctt gaa tta agg gtt cta acg cct gaa	96
Leu Asn Tyr Glu Asp Gly Glu Leu Glu Leu Arg Val Leu Thr Pro Glu	
20 25 30	
att gtg cgt gta ttt gaa aat cgt ggc aat gct agc aat tca tat gct	144
Ile Val Arg Val Phe Glu Asn Arg Gly Asn Ala Ser Asn Ser Tyr Ala	
35 40 45	
atc gct ggt gat aag gaa ata aaa act aat ttt cgt att gaa gaa aaa	192
Ile Ala Gly Asp Lys Glu Ile Lys Thr Asn Phe Arg Ile Glu Glu Lys	
50 55 60	
gat gat cat gca gag tta tca aca gaa aag ttg ttc gta aaa att tac	240
Asp Asp His Ala Glu Leu Ser Thr Glu Lys Leu Phe Val Lys Ile Tyr	
65 70 75 80	
gat gac aaa aag att gat gtt tat gat gaa aag gat cat cca ttg atc	288
Asp Asp Lys Lys Ile Asp Val Tyr Asp Glu Lys Asp His Pro Leu Ile	
85 90 95	
att gat tat cgc ggt gag cgt acg ccg att gat cgt caa atg gac gag	336
Ile Asp Tyr Arg Gly Glu Arg Thr Pro Ile Asp Arg Gln Met Asp Glu	
100 105 110	
gaa cat aaa aaa tcg gca gaa tca gaa ggt cat gag gtt gct ggt agt	384
Glu His Lys Lys Ser Ala Glu Ser Glu Gly His Glu Val Ala Gly Ser	
115 120 125	
aaa aaa gaa gat aaa aac tat tat gaa atc gtt aaa aaa cta gct agt	432
Lys Lys Glu Asp Lys Asn Tyr Tyr Glu Ile Val Lys Lys Leu Ala Ser	
130 135 140	
gat gaa caa ttt tac ggc tta ggt gat aag act ggc ttt tta aat aag	480
Asp Glu Gln Phe Tyr Gly Leu Gly Asp Lys Thr Gly Phe Leu Asn Lys	
145 150 155 160	
cgt cat tat gcc tat aat aac tgg aat act gac gat cca gca cct caa	528
Arg His Tyr Ala Tyr Asn Asn Trp Asn Thr Asp Asp Pro Ala Pro Gln	
165 170 175	

gtt gaa agc ttc cca agt ctt tat aag tcg gtt ccg atc ttg ctc ggc	576
Val Glu Ser Phe Pro Ser Leu Tyr Lys Ser Val Pro Ile Leu Leu Gly	
180 185 190	
tta aaa gat ggt cat ccc tat ggg att ttc ttt gac aat act tat cgt	624
Leu Lys Asp Gly His Pro Tyr Gly Ile Phe Phe Asp Asn Thr Tyr Arg	
195 200 205	
aac cac att gac tta ggt aaa gaa agt aac gat tat tac tac tac tcc	672
Asn His Ile Asp Leu Gly Lys Glu Ser Asn Asp Tyr Tyr Tyr Tyr Ser	
210 215 220	
gca gtt gat ggc aac att gat tac tac atc att ggt ggt gat tca ctt	720
Ala Val Asp Gly Asn Ile Asp Tyr Tyr Ile Ile Gly Gly Asp Ser Leu	
225 230 235 240	
aaa gaa att atc acc aac tac act tac ttg act ggt cgt gta cca atg	768
Lys Glu Ile Ile Thr Asn Tyr Thr Tyr Leu Thr Gly Arg Val Pro Met	
245 250 255	
ccg cag aaa tgg acc ttg ggc tat caa cag tct cgc tgg ggc tac agt	816
Pro Gln Lys Trp Thr Leu Gly Tyr Gln Gln Ser Arg Trp Gly Tyr Ser	
260 265 270	
gtc agc caa aag caa gtt gag aaa att gcg gaa aac ttg cgc aag tat	864
Val Ser Gln Lys Gln Val Glu Lys Ile Ala Glu Asn Leu Arg Lys Tyr	
275 280 285	
gat ttg ccg tgt gac gtt ttg cat ctt gat atc gat tat atg cgt ggg	912
Asp Leu Pro Cys Asp Val Leu His Leu Asp Ile Asp Tyr Met Arg Gly	
290 295 300	
tat cgt gta ttt acc tgg aga aaa gat act tat gaa tca cca gat aaa	960
Tyr Arg Val Phe Thr Trp Arg Lys Asp Thr Tyr Glu Ser Pro Asp Lys	
305 310 315 320	
ttc atc aag aag atg cgt aaa ttg ggc ttt aga atc atc acg att att	1008
Phe Ile Lys Lys Met Arg Lys Leu Gly Phe Arg Ile Ile Thr Ile Ile	
325 330 335	
gac cca ggc gta aag aaa gat gat gac tat aag att tac aag gaa ggt	1056
Asp Pro Gly Val Lys Lys Asp Asp Asp Tyr Lys Ile Tyr Lys Glu Gly	
340 345 350	
ctt gaa aaa ggc tac ttc gtt aag gct cca gat ggt acg gtt tat gta	1104
Leu Glu Lys Gly Tyr Phe Val Lys Ala Pro Asp Gly Thr Val Tyr Val	
355 360 365	
aat gaa gtt tgg cca ggc gat gct gtc ttc cca gac ttt ggt cgc aaa	1152
Asn Glu Val Trp Pro Gly Asp Ala Val Phe Pro Asp Phe Gly Arg Lys	
370 375 380	
gaa gta cgt aaa tgg tgg gct aga aat tgt aag tac tta gtt gat ctt	1200
Glu Val Arg Lys Trp Trp Ala Arg Asn Cys Lys Tyr Leu Val Asp Leu	
385 390 395 400	

ggc gtt tca ggt atc tgg gac gat atg aat gaa cct gca tca ttt aga	1248
Gly Val Ser Gly Ile Trp Asp Asp Met Asn Glu Pro Ala Ser Phe Arg	
405 410 415	
ggg gaa att cca caa gat att gtc ttt cat aac gaa gag caa gct tca	1296
Gly Glu Ile Pro Gln Asp Ile Val Phe His Asn Glu Glu Gln Ala Ser	
420 425 430	
act cat aag aag atg cac aat gtc tat ggt cat aat atg gct aaa gca	1344
Thr His Lys Lys Met His Asn Val Tyr Gly His Asn Met Ala Lys Ala	
435 440 445	
act tat gaa ggt ttg aag aaa tat tca ggc aag cgt ccc ttt gtc att	1392
Thr Tyr Glu Gly Leu Lys Lys Tyr Ser Gly Lys Arg Pro Phe Val Ile	
450 455 460	
acg cgt gcg gca tat gca gga acg caa aag ttt tcc aca gtt tgg act	1440
Thr Arg Ala Ala Tyr Ala Gly Thr Gln Lys Phe Ser Thr Val Trp Thr	
465 470 475 480	
ggg gat aac caa agt tta tgg acg cat gtc caa atg atg att ccg caa	1488
Gly Asp Asn Gln Ser Leu Trp Thr His Val Gln Met Met Ile Pro Gln	
485 490 495	
tta tgt aac ttg gga atg agt gga ttt agt ttt gcc ggt act gat att	1536
Leu Cys Asn Leu Gly Met Ser Gly Phe Ser Phe Ala Gly Thr Asp Ile	
500 505 510	
ggg ggt ttc ggt gct gat acg acg cca gaa tta ttg act cgt tgg atc	1584
Gly Gly Phe Gly Ala Asp Thr Thr Pro Glu Leu Leu Thr Arg Trp Ile	
515 520 525	
gaa ggt gca tta ttt agt ccg ttg tac aga aac cat gcg gct cta ggt	1632
Glu Gly Ala Leu Phe Ser Pro Leu Tyr Arg Asn His Ala Ala Leu Gly	
530 535 540	
act cgc tca caa gag cca tgg gta ttt ggt gaa cca act ttg tca att	1680
Thr Arg Ser Gln Glu Pro Trp Val Phe Gly Glu Pro Thr Leu Ser Ile	
545 550 555 560	
tac cgt aaa tac ttg aaa ctt cgc tac cgc ttt att cca tat ctt tac	1728
Tyr Arg Lys Tyr Leu Lys Leu Arg Tyr Arg Phe Ile Pro Tyr Leu Tyr	
565 570 575	
gat gaa ttt tat cgt gaa act agg aca ggt ttg cca att atg cgg cca	1776
Asp Glu Phe Tyr Arg Glu Thr Arg Thr Gly Leu Pro Ile Met Arg Pro	
580 585 590	
ctt gtc ttg aat tat gaa aat gat cca cag gtg tat aac ttg aat gat	1824
Leu Val Leu Asn Tyr Glu Asn Asp Pro Gln Val Tyr Asn Leu Asn Asp	
595 600 605	
gag tat atg gtt ggc gag gat att ttg gca gcc cca gtt gtt caa gag	1872
Glu Tyr Met Val Gly Glu Asp Ile Leu Ala Ala Pro Val Val Gln Glu	
610 615 620	
ggg caa act aag cgt gcc gta tat ttg cca aaa gga aaa tgg att gat	1920

Gly Gln Thr Lys Arg Ala Val Tyr Leu Pro Lys Gly Lys Trp Ile Asp
 625 630 635 640
 ttt tgg aat ggt gtt gaa tat tct gga aag acc acg att ttg gtt gat 1968
 Phe Trp Asn Gly Val Glu Tyr Ser Gly Lys Thr Thr Ile Leu Val Asp
 645 650 655
 gca cca att ggt aaa ttg cca ttg ttc att aag aag aat act atc ctg 2016
 Ala Pro Ile Gly Lys Leu Pro Leu Phe Ile Lys Lys Asn Thr Ile Leu
 660 665 670
 cca tgg ggc aag gaa gta agt cac att tcc gat gag cca gac gag agt 2064
 Pro Trp Gly Lys Glu Val Ser His Ile Ser Asp Glu Pro Asp Glu Ser
 675 680 685
 atg acc ttt aga gta ttt ggt aaa aag ggt aag tac att cac tat caa 2112
 Met Thr Phe Arg Val Phe Gly Lys Lys Gly Lys Tyr Ile His Tyr Gln
 690 695 700
 gat aac gga act gac ttc aag tac caa aag ggc gaa tac aac ttg tac 2160
 Asp Asn Gly Thr Asp Phe Lys Tyr Gln Lys Gly Glu Tyr Asn Leu Tyr
 705 710 715 720
 aag gtt aag gta agt aag gat ggt agc gta aag gtt aag ctt gaa aag 2208
 Lys Val Lys Val Ser Lys Asp Gly Ser Val Lys Val Lys Leu Glu Lys
 725 730 735
 cat ggc ttc ggt cct gta tat cgt aga att acg gtt caa ttg cct aat 2256
 His Gly Phe Gly Pro Val Tyr Arg Arg Ile Thr Val Gln Leu Pro Asn
 740 745 750
 aag aag gtt gaa ttt aag tac aag aat ggt gaa tac gtt aga aaa 2301
 Lys Lys Val Glu Phe Lys Tyr Lys Asn Gly Glu Tyr Val Arg Lys
 755 760 765

<210> 264

<211> 767

<212> PRT

<213> Lactobacillus acidophilus

<400> 264

Met Ala Asn Lys Leu Lys Asn Phe Ile Gln Asp Gly Gln Lys Val Thr
 1 5 10 15
 Leu Asn Tyr Glu Asp Gly Glu Leu Glu Leu Arg Val Leu Thr Pro Glu
 20 25 30
 Ile Val Arg Val Phe Glu Asn Arg Gly Asn Ala Ser Asn Ser Tyr Ala
 35 40 45
 Ile Ala Gly Asp Lys Glu Ile Lys Thr Asn Phe Arg Ile Glu Glu Lys
 50 55 60
 Asp Asp His Ala Glu Leu Ser Thr Glu Lys Leu Phe Val Lys Ile Tyr
 65 70 75 80
 Asp Asp Lys Lys Ile Asp Val Tyr Asp Glu Lys Asp His Pro Leu Ile
 85 90 95
 Ile Asp Tyr Arg Gly Glu Arg Thr Pro Ile Asp Arg Gln Met Asp Glu
 100 105 110

Glu His Lys Lys Ser Ala Glu Ser Glu Gly His Glu Val Ala Gly Ser
 115 120 125
 Lys Lys Glu Asp Lys Asn Tyr Tyr Glu Ile Val Lys Lys Leu Ala Ser
 130 135 140
 Asp Glu Gln Phe Tyr Gly Leu Gly Asp Lys Thr Gly Phe Leu Asn Lys
 145 150 155 160
 Arg His Tyr Ala Tyr Asn Asn Trp Asn Thr Asp Asp Pro Ala Pro Gln
 165 170 175
 Val Glu Ser Phe Pro Ser Leu Tyr Lys Ser Val Pro Ile Leu Leu Gly
 180 185 190
 Leu Lys Asp Gly His Pro Tyr Gly Ile Phe Phe Asp Asn Thr Tyr Arg
 195 200 205
 Asn His Ile Asp Leu Gly Lys Glu Ser Asn Asp Tyr Tyr Tyr Tyr Ser
 210 215 220
 Ala Val Asp Gly Asn Ile Asp Tyr Tyr Ile Ile Gly Gly Asp Ser Leu
 225 230 235 240
 Lys Glu Ile Ile Thr Asn Tyr Thr Tyr Leu Thr Gly Arg Val Pro Met
 245 250 255
 Pro Gln Lys Trp Thr Leu Gly Tyr Gln Gln Ser Arg Trp Gly Tyr Ser
 260 265 270
 Val Ser Gln Lys Gln Val Glu Lys Ile Ala Glu Asn Leu Arg Lys Tyr
 275 280 285
 Asp Leu Pro Cys Asp Val Leu His Leu Asp Ile Asp Tyr Met Arg Gly
 290 295 300
 Tyr Arg Val Phe Thr Trp Arg Lys Asp Thr Tyr Glu Ser Pro Asp Lys
 305 310 315 320
 Phe Ile Lys Lys Met Arg Lys Leu Gly Phe Arg Ile Ile Thr Ile Ile
 325 330 335
 Asp Pro Gly Val Lys Lys Asp Asp Asp Tyr Lys Ile Tyr Lys Glu Gly
 340 345 350
 Leu Glu Lys Gly Tyr Phe Val Lys Ala Pro Asp Gly Thr Val Tyr Val
 355 360 365
 Asn Glu Val Trp Pro Gly Asp Ala Val Phe Pro Asp Phe Gly Arg Lys
 370 375 380
 Glu Val Arg Lys Trp Trp Ala Arg Asn Cys Lys Tyr Leu Val Asp Leu
 385 390 395 400
 Gly Val Ser Gly Ile Trp Asp Asp Met Asn Glu Pro Ala Ser Phe Arg
 405 410 415
 Gly Glu Ile Pro Gln Asp Ile Val Phe His Asn Glu Glu Gln Ala Ser
 420 425 430
 Thr His Lys Lys Met His Asn Val Tyr Gly His Asn Met Ala Lys Ala
 435 440 445
 Thr Tyr Glu Gly Leu Lys Lys Tyr Ser Gly Lys Arg Pro Phe Val Ile
 450 455 460
 Thr Arg Ala Ala Tyr Ala Gly Thr Gln Lys Phe Ser Thr Val Trp Thr
 465 470 475 480
 Gly Asp Asn Gln Ser Leu Trp Thr His Val Gln Met Met Ile Pro Gln
 485 490 495
 Leu Cys Asn Leu Gly Met Ser Gly Phe Ser Phe Ala Gly Thr Asp Ile
 500 505 510
 Gly Gly Phe Gly Ala Asp Thr Thr Pro Glu Leu Leu Thr Arg Trp Ile
 515 520 525
 Glu Gly Ala Leu Phe Ser Pro Leu Tyr Arg Asn His Ala Ala Leu Gly
 530 535 540
 Thr Arg Ser Gln Glu Pro Trp Val Phe Gly Glu Pro Thr Leu Ser Ile
 545 550 555 560
 Tyr Arg Lys Tyr Leu Lys Leu Arg Tyr Arg Phe Ile Pro Tyr Leu Tyr

```

                    565                    570                    575
Asp Glu Phe Tyr Arg Glu Thr Arg Thr Gly Leu Pro Ile Met Arg Pro
                    580                    585                    590
Leu Val Leu Asn Tyr Glu Asn Asp Pro Gln Val Tyr Asn Leu Asn Asp
                    595                    600                    605
Glu Tyr Met Val Gly Glu Asp Ile Leu Ala Ala Pro Val Val Gln Glu
                    610                    615                    620
Gly Gln Thr Lys Arg Ala Val Tyr Leu Pro Lys Gly Lys Trp Ile Asp
625                    630                    635                    640
Phe Trp Asn Gly Val Glu Tyr Ser Gly Lys Thr Thr Ile Leu Val Asp
                    645                    650                    655
Ala Pro Ile Gly Lys Leu Pro Leu Phe Ile Lys Lys Asn Thr Ile Leu
                    660                    665                    670
Pro Trp Gly Lys Glu Val Ser His Ile Ser Asp Glu Pro Asp Glu Ser
                    675                    680                    685
Met Thr Phe Arg Val Phe Gly Lys Lys Gly Lys Tyr Ile His Tyr Gln
690                    695                    700
Asp Asn Gly Thr Asp Phe Lys Tyr Gln Lys Gly Glu Tyr Asn Leu Tyr
705                    710                    715                    720
Lys Val Lys Val Ser Lys Asp Gly Ser Val Lys Val Lys Leu Glu Lys
                    725                    730                    735
His Gly Phe Gly Pro Val Tyr Arg Arg Ile Thr Val Gln Leu Pro Asn
                    740                    745                    750
Lys Lys Val Glu Phe Lys Tyr Lys Asn Gly Glu Tyr Val Arg Lys
                    755                    760                    765

```

<210> 265

<211> 1632

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 264 - glucan 1,6-alpha-glucosidase

<220>

<221> CDS

<222> (1)...(1632)

<400> 265

```

gtg agg gta aaa att atg gct tca tgg tgg aaa aat gct gtt gtt tat   48
Met Arg Val Lys Ile Met Ala Ser Trp Trp Lys Asn Ala Val Val Tyr
 1              5              10              15

```

```

cag gtt tat cct aag tct ttc caa gac agt aac ggt gat gga ata gga   96
Gln Val Tyr Pro Lys Ser Phe Gln Asp Ser Asn Gly Asp Gly Ile Gly
          20              25              30

```

```

gat ttg caa ggg att att tca aga tta gac tat cta gaa aaa tta gga   144
Asp Leu Gln Gly Ile Ile Ser Arg Leu Asp Tyr Leu Glu Lys Leu Gly
          35              40              45

```

```

att gat gct att tgg ctt tca cca gtt tat caa tct cct ggt gtt gat   192
Ile Asp Ala Ile Trp Leu Ser Pro Val Tyr Gln Ser Pro Gly Val Asp

```

50	55	60	
aat gga tat gat att tct gat tat gaa gcg att gat cca cag tat ggc			240
Asn Gly Tyr Asp Ile Ser Asp Tyr Glu Ala Ile Asp Pro Gln Tyr Gly			
65	70	75	80
aca atg gca gat atg gac gag tta att agc aag gct aaa gaa cat cat			288
Thr Met Ala Asp Met Asp Glu Leu Ile Ser Lys Ala Lys Glu His His			
	85	90	95
atc aag ata gtg atg gac tta gtg gtt aat cat act tct gat caa cat			336
Ile Lys Ile Val Met Asp Leu Val Val Asn His Thr Ser Asp Gln His			
	100	105	110
aag tgg ttt gta gag gcc aaa aaa gga aag gat aat caa tat cgt gat			384
Lys Trp Phe Val Glu Ala Lys Lys Gly Lys Asp Asn Gln Tyr Arg Asp			
	115	120	125
tat tat att tgg cgt gat cca gtt gat gaa cat gag cct aat gac tta			432
Tyr Tyr Ile Trp Arg Asp Pro Val Asp Glu His Glu Pro Asn Asp Leu			
	130	135	140
aaa tct gct ttt tca ggt tct gct tgg aaa tat gat gaa aga agt gga			480
Lys Ser Ala Phe Ser Gly Ser Ala Trp Lys Tyr Asp Glu Arg Ser Gly			
	145	150	155
caa tat tat cta cat ttc ttt gct gat caa cag cct gat ttg aat tgg			528
Gln Tyr Tyr Leu His Phe Phe Ala Asp Gln Gln Pro Asp Leu Asn Trp			
	165	170	175
caa aat acc gag tta cgt cag aaa atc tac aac atg atg aac ttt tgg			576
Gln Asn Thr Glu Leu Arg Gln Lys Ile Tyr Asn Met Met Asn Phe Trp			
	180	185	190
ctt gat aag gga att ggc ggt ttt cgt atg gat gta att gaa tta atc			624
Leu Asp Lys Gly Ile Gly Gly Phe Arg Met Asp Val Ile Glu Leu Ile			
	195	200	205
ggg aag gat cca gac aag aac att cgt gaa aat ggg cca atg cta cat			672
Gly Lys Asp Pro Asp Lys Asn Ile Arg Glu Asn Gly Pro Met Leu His			
	210	215	220
cca tat tta caa gaa atg aat aaa gct act ttt ggt aaa cgt gat gtg			720
Pro Tyr Leu Gln Glu Met Asn Lys Ala Thr Phe Gly Lys Arg Asp Val			
	225	230	235
atg aca gta ggt gaa act tgg aat gca aca cca aag att gcg gaa gaa			768
Met Thr Val Gly Glu Thr Trp Asn Ala Thr Pro Lys Ile Ala Glu Glu			
	245	250	255
tat tct gat cct gat cgt cat gaa ttg tca atg gtc ttt caa ttt gaa			816
Tyr Ser Asp Pro Asp Arg His Glu Leu Ser Met Val Phe Gln Phe Glu			
	260	265	270
aat caa tct tta gat caa caa cct ggt aaa gaa aag tgg gat tta aaa			864
Asn Gln Ser Leu Asp Gln Gln Pro Gly Lys Glu Lys Trp Asp Leu Lys			
	275	280	285

cct ctt gat tta gga gaa ttg aaa aaa gta ttg gtt aag tgg caa aca	912
Pro Leu Asp Leu Gly Glu Leu Lys Lys Val Leu Val Lys Trp Gln Thr	
290 295 300	
aaa atc gat ttt gat cat gct tgg aat agt ttg ttt tgg gag aat cac	960
Lys Ile Asp Phe Asp His Ala Trp Asn Ser Leu Phe Trp Glu Asn His	
305 310 315 320	
gac att ccg cga gtt att tcg cgc tgg ggt aat gat caa gaa tac cgt	1008
Asp Ile Pro Arg Val Ile Ser Arg Trp Gly Asn Asp Gln Glu Tyr Arg	
325 330 335	
gtc caa tgc gcc aaa atg ttt gca att att tta cat atg atg cac ggt	1056
Val Gln Cys Ala Lys Met Phe Ala Ile Ile Leu His Met Met His Gly	
340 345 350	
aca cct tat att ttt aat ggt gaa gaa att ggg atg act aat tgt cct	1104
Thr Pro Tyr Ile Phe Asn Gly Glu Glu Ile Gly Met Thr Asn Cys Pro	
355 360 365	
gtt aaa aat att gat gag gtt gaa gat att gaa agt att aat atg tat	1152
Val Lys Asn Ile Asp Glu Val Glu Asp Ile Glu Ser Ile Asn Met Tyr	
370 375 380	
aac gaa cgt tta gcg gaa ggt tat gat gaa gaa gag ttg att cat gca	1200
Asn Glu Arg Leu Ala Glu Gly Tyr Asp Glu Glu Glu Leu Ile His Ala	
385 390 395 400	
atc aat gta aaa ggt cgt gat aat gca cgt cga cca atg caa tgg aat	1248
Ile Asn Val Lys Gly Arg Asp Asn Ala Arg Arg Pro Met Gln Trp Asn	
405 410 415	
gat gaa aaa aat gct ggc ttt tct gaa gtt gat cca tgg cta agt gta	1296
Asp Glu Lys Asn Ala Gly Phe Ser Glu Val Asp Pro Trp Leu Ser Val	
420 425 430	
aat cct aat tat aag gac att aat gtt gaa aat gcg tta gca gat cca	1344
Asn Pro Asn Tyr Lys Asp Ile Asn Val Glu Asn Ala Leu Ala Asp Pro	
435 440 445	
aat tcg att ttt tat act tat caa aaa ttg att aaa tta cgt cat gaa	1392
Asn Ser Ile Phe Tyr Thr Tyr Gln Lys Leu Ile Lys Leu Arg His Glu	
450 455 460	
aat ccg atc gta gtt gat ggt gat ttt tca tta gtg tct aat aca caa	1440
Asn Pro Ile Val Val Asp Gly Asp Phe Ser Leu Val Ser Asn Thr Gln	
465 470 475 480	
gat gca gtg ctt gct tat tat cgc att ttg aat gat aaa aaa tgg ttg	1488
Asp Ala Val Leu Ala Tyr Tyr Arg Ile Leu Asn Asp Lys Lys Trp Leu	
485 490 495	
gta gta gct aac tta tct aat gag gag cag aat ttt gta tct aat gat	1536
Val Val Ala Asn Leu Ser Asn Glu Glu Gln Asn Phe Val Ser Asn Asp	
500 505 510	

caa att gaa acg atc ctc agc aac tat cca gaa aga aat aat gta caa 1584
 Gln Ile Glu Thr Ile Leu Ser Asn Tyr Pro Glu Arg Asn Asn Val Gln
 515 520 525

aat atc acc ctt aaa cca tat gag gct ttc ata agc aaa gta att gaa 1632
 Asn Ile Thr Leu Lys Pro Tyr Glu Ala Phe Ile Ser Lys Val Ile Glu
 530 535 540

<210> 266

<211> 544

<212> PRT

<213> Lactobacillus acidophilus

<400> 266

Met Arg Val Lys Ile Met Ala Ser Trp Trp Lys Asn Ala Val Val Tyr
 1 5 10 15
 Gln Val Tyr Pro Lys Ser Phe Gln Asp Ser Asn Gly Asp Gly Ile Gly
 20 25 30
 Asp Leu Gln Gly Ile Ile Ser Arg Leu Asp Tyr Leu Glu Lys Leu Gly
 35 40 45
 Ile Asp Ala Ile Trp Leu Ser Pro Val Tyr Gln Ser Pro Gly Val Asp
 50 55 60
 Asn Gly Tyr Asp Ile Ser Asp Tyr Glu Ala Ile Asp Pro Gln Tyr Gly
 65 70 75 80
 Thr Met Ala Asp Met Asp Glu Leu Ile Ser Lys Ala Lys Glu His His
 85 90 95
 Ile Lys Ile Val Met Asp Leu Val Val Asn His Thr Ser Asp Gln His
 100 105 110
 Lys Trp Phe Val Glu Ala Lys Lys Gly Lys Asp Asn Gln Tyr Arg Asp
 115 120 125
 Tyr Tyr Ile Trp Arg Asp Pro Val Asp Glu His Glu Pro Asn Asp Leu
 130 135 140
 Lys Ser Ala Phe Ser Gly Ser Ala Trp Lys Tyr Asp Glu Arg Ser Gly
 145 150 155 160
 Gln Tyr Tyr Leu His Phe Phe Ala Asp Gln Gln Pro Asp Leu Asn Trp
 165 170 175
 Gln Asn Thr Glu Leu Arg Gln Lys Ile Tyr Asn Met Met Asn Phe Trp
 180 185 190
 Leu Asp Lys Gly Ile Gly Gly Phe Arg Met Asp Val Ile Glu Leu Ile
 195 200 205
 Gly Lys Asp Pro Asp Lys Asn Ile Arg Glu Asn Gly Pro Met Leu His
 210 215 220
 Pro Tyr Leu Gln Glu Met Asn Lys Ala Thr Phe Gly Lys Arg Asp Val
 225 230 235 240
 Met Thr Val Gly Glu Thr Trp Asn Ala Thr Pro Lys Ile Ala Glu Glu
 245 250 255
 Tyr Ser Asp Pro Asp Arg His Glu Leu Ser Met Val Phe Gln Phe Glu
 260 265 270
 Asn Gln Ser Leu Asp Gln Gln Pro Gly Lys Glu Lys Trp Asp Leu Lys
 275 280 285
 Pro Leu Asp Leu Gly Glu Leu Lys Lys Val Leu Val Lys Trp Gln Thr
 290 295 300
 Lys Ile Asp Phe Asp His Ala Trp Asn Ser Leu Phe Trp Glu Asn His
 305 310 315 320
 Asp Ile Pro Arg Val Ile Ser Arg Trp Gly Asn Asp Gln Glu Tyr Arg

```

          325          330          335
Val Gln Cys Ala Lys Met Phe Ala Ile Ile Leu His Met Met His Gly
          340          345          350
Thr Pro Tyr Ile Phe Asn Gly Glu Glu Ile Gly Met Thr Asn Cys Pro
          355          360          365
Val Lys Asn Ile Asp Glu Val Glu Asp Ile Glu Ser Ile Asn Met Tyr
          370          375          380
Asn Glu Arg Leu Ala Glu Gly Tyr Asp Glu Glu Glu Leu Ile His Ala
          385          390          395
Ile Asn Val Lys Gly Arg Asp Asn Ala Arg Arg Pro Met Gln Trp Asn
          405          410          415
Asp Glu Lys Asn Ala Gly Phe Ser Glu Val Asp Pro Trp Leu Ser Val
          420          425          430
Asn Pro Asn Tyr Lys Asp Ile Asn Val Glu Asn Ala Leu Ala Asp Pro
          435          440          445
Asn Ser Ile Phe Tyr Thr Tyr Gln Lys Leu Ile Lys Leu Arg His Glu
          450          455          460
Asn Pro Ile Val Val Asp Gly Asp Phe Ser Leu Val Ser Asn Thr Gln
          465          470          475
Asp Ala Val Leu Ala Tyr Tyr Arg Ile Leu Asn Asp Lys Lys Trp Leu
          485          490          495
Val Val Ala Asn Leu Ser Asn Glu Glu Gln Asn Phe Val Ser Asn Asp
          500          505          510
Gln Ile Glu Thr Ile Leu Ser Asn Tyr Pro Glu Arg Asn Asn Val Gln
          515          520          525
Asn Ile Thr Leu Lys Pro Tyr Glu Ala Phe Ile Ser Lys Val Ile Glu
          530          535          540

```

<210> 267

<211> 3012

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 143 - ALPHA-GLUCOSIDASE II

<220>

<221> CDS

<222> (1)...(3012)

<400> 267

```

atg aca caa aat acg caa ata gaa aga cac caa tta ggt cag ctt atc   48
Met Thr Gln Asn Thr Gln Ile Glu Arg His Gln Leu Gly Gln Leu Ile
  1              5              10              15

```

```

ggt gcc aat aaa cgc gat cat tat tat gaa ctc cac tat tcc acc gga   96
Gly Ala Asn Lys Arg Asp His Tyr Tyr Glu Leu His Tyr Ser Thr Gly
          20              25              30

```

```

gaa gtt gct cgt ctt tat att tta gct gaa gga ata ttc cgt tat ttt   144
Glu Val Ala Arg Leu Tyr Ile Leu Ala Glu Gly Ile Phe Arg Tyr Phe
          35              40              45

```

ctt gat ccg gct aag gaa ttc gac gaa aat cac tcc tct ttt gtt gac	192
Leu Asp Pro Ala Lys Glu Phe Asp Glu Asn His Ser Ser Phe Val Asp	
50 55 60	
cta aca caa ttt gat aat agt tat ttt gaa aaa tcc aag cct aaa gct	240
Leu Thr Gln Phe Asp Asn Ser Tyr Phe Glu Lys Ser Lys Pro Lys Ala	
65 70 75 80	
aca agc gat tct ttg att att caa tct ggt aat tac caa tta atc ttt	288
Thr Ser Asp Ser Leu Ile Ile Gln Ser Gly Asn Tyr Gln Leu Ile Phe	
85 90 95	
tgg caa aaa cca gca gta atg aat att ttt gat gag act tta cac cgt	336
Trp Gln Lys Pro Ala Val Met Asn Ile Phe Asp Glu Thr Leu His Arg	
100 105 110	
aac cgc gtt gtt cag ctt agt ccg ctt gaa cta gat caa aat caa act	384
Asn Arg Val Val Gln Leu Ser Pro Leu Glu Leu Asp Gln Asn Gln Thr	
115 120 125	
acc gaa att tta aag caa cat aaa aat gaa ttt tat ttc ggt ggt ggg	432
Thr Glu Ile Leu Lys Gln His Lys Asn Glu Phe Tyr Phe Gly Gly Gly	
130 135 140	
atg caa aat ggc tac ttc agc cac aag ggt caa atc att gat att aaa	480
Met Gln Asn Gly Tyr Phe Ser His Lys Gly Gln Ile Ile Asp Ile Lys	
145 150 155 160	
cgt gac aaa att act ggt aaa ggt ggc gta tta aca cag gtt cca ttt	528
Arg Asp Lys Ile Thr Gly Lys Gly Gly Val Leu Thr Gln Val Pro Phe	
165 170 175	
ttc tgg gca aat tcc ggc ttt ggt gaa tta aga aat act act gcc cct	576
Phe Trp Ala Asn Ser Gly Phe Gly Glu Leu Arg Asn Thr Thr Ala Pro	
180 185 190	
ggt caa tat gat ttt ggc aaa aaa gat gaa gat gcc gta atc tta cgt	624
Gly Gln Tyr Asp Phe Gly Lys Lys Asp Glu Asp Ala Val Ile Leu Arg	
195 200 205	
cat gac tct caa ata ttt gat aca ttc tat ctt ttg ggt aac tct cct	672
His Asp Ser Gln Ile Phe Asp Thr Phe Tyr Leu Leu Gly Asn Ser Pro	
210 215 220	
aca gat att ttg gaa aaa tat tat gtt cta acc ggt aag cca tta atg	720
Thr Asp Ile Leu Glu Lys Tyr Tyr Val Leu Thr Gly Lys Pro Leu Met	
225 230 235 240	
cca cct aaa tat gca ttg ggc ttg gga cat gtc ggc aac ttt ttg act	768
Pro Pro Lys Tyr Ala Leu Gly Leu Gly His Val Gly Asn Phe Leu Thr	
245 250 255	
acc cta tgg caa cct ggt gaa gct aaa gaa cgc aac gcc act atg ttt	816
Thr Leu Trp Gln Pro Gly Glu Ala Lys Glu Arg Asn Ala Thr Met Phe	
260 265 270	
gaa gat ggt aac tat tac acc aga act act aat ccg gaa aat gct aat	864

Glu Asp Gly Asn Tyr Tyr Thr Arg Thr Thr Asn Pro Glu Asn Ala Asn	
275 280 285	
ggg aag gca tca tta aat ggt gag gaa gaa tat caa ttc tcc gct cgt	912
Gly Lys Ala Ser Leu Asn Gly Glu Glu Glu Tyr Gln Phe Ser Ala Arg	
290 295 300	
gca atg att gat cgt tat caa aag caa cat ttc aaa cta agc tgg att	960
Ala Met Ile Asp Arg Tyr Gln Lys Gln His Phe Lys Leu Ser Trp Ile	
305 310 315 320	
gta ccc aac tac aat atc caa gat gtt gat gcc gag caa atg acc agt	1008
Val Pro Asn Tyr Asn Ile Gln Asp Val Asp Ala Glu Gln Met Thr Ser	
325 330 335	
ttt agc gat tat gct gcg tca aga gaa gtt aat gct ggc gtt tgg agc	1056
Phe Ser Asp Tyr Ala Ala Ser Arg Glu Val Asn Ala Gly Val Trp Ser	
340 345 350	
ggg gac gaa aca cca aag act gct ccc gac act act ttt att caa act	1104
Gly Asp Glu Thr Pro Lys Thr Ala Pro Asp Thr Thr Phe Ile Gln Thr	
355 360 365	
gat act agt gat cct aaa aca ctt aaa aat gac tca ctg atc tta cgt	1152
Asp Thr Ser Asp Pro Lys Thr Leu Lys Asn Asp Ser Leu Ile Leu Arg	
370 375 380	
gat aat tta aag cgt aaa cgt cca ctt att ttt tca aat aca ggt att	1200
Asp Asn Leu Lys Arg Lys Arg Pro Leu Ile Phe Ser Asn Thr Gly Ile	
385 390 395 400	
gcc ggt agt caa aac aga ata atg ttg gcc ttt ggc gat att ggc ggt	1248
Ala Gly Ser Gln Asn Arg Ile Met Leu Ala Phe Gly Asp Ile Gly Gly	
405 410 415	
aat tgg gaa aat att cca act caa gtt gcc ggc ttt tta ggt gca agt	1296
Asn Trp Glu Asn Ile Pro Thr Gln Val Ala Gly Phe Leu Gly Ala Ser	
420 425 430	
tta tct ggt caa cca tta gtt ggt agt gca gtt gac gga act gtt ggt	1344
Leu Ser Gly Gln Pro Leu Val Gly Ser Ala Val Asp Gly Thr Val Gly	
435 440 445	
gga ggt aat gct caa atc agt atc cgt gat ttt gaa tgg aag gca ttc	1392
Gly Gly Asn Ala Gln Ile Ser Ile Arg Asp Phe Glu Trp Lys Ala Phe	
450 455 460	
acg cct att ctt ttc aat ctt gac gat caa ggc aat ttt agt aaa acg	1440
Thr Pro Ile Leu Phe Asn Leu Asp Asp Gln Gly Asn Phe Ser Lys Thr	
465 470 475 480	
cca ttt gct tat aac agc aag atg acc aag att aac cgc gca tat cta	1488
Pro Phe Ala Tyr Asn Ser Lys Met Thr Lys Ile Asn Arg Ala Tyr Leu	
485 490 495	
aag ctc cgt gaa caa ctt caa act tac atg tat acg ctc atc tat cgt	1536
Lys Leu Arg Glu Gln Leu Gln Thr Tyr Met Tyr Thr Leu Ile Tyr Arg	

500	505	510	
gcg caa gtt ggt gaa cct atc atg aga cca tta ttt tta gaa ttt cct Ala Gln Val Gly Glu Pro Ile Met Arg Pro Leu Phe Leu Glu Phe Pro 515 520 525			1584
cat gag caa atc aat tac aca tca caa gtt ggt cac gaa ttc atg ctt His Glu Gln Ile Asn Tyr Thr Ser Gln Val Gly His Glu Phe Met Leu 530 535 540			1632
ggt cct aac ttg ctt att tca cca att gta aac ggc cga gaa gat ggt Gly Pro Asn Leu Leu Ile Ser Pro Ile Val Asn Gly Arg Glu Asp Gly 545 550 555 560			1680
aat ggg aat tca aga aaa gac aat ctt tac tta cca aat cac cgt acc Asn Gly Asn Ser Arg Lys Asp Asn Leu Tyr Leu Pro Asn His Arg Thr 565 570 575			1728
atg tgg atc gat tta ttc gat ggt aaa aag ttc tta ggt ggc cgc gtt Met Trp Ile Asp Leu Phe Asp Gly Lys Lys Phe Leu Gly Gly Arg Val 580 585 590			1776
tat aac aaa cag tct tat cca tct tgg cat tta cct gtc ttt gta cgt Tyr Asn Lys Gln Ser Tyr Pro Ser Trp His Leu Pro Val Phe Val Arg 595 600 605			1824
ggc gga tca atc ttt gac ttg ggt gat cgt aat tac gtt ctt tac cca Gly Gly Ser Ile Phe Asp Leu Gly Asp Arg Asn Tyr Val Leu Tyr Pro 610 615 620			1872
caa gga cgt agc aaa atg gtt act tac gat gat aat ggc tac aat gat Gln Gly Arg Ser Lys Met Val Thr Tyr Asp Asp Asn Gly Tyr Asn Asp 625 630 635 640			1920
tat tct aga aat cat gta gca acg cag att act agt gat ctt gaa gca Tyr Ser Arg Asn His Val Ala Thr Gln Ile Thr Ser Asp Leu Glu Ala 645 650 655			1968
agc aag tta act att acc att gat cca act caa ggt gat ttc agt act Ser Lys Leu Thr Ile Thr Ile Asp Pro Thr Gln Gly Asp Phe Ser Thr 660 665 670			2016
ttc caa acg gaa aac acc act aat cta aat att atg tgt gat ggt tat Phe Gln Thr Glu Asn Thr Thr Asn Leu Asn Ile Met Cys Asp Gly Tyr 675 680 685			2064
cca gac ggt tta acc gtt aag att aat gat caa gtt gtc aat atg caa Pro Asp Gly Leu Thr Val Lys Ile Asn Asp Gln Val Val Asn Met Gln 690 695 700			2112
gaa tat ggc act gtt gat aca ttc gca cat gca aaa gaa ggt ttc ttc Glu Tyr Gly Thr Val Asp Thr Phe Ala His Ala Lys Glu Gly Phe Phe 705 710 715 720			2160
ttt aat acc aac tac agc tgg atg cct gaa ttt gat caa tat caa gaa Phe Asn Thr Asn Tyr Ser Trp Met Pro Glu Phe Asp Gln Tyr Gln Gln 725 730 735			2208

aag aag caa aca gct tta caa att aaa ttg gct aaa cgg gat att act	2256
Lys Lys Gln Thr Ala Leu Gln Ile Lys Leu Ala Lys Arg Asp Ile Thr	
740 745 750	
gat tca aag att gaa atc act atc cgt aac ttc aga tat ggt aat gaa	2304
Asp Ser Lys Ile Glu Ile Thr Ile Arg Asn Phe Arg Tyr Gly Asn Glu	
755 760 765	
act ttg gtt cac gca att act gat tca ttg ctt cac tca cca aag cag	2352
Thr Leu Val His Ala Ile Thr Asp Ser Leu Leu His Ser Pro Lys Gln	
770 775 780	
cca atg gtc gat cct gat aaa att agt tca cat tca ttg act gtt gtt	2400
Pro Met Val Asp Pro Asp Lys Ile Ser Ser His Ser Leu Thr Val Val	
785 790 795 800	
tgg cca caa tta acc gat aag gtc caa att gaa gtt aac ggc att ttg	2448
Trp Pro Gln Leu Thr Asp Lys Val Gln Ile Glu Val Asn Gly Ile Leu	
805 810 815	
cat gat ggc att gat ggt agc tca ttt acc ttc cac gaa tta gtg cca	2496
His Asp Gly Ile Asp Gly Ser Ser Phe Thr Phe His Glu Leu Val Pro	
820 825 830	
aat act cgc tac act tta cgc ttg aga tat gtt gct ggt aat aaa gtt	2544
Asn Thr Arg Tyr Thr Leu Arg Leu Arg Tyr Val Ala Gly Asn Lys Val	
835 840 845	
tct gaa tgg tca gaa cca ttt ggt gca att acc aaa ccg gat cca atg	2592
Ser Glu Trp Ser Glu Pro Phe Gly Ala Ile Thr Lys Pro Asp Pro Met	
850 855 860	
aat tac gct atc agt aat atc cat gtc acc agt agt tta acc agt caa	2640
Asn Tyr Ala Ile Ser Asn Ile His Val Thr Ser Ser Leu Thr Ser Gln	
865 870 875 880	
aaa gat cat cca att gaa tat ttg act gat cta aag ctt gcc agc gaa	2688
Lys Asp His Pro Ile Glu Tyr Leu Thr Asp Leu Lys Leu Ala Ser Glu	
885 890 895	
tgg gaa act att aac ggc gta agt gaa gac aaa cca ctt gaa tta aac	2736
Trp Glu Thr Ile Asn Gly Val Ser Glu Asp Lys Pro Leu Glu Leu Asn	
900 905 910	
ttc aag ttc gac cat ttg gaa cac tta agt aga atg gtt ttg gta cct	2784
Phe Lys Phe Asp His Leu Glu His Leu Ser Arg Met Val Leu Val Pro	
915 920 925	
aga aag att gat cat caa ggc gat cca gtt gag gtc agc gtt gaa acc	2832
Arg Lys Ile Asp His Gln Gly Asp Pro Val Glu Val Ser Val Glu Thr	
930 935 940	
tca atg gat ggt act aac ttt aag cca tac gac gaa cga ctt act tgg	2880
Ser Met Asp Gly Thr Asn Phe Lys Pro Tyr Asp Glu Arg Leu Thr Trp	
945 950 955 960	

aag tct gac agc aag aat aaa gtt gtc ggc ttg agg gat gta gaa gct 2928
 Lys Ser Asp Ser Lys Asn Lys Val Val Gly Leu Arg Asp Val Glu Ala
 965 970 975

 aag gca atc aga tta aag gtt tat aag tca tct ggc cca ttt gtg gca 2976
 Lys Ala Ile Arg Leu Lys Val Tyr Lys Ser Ser Gly Pro Phe Val Ala
 980 985 990

 gct aag gaa gtt atc ttc ttt aga gag aag aaa gat 3012
 Ala Lys Glu Val Ile Phe Phe Arg Glu Lys Lys Asp
 995 1000

<210> 268

<211> 1004

<212> PRT

<213> Lactobacillus acidophilus

<400> 268

Met Thr Gln Asn Thr Gln Ile Glu Arg His Gln Leu Gly Gln Leu Ile
 1 5 10 15
 Gly Ala Asn Lys Arg Asp His Tyr Tyr Glu Leu His Tyr Ser Thr Gly
 20 25 30
 Glu Val Ala Arg Leu Tyr Ile Leu Ala Glu Gly Ile Phe Arg Tyr Phe
 35 40 45
 Leu Asp Pro Ala Lys Glu Phe Asp Glu Asn His Ser Ser Phe Val Asp
 50 55 60
 Leu Thr Gln Phe Asp Asn Ser Tyr Phe Glu Lys Ser Lys Pro Lys Ala
 65 70 75 80
 Thr Ser Asp Ser Leu Ile Ile Gln Ser Gly Asn Tyr Gln Leu Ile Phe
 85 90 95
 Trp Gln Lys Pro Ala Val Met Asn Ile Phe Asp Glu Thr Leu His Arg
 100 105 110
 Asn Arg Val Val Gln Leu Ser Pro Leu Glu Leu Asp Gln Asn Gln Thr
 115 120 125
 Thr Glu Ile Leu Lys Gln His Lys Asn Glu Phe Tyr Phe Gly Gly Gly
 130 135 140
 Met Gln Asn Gly Tyr Phe Ser His Lys Gly Gln Ile Ile Asp Ile Lys
 145 150 155 160
 Arg Asp Lys Ile Thr Gly Lys Gly Gly Val Leu Thr Gln Val Pro Phe
 165 170 175
 Phe Trp Ala Asn Ser Gly Phe Gly Glu Leu Arg Asn Thr Thr Ala Pro
 180 185 190
 Gly Gln Tyr Asp Phe Gly Lys Lys Asp Glu Asp Ala Val Ile Leu Arg
 195 200 205
 His Asp Ser Gln Ile Phe Asp Thr Phe Tyr Leu Leu Gly Asn Ser Pro
 210 215 220
 Thr Asp Ile Leu Glu Lys Tyr Tyr Val Leu Thr Gly Lys Pro Leu Met
 225 230 235 240
 Pro Pro Lys Tyr Ala Leu Gly Leu Gly His Val Gly Asn Phe Leu Thr
 245 250 255
 Thr Leu Trp Gln Pro Gly Glu Ala Lys Glu Arg Asn Ala Thr Met Phe
 260 265 270
 Glu Asp Gly Asn Tyr Tyr Thr Arg Thr Thr Asn Pro Glu Asn Ala Asn
 275 280 285
 Gly Lys Ala Ser Leu Asn Gly Glu Glu Glu Tyr Gln Phe Ser Ala Arg
 290 295 300

Ala Met Ile Asp Arg Tyr Gln Lys Gln His Phe Lys Leu Ser Trp Ile
 305 310 315 320
 Val Pro Asn Tyr Asn Ile Gln Asp Val Asp Ala Glu Gln Met Thr Ser
 325 330 335
 Phe Ser Asp Tyr Ala Ala Ser Arg Glu Val Asn Ala Gly Val Trp Ser
 340 345 350
 Gly Asp Glu Thr Pro Lys Thr Ala Pro Asp Thr Thr Phe Ile Gln Thr
 355 360 365
 Asp Thr Ser Asp Pro Lys Thr Leu Lys Asn Asp Ser Leu Ile Leu Arg
 370 375 380
 Asp Asn Leu Lys Arg Lys Arg Pro Leu Ile Phe Ser Asn Thr Gly Ile
 385 390 395 400
 Ala Gly Ser Gln Asn Arg Ile Met Leu Ala Phe Gly Asp Ile Gly Gly
 405 410 415
 Asn Trp Glu Asn Ile Pro Thr Gln Val Ala Gly Phe Leu Gly Ala Ser
 420 425 430
 Leu Ser Gly Gln Pro Leu Val Gly Ser Ala Val Asp Gly Thr Val Gly
 435 440 445
 Gly Gly Asn Ala Gln Ile Ser Ile Arg Asp Phe Glu Trp Lys Ala Phe
 450 455 460
 Thr Pro Ile Leu Phe Asn Leu Asp Asp Gln Gly Asn Phe Ser Lys Thr
 465 470 475 480
 Pro Phe Ala Tyr Asn Ser Lys Met Thr Lys Ile Asn Arg Ala Tyr Leu
 485 490 495
 Lys Leu Arg Glu Gln Leu Gln Thr Tyr Met Tyr Thr Leu Ile Tyr Arg
 500 505 510
 Ala Gln Val Gly Glu Pro Ile Met Arg Pro Leu Phe Leu Glu Phe Pro
 515 520 525
 His Glu Gln Ile Asn Tyr Thr Ser Gln Val Gly His Glu Phe Met Leu
 530 535 540
 Gly Pro Asn Leu Leu Ile Ser Pro Ile Val Asn Gly Arg Glu Asp Gly
 545 550 555 560
 Asn Gly Asn Ser Arg Lys Asp Asn Leu Tyr Leu Pro Asn His Arg Thr
 565 570 575
 Met Trp Ile Asp Leu Phe Asp Gly Lys Lys Phe Leu Gly Gly Arg Val
 580 585 590
 Tyr Asn Lys Gln Ser Tyr Pro Ser Trp His Leu Pro Val Phe Val Arg
 595 600 605
 Gly Gly Ser Ile Phe Asp Leu Gly Asp Arg Asn Tyr Val Leu Tyr Pro
 610 615 620
 Gln Gly Arg Ser Lys Met Val Thr Tyr Asp Asp Asn Gly Tyr Asn Asp
 625 630 635 640
 Tyr Ser Arg Asn His Val Ala Thr Gln Ile Thr Ser Asp Leu Glu Ala
 645 650 655
 Ser Lys Leu Thr Ile Thr Ile Asp Pro Thr Gln Gly Asp Phe Ser Thr
 660 665 670
 Phe Gln Thr Glu Asn Thr Thr Asn Leu Asn Ile Met Cys Asp Gly Tyr
 675 680 685
 Pro Asp Gly Leu Thr Val Lys Ile Asn Asp Gln Val Val Asn Met Gln
 690 695 700
 Glu Tyr Gly Thr Val Asp Thr Phe Ala His Ala Lys Glu Gly Phe Phe
 705 710 715 720
 Phe Asn Thr Asn Tyr Ser Trp Met Pro Glu Phe Asp Gln Tyr Gln Glu
 725 730 735
 Lys Lys Gln Thr Ala Leu Gln Ile Lys Leu Ala Lys Arg Asp Ile Thr
 740 745 750
 Asp Ser Lys Ile Glu Ile Thr Ile Arg Asn Phe Arg Tyr Gly Asn Glu

```

      755      760      765
Thr Leu Val His Ala Ile Thr Asp Ser Leu Leu His Ser Pro Lys Gln
770      775      780
Pro Met Val Asp Pro Asp Lys Ile Ser Ser His Ser Leu Thr Val Val
785      790      795      800
Trp Pro Gln Leu Thr Asp Lys Val Gln Ile Glu Val Asn Gly Ile Leu
805      810      815
His Asp Gly Ile Asp Gly Ser Ser Phe Thr Phe His Glu Leu Val Pro
820      825      830
Asn Thr Arg Tyr Thr Leu Arg Leu Arg Tyr Val Ala Gly Asn Lys Val
835      840      845
Ser Glu Trp Ser Glu Pro Phe Gly Ala Ile Thr Lys Pro Asp Pro Met
850      855      860
Asn Tyr Ala Ile Ser Asn Ile His Val Thr Ser Ser Leu Thr Ser Gln
865      870      875      880
Lys Asp His Pro Ile Glu Tyr Leu Thr Asp Leu Lys Leu Ala Ser Glu
885      890      895
Trp Glu Thr Ile Asn Gly Val Ser Glu Asp Lys Pro Leu Glu Leu Asn
900      905      910
Phe Lys Phe Asp His Leu Glu His Leu Ser Arg Met Val Leu Val Pro
915      920      925
Arg Lys Ile Asp His Gln Gly Asp Pro Val Glu Val Ser Val Glu Thr
930      935      940
Ser Met Asp Gly Thr Asn Phe Lys Pro Tyr Asp Glu Arg Leu Thr Trp
945      950      955      960
Lys Ser Asp Ser Lys Asn Lys Val Val Gly Leu Arg Asp Val Glu Ala
965      970      975
Lys Ala Ile Arg Leu Lys Val Tyr Lys Ser Ser Gly Pro Phe Val Ala
980      985      990
Ala Lys Glu Val Ile Phe Phe Arg Glu Lys Lys Asp
995      1000

```

<210> 269

<211> 1710

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1014 - Dextran glucosidase

<220>

<221> CDS

<222> (1)...(1710)

<400> 269

```

ttg ttg att ttg caa gaa gac aga aga tta aat tgt aag gag aaa agt 48
Met Leu Ile Leu Gln Glu Asp Arg Arg Leu Asn Cys Lys Glu Lys Ser
1      5      10      15

```

```

atg att aat tta ggc aaa aaa ata att tat caa att tat cct aaa tct 96
Met Ile Asn Leu Gly Lys Lys Ile Ile Tyr Gln Ile Tyr Pro Lys Ser
20      25      30

```

ttc tat gat tca aat ggc gat ggg gta gga gat ctt caa gga atc att	144
Phe Tyr Asp Ser Asn Gly Asp Gly Val Gly Asp Leu Gln Gly Ile Ile	
35 40 45	
caa aag att gat tat att aag aag tta aat gta gac atg atc tgg ttt	192
Gln Lys Ile Asp Tyr Ile Lys Lys Leu Asn Val Asp Met Ile Trp Phe	
50 55 60	
aat cca ttt ttt gtt tca ccg caa aat gat aat ggt tat gat att gct	240
Asn Pro Phe Phe Val Ser Pro Gln Asn Asp Asn Gly Tyr Asp Ile Ala	
65 70 75 80	
gat tat tac aac att gat cct cgc ttt ggt aca atg gct gat ttt gag	288
Asp Tyr Tyr Asn Ile Asp Pro Arg Phe Gly Thr Met Ala Asp Phe Glu	
85 90 95	
aaa ttg gta aag aag ctg aaa gaa atc ggt gtg ggt gta atg cta gat	336
Lys Leu Val Lys Lys Leu Lys Glu Ile Gly Val Gly Val Met Leu Asp	
100 105 110	
atg gtg ctc aat cac tgc tca act gaa aat att tgg ttt aaa aaa gca	384
Met Val Leu Asn His Cys Ser Thr Glu Asn Ile Trp Phe Lys Lys Ala	
115 120 125	
ctt gct ggc aat gaa aag tat cgt aaa ttt ttc tac ttg aga aaa gga	432
Leu Ala Gly Asn Glu Lys Tyr Arg Lys Phe Phe Tyr Leu Arg Lys Gly	
130 135 140	
aaa aac gga ggt tta cct aat aat tgg caa agt aaa ttc ggt ggt act	480
Lys Asn Gly Gly Leu Pro Asn Asn Trp Gln Ser Lys Phe Gly Gly Thr	
145 150 155 160	
gct tgg tca aaa ttt ggt gat acc gat tac tac tac ctt cac ttg tat	528
Ala Trp Ser Lys Phe Gly Asp Thr Asp Tyr Tyr Tyr Leu His Leu Tyr	
165 170 175	
gat cca act caa gca gat ctt gat tgg cat aat cct gaa gtt cgt aaa	576
Asp Pro Thr Gln Ala Asp Leu Asp Trp His Asn Pro Glu Val Arg Lys	
180 185 190	
gaa tta ttt aaa gtg gtt aac ttt tgg cgt agt aaa ggt gtc cat ggc	624
Glu Leu Phe Lys Val Val Asn Phe Trp Arg Ser Lys Gly Val His Gly	
195 200 205	
ttc cgc ttt gat gta att aat gtt acg ggt aaa gcg gaa aaa cta gtt	672
Phe Arg Phe Asp Val Ile Asn Val Thr Gly Lys Ala Glu Lys Leu Val	
210 215 220	
gat tca aca gat cct gta gaa gaa aag agt ttg tac act gat act cca	720
Asp Ser Thr Asp Pro Val Glu Glu Lys Ser Leu Tyr Thr Asp Thr Pro	
225 230 235 240	
att gtt cat aaa tac tta aaa gag ctt aat gct gca act ttt ggt caa	768
Ile Val His Lys Tyr Leu Lys Glu Leu Asn Ala Ala Thr Phe Gly Gln	
245 250 255	
gac cct gaa tca att act gtg gga gaa atg tca tca acg acg att gcc	816

Asp	Pro	Glu	Ser	Ile	Thr	Val	Gly	Glu	Met	Ser	Ser	Thr	Thr	Ile	Ala	
			260					265					270			
aac	tca	att	gaa	tat	tca	aaa	cca	agt	gaa	cat	gaa	tta	tca	atg	gtt	864
Asn	Ser	Ile	Glu	Tyr	Ser	Lys	Pro	Ser	Glu	His	Glu	Leu	Ser	Met	Val	
		275					280					285				
ttc	act	ttc	cat	cat	ttg	aaa	gtt	gac	tat	cag	gat	ggg	gaa	aag	tgg	912
Phe	Thr	Phe	His	His	Leu	Lys	Val	Asp	Tyr	Gln	Asp	Gly	Glu	Lys	Trp	
	290					295					300					
tct	aag	atg	cca	ttt	gat	ttt	atg	aaa	tta	aag	gaa	tta	ttc	act	gaa	960
Ser	Lys	Met	Pro	Phe	Asp	Phe	Met	Lys	Leu	Lys	Glu	Leu	Phe	Thr	Glu	
305					310					315					320	
tgg	caa	gaa	aaa	atg	gat	caa	ggg	gat	ggc	tgg	aac	gca	tta	ttc	tgg	1008
Trp	Gln	Glu	Lys	Met	Asp	Gln	Gly	Asp	Gly	Trp	Asn	Ala	Leu	Phe	Trp	
			325					330						335		
gac	aat	cat	gat	cag	cct	tgg	gca	tta	act	aga	ttt	ggg	gat	act	ggg	1056
Asp	Asn	His	Asp	Gln	Pro	Trp	Ala	Leu	Thr	Arg	Phe	Gly	Asp	Thr	Gly	
			340					345					350			
aag	tat	cgt	gga	aag	tca	gct	gaa	atg	ctt	gcc	aca	gca	act	cat	ctt	1104
Lys	Tyr	Arg	Gly	Lys	Ser	Ala	Glu	Met	Leu	Ala	Thr	Ala	Thr	His	Leu	
		355					360					365				
atg	cgg	gga	aca	cca	tat	att	tat	atg	ggg	gaa	gaa	att	ggg	atg	att	1152
Met	Arg	Gly	Thr	Pro	Tyr	Ile	Tyr	Met	Gly	Glu	Glu	Ile	Gly	Met	Ile	
	370					375						380				
gat	cct	gat	tat	tct	tca	atg	gat	gat	tac	gta	gat	gtt	gag	gcc	aag	1200
Asp	Pro	Asp	Tyr	Ser	Ser	Met	Asp	Asp	Tyr	Val	Asp	Val	Glu	Ala	Lys	
385					390					395					400	
aat	gct	ttt	aag	gct	tta	act	aaa	aaa	ggg	ttg	agt	gat	aaa	gaa	gct	1248
Asn	Ala	Phe	Lys	Ala	Leu	Thr	Lys	Lys	Gly	Leu	Ser	Asp	Lys	Glu	Ala	
				405					410					415		
ttt	gaa	ata	gtt	aaa	tca	aaa	gct	cgt	gac	aat	tca	cgt	gta	cca	atg	1296
Phe	Glu	Ile	Val	Lys	Ser	Lys	Ala	Arg	Asp	Asn	Ser	Arg	Val	Pro	Met	
			420					425					430			
cat	tgg	aat	agt	gaa	aaa	tat	gca	ggg	ttt	agt	gaa	cat	aag	ccg	tgg	1344
His	Trp	Asn	Ser	Glu	Lys	Tyr	Ala	Gly	Phe	Ser	Glu	His	Lys	Pro	Trp	
		435					440					445				
ctc	ata	cca	act	gat	caa	gaa	aaa	att	aat	gtt	gaa	gag	gaa	tta	gca	1392
Leu	Ile	Pro	Thr	Asp	Gln	Glu	Lys	Ile	Asn	Val	Glu	Glu	Glu	Leu	Ala	
		450				455					460					
cat	ggg	gaa	att	ttt	aat	tac	tat	caa	aag	tta	att	aag	ctg	cgt	aga	1440
His	Gly	Glu	Ile	Phe	Asn	Tyr	Tyr	Gln	Lys	Leu	Ile	Lys	Leu	Arg	Arg	
465					470					475					480	
agc	gaa	gat	tta	atc	tct	gat	ggg	cat	att	aag	atg	ttc	ttg	aaa	gat	1488
Ser	Glu	Asp	Leu	Ile	Ser	Asp	Gly	His	Ile	Lys	Met	Phe	Leu	Lys	Asp	

485										490					495					
gat	ccg	cag	ggt	ttt	gct	tat	gaa	cgc	tac	tta	aaa	gat	agt	gat	aaa	1536				
Asp	Pro	Gln	Val	Phe	Ala	Tyr	Glu	Arg	Tyr	Leu	Lys	Asp	Ser	Asp	Lys					
500					505					510										
aag	tta	ttg	gta	ttt	act	aac	ttc	tat	ggg	aaa	gaa	cat	agt	ggt	aaa	1584				
Lys	Leu	Leu	Val	Phe	Thr	Asn	Phe	Tyr	Gly	Lys	Glu	His	Ser	Val	Lys					
515					520					525										
tta	ccc	gaa	gaa	tat	caa	aac	aaa	gaa	tac	caa	ggt	tta	att	aac	aat	1632				
Leu	Pro	Glu	Glu	Tyr	Gln	Asn	Lys	Glu	Tyr	Gln	Val	Leu	Ile	Asn	Asn					
530					535					540										
tat	gat	act	aaa	gat	agc	caa	tta	acc	gat	gaa	att	ata	ttg	aag	cca	1680				
Tyr	Asp	Thr	Lys	Asp	Ser	Gln	Leu	Thr	Asp	Glu	Ile	Ile	Leu	Lys	Pro					
545					550					555					560					
tat	gaa	gca	tta	gct	att	aaa	att	aaa	caa							1710				
Tyr	Glu	Ala	Leu	Ala	Ile	Lys	Ile	Lys	Gln											
565					570															

<210> 270

<211> 570

<212> PRT

<213> Lactobacillus acidophilus

<400> 270

Met	Leu	Ile	Leu	Gln	Glu	Asp	Arg	Arg	Leu	Asn	Cys	Lys	Glu	Lys	Ser
1				5					10					15	
Met	Ile	Asn	Leu	Gly	Lys	Lys	Ile	Ile	Tyr	Gln	Ile	Tyr	Pro	Lys	Ser
			20					25					30		
Phe	Tyr	Asp	Ser	Asn	Gly	Asp	Gly	Val	Gly	Asp	Leu	Gln	Gly	Ile	Ile
		35				40						45			
Gln	Lys	Ile	Asp	Tyr	Ile	Lys	Lys	Leu	Asn	Val	Asp	Met	Ile	Trp	Phe
		50				55					60				
Asn	Pro	Phe	Phe	Val	Ser	Pro	Gln	Asn	Asp	Asn	Gly	Tyr	Asp	Ile	Ala
65				70					75					80	
Asp	Tyr	Tyr	Asn	Ile	Asp	Pro	Arg	Phe	Gly	Thr	Met	Ala	Asp	Phe	Glu
			85					90					95		
Lys	Leu	Val	Lys	Lys	Leu	Lys	Glu	Ile	Gly	Val	Gly	Val	Met	Leu	Asp
			100				105					110			
Met	Val	Leu	Asn	His	Cys	Ser	Thr	Glu	Asn	Ile	Trp	Phe	Lys	Lys	Ala
		115					120					125			
Leu	Ala	Gly	Asn	Glu	Lys	Tyr	Arg	Lys	Phe	Phe	Tyr	Leu	Arg	Lys	Gly
	130					135					140				
Lys	Asn	Gly	Gly	Leu	Pro	Asn	Asn	Trp	Gln	Ser	Lys	Phe	Gly	Gly	Thr
145				150					155					160	
Ala	Trp	Ser	Lys	Phe	Gly	Asp	Thr	Asp	Tyr	Tyr	Tyr	Leu	His	Leu	Tyr
			165					170					175		
Asp	Pro	Thr	Gln	Ala	Asp	Leu	Asp	Trp	His	Asn	Pro	Glu	Val	Arg	Lys
		180					185					190			
Glu	Leu	Phe	Lys	Val	Val	Asn	Phe	Trp	Arg	Ser	Lys	Gly	Val	His	Gly
	195					200						205			
Phe	Arg	Phe	Asp	Val	Ile	Asn	Val	Thr	Gly	Lys	Ala	Glu	Lys	Leu	Val
210						215					220				

```

Asp Ser Thr Asp Pro Val Glu Glu Lys Ser Leu Tyr Thr Asp Thr Pro
225          230          235          240
Ile Val His Lys Tyr Leu Lys Glu Leu Asn Ala Ala Thr Phe Gly Gln
          245          250          255
Asp Pro Glu Ser Ile Thr Val Gly Glu Met Ser Ser Thr Thr Ile Ala
          260          265          270
Asn Ser Ile Glu Tyr Ser Lys Pro Ser Glu His Glu Leu Ser Met Val
          275          280          285
Phe Thr Phe His His Leu Lys Val Asp Tyr Gln Asp Gly Glu Lys Trp
          290          295          300
Ser Lys Met Pro Phe Asp Phe Met Lys Leu Lys Glu Leu Phe Thr Glu
305          310          315          320
Trp Gln Glu Lys Met Asp Gln Gly Asp Gly Trp Asn Ala Leu Phe Trp
          325          330          335
Asp Asn His Asp Gln Pro Trp Ala Leu Thr Arg Phe Gly Asp Thr Gly
          340          345          350
Lys Tyr Arg Gly Lys Ser Ala Glu Met Leu Ala Thr Ala Thr His Leu
          355          360          365
Met Arg Gly Thr Pro Tyr Ile Tyr Met Gly Glu Glu Ile Gly Met Ile
          370          375          380
Asp Pro Asp Tyr Ser Ser Met Asp Asp Tyr Val Asp Val Glu Ala Lys
385          390          395          400
Asn Ala Phe Lys Ala Leu Thr Lys Lys Gly Leu Ser Asp Lys Glu Ala
          405          410          415
Phe Glu Ile Val Lys Ser Lys Ala Arg Asp Asn Ser Arg Val Pro Met
          420          425          430
His Trp Asn Ser Glu Lys Tyr Ala Gly Phe Ser Glu His Lys Pro Trp
          435          440          445
Leu Ile Pro Thr Asp Gln Glu Lys Ile Asn Val Glu Glu Glu Leu Ala
          450          455          460
His Gly Glu Ile Phe Asn Tyr Tyr Gln Lys Leu Ile Lys Leu Arg Arg
465          470          475          480
Ser Glu Asp Leu Ile Ser Asp Gly His Ile Lys Met Phe Leu Lys Asp
          485          490          495
Asp Pro Gln Val Phe Ala Tyr Glu Arg Tyr Leu Lys Asp Ser Asp Lys
          500          505          510
Lys Leu Leu Val Phe Thr Asn Phe Tyr Gly Lys Glu His Ser Val Lys
          515          520          525
Leu Pro Glu Glu Tyr Gln Asn Lys Glu Tyr Gln Val Leu Ile Asn Asn
          530          535          540
Tyr Asp Thr Lys Asp Ser Gln Leu Thr Asp Glu Ile Ile Leu Lys Pro
545          550          555          560
Tyr Glu Ala Leu Ala Ile Lys Ile Lys Gln
          565          570

```

<210> 271

<211> 1914

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 680 - 1,4-alpha-glucan branching enzyme

<220>

<221> CDS

<222> (1)...(1914)

<400> 271

atg gta acg ata gtg gag gtt aaa caa cat att aaa aaa ttt gca gct	48
Met Val Thr Ile Val Glu Val Lys Gln His Ile Lys Lys Phe Ala Ala	
1 5 10 15	
ggc aat gag cta tat ctt caa gaa gta tta ggg tgt cat tat gaa aat	96
Gly Asn Glu Leu Tyr Leu Gln Glu Val Leu Gly Cys His Tyr Glu Asn	
20 25 30	
gat atc tat act ttt aga gta tgg gca cca aat gcg caa aaa gtt tgg	144
Asp Ile Tyr Thr Phe Arg Val Trp Ala Pro Asn Ala Gln Lys Val Trp	
35 40 45	
cta gtt ggc gat ttt aat gat tgg gat aaa tca tta gaa atg agt cag	192
Leu Val Gly Asp Phe Asn Asp Trp Asp Lys Ser Leu Glu Met Ser Gln	
50 55 60	
act tta gat gga gtt tgg gaa ata aag acc agc tta ccc aaa gaa gga	240
Thr Leu Asp Gly Val Trp Glu Ile Lys Thr Ser Leu Pro Lys Glu Gly	
65 70 75 80	
cag cta tat aag ttt cta gtt aaa caa gct gat ggt cgt gag gta atg	288
Gln Leu Tyr Lys Phe Leu Val Lys Gln Ala Asp Gly Arg Glu Val Met	
85 90 95	
aaa att gat cct atg gcg ttc gaa tta gag cct aga cca ggc agt gca	336
Lys Ile Asp Pro Met Ala Phe Glu Leu Glu Pro Arg Pro Gly Ser Ala	
100 105 110	
gct gtg att gtt aag tta cct aat aaa aag tgg ctt gac ggt gca tgg	384
Ala Val Ile Val Lys Leu Pro Asn Lys Lys Trp Leu Asp Gly Ala Trp	
115 120 125	
atg gga cga aat aaa aga tcg aat cat ttt gct cga cca att aat att	432
Met Gly Arg Asn Lys Arg Ser Asn His Phe Ala Arg Pro Ile Asn Ile	
130 135 140	
tat gaa gta cat gct agt tca tgg aaa aga cat aca gat ggg tct ctg	480
Tyr Glu Val His Ala Ser Ser Trp Lys Arg His Thr Asp Gly Ser Leu	
145 150 155 160	
tat act ttg aag gat tta caa aag gaa tta att ccg tat gtt aaa gaa	528
Tyr Thr Leu Lys Asp Leu Gln Lys Glu Leu Ile Pro Tyr Val Lys Glu	
165 170 175	
caa gga ttt aat tat atc gaa ttt ttg cct tta aca gca cat cct tta	576
Gln Gly Phe Asn Tyr Ile Glu Phe Leu Pro Leu Thr Ala His Pro Leu	
180 185 190	
gat gct tca tgg gga tat caa aca att ggt tat tat gct ttg gag cgt	624
Asp Ala Ser Trp Gly Tyr Gln Thr Ile Gly Tyr Tyr Ala Leu Glu Arg	
195 200 205	

act tat ggt aca cca cga gag ctg caa gat ttt gtt gaa gca tgt cac	672
Thr Tyr Gly Thr Pro Arg Glu Leu Gln Asp Phe Val Glu Ala Cys His	
210 215 220	
aaa gaa aac atc ggt gtt ttg gct gat tgg gta cca gga cac ttt tgt	720
Lys Glu Asn Ile Gly Val Leu Ala Asp Trp Val Pro Gly His Phe Cys	
225 230 235 240	
att aat gat gat gcc ttg gct tat tat gat ggc aca cca tgt tat gaa	768
Ile Asn Asp Asp Ala Leu Ala Tyr Tyr Asp Gly Thr Pro Cys Tyr Glu	
245 250 255	
ttt agc gaa aaa tgg aga gcc gaa aat aaa ggc tgg gga gct cta aat	816
Phe Ser Glu Lys Trp Arg Ala Glu Asn Lys Gly Trp Gly Ala Leu Asn	
260 265 270	
ttt gat tta ggc aaa ccg gaa gtg caa tca ttt tta ctt tct agt gcc	864
Phe Asp Leu Gly Lys Pro Glu Val Gln Ser Phe Leu Leu Ser Ser Ala	
275 280 285	
cta ttt tgg cta gaa ttt tat cat ttg gat ggc ttg aga gtt gat gct	912
Leu Phe Trp Leu Glu Phe Tyr His Leu Asp Gly Leu Arg Val Asp Ala	
290 295 300	
gtt tct aac atg att tat cgc gat tat gac cgc agt gac ggt gaa tgg	960
Val Ser Asn Met Ile Tyr Arg Asp Tyr Asp Arg Ser Asp Gly Glu Trp	
305 310 315 320	
aaa aca gat aaa ttt ggt gga aat cgt aat tta gag ggg ata gaa ttc	1008
Lys Thr Asp Lys Phe Gly Gly Asn Arg Asn Leu Glu Gly Ile Glu Phe	
325 330 335	
cta caa aaa cta aat cga acc att aaa ggc aaa cat cca gaa tgt tta	1056
Leu Gln Lys Leu Asn Arg Thr Ile Lys Gly Lys His Pro Glu Cys Leu	
340 345 350	
atg att gcc gag gaa agt tct gct caa gta aag ata act ggt cga ata	1104
Met Ile Ala Glu Glu Ser Ser Ala Gln Val Lys Ile Thr Gly Arg Ile	
355 360 365	
gaa gat ggt ggg tta ggt ttt gat ttt aaa tgg aat atg ggt tgg atg	1152
Glu Asp Gly Gly Leu Gly Phe Asp Phe Lys Trp Asn Met Gly Trp Met	
370 375 380	
aac gat att tta cgt ttt tat gag atg gac cca tta ttt aga aaa ttt	1200
Asn Asp Ile Leu Arg Phe Tyr Glu Met Asp Pro Leu Phe Arg Lys Phe	
385 390 395 400	
aat ttt aat cta gct act ttt tca ttc atg tat cga atg agt gaa aac	1248
Asn Phe Asn Leu Ala Thr Phe Ser Phe Met Tyr Arg Met Ser Glu Asn	
405 410 415	
ttt att tta cct tta tca cat gac gag gtt gtt cat ggt aag cga agc	1296
Phe Ile Leu Pro Leu Ser His Asp Glu Val Val His Gly Lys Arg Ser	
420 425 430	
cta atg aat aaa atg ttt ggc gac cgt gat aag caa ttt gct caa tta	1344

Leu Met Asn Lys Met Phe Gly Asp Arg Asp Lys Gln Phe Ala Gln Leu
 435 440 445
 cgt aat tta ctt aca ttg caa atg acc tat cct ggt aaa aag ctt tta 1392
 Arg Asn Leu Leu Thr Leu Gln Met Thr Tyr Pro Gly Lys Lys Leu Leu
 450 455 460
 ttt atg gga agt gaa ttt gga caa tat ctt gaa tgg cga tat aac gat 1440
 Phe Met Gly Ser Glu Phe Gly Gln Tyr Leu Glu Trp Arg Tyr Asn Asp
 465 470 475 480
 ggc tta gat tgg gca gaa tta aag gat gaa ctg aat gct aaa atg aag 1488
 Gly Leu Asp Trp Ala Glu Leu Lys Asp Glu Leu Asn Ala Lys Met Lys
 485 490 495
 cat ttt gat caa gat tta aat agt ttt tat tta aat gag ccg gct ttg 1536
 His Phe Asp Gln Asp Leu Asn Ser Phe Tyr Leu Asn Glu Pro Ala Leu
 500 505 510
 tgg caa tta gaa caa aga gaa gat tct gtt caa att att gac gca gat 1584
 Trp Gln Leu Glu Gln Arg Glu Asp Ser Val Gln Ile Ile Asp Ala Asp
 515 520 525
 aat aaa gat gag tca gtc ttg tca ttt att cgt caa ggt aaa act aga 1632
 Asn Lys Asp Glu Ser Val Leu Ser Phe Ile Arg Gln Gly Lys Thr Arg
 530 535 540
 cat gac ttt tta ata gtt att ttg aat ttt aca cct gtt gat cga aaa 1680
 His Asp Phe Leu Ile Val Ile Leu Asn Phe Thr Pro Val Asp Arg Lys
 545 550 555 560
 aaa att aca att ggt gtt cca tat gct ggt aaa tat tgt gaa gtc ttt 1728
 Lys Ile Thr Ile Gly Val Pro Tyr Ala Gly Lys Tyr Cys Glu Val Phe
 565 570 575
 aat agt gcc aga aaa gaa tat ggt ggc agt tgg aac caa gaa aag cag 1776
 Asn Ser Ala Arg Lys Glu Tyr Gly Gly Ser Trp Asn Gln Glu Lys Gln
 580 585 590
 aat ttg aaa act caa aat aat tca ttt aag aat ttt aat tat caa gtg 1824
 Asn Leu Lys Thr Gln Asn Asn Ser Phe Lys Asn Phe Asn Tyr Gln Val
 595 600 605
 caa ttg gat ata ccg ggt ttt agt gct gtg att tta aaa cct gta gat 1872
 Gln Leu Asp Ile Pro Gly Phe Ser Ala Val Ile Leu Lys Pro Val Asp
 610 615 620
 gtt cat ata aaa aga aga att aat aga aaa aca aaa act aag 1914
 Val His Ile Lys Arg Arg Ile Asn Arg Lys Thr Lys Thr Lys
 625 630 635

<210> 272

<211> 638

<212> PRT

<213> Lactobacillus acidophilus

<400> 272

```

Met Val Thr Ile Val Glu Val Lys Gln His Ile Lys Lys Phe Ala Ala
 1          5          10          15
Gly Asn Glu Leu Tyr Leu Gln Glu Val Leu Gly Cys His Tyr Glu Asn
          20          25          30
Asp Ile Tyr Thr Phe Arg Val Trp Ala Pro Asn Ala Gln Lys Val Trp
          35          40          45
Leu Val Gly Asp Phe Asn Asp Trp Asp Lys Ser Leu Glu Met Ser Gln
          50          55          60
Thr Leu Asp Gly Val Trp Glu Ile Lys Thr Ser Leu Pro Lys Glu Gly
65          70          75          80
Gln Leu Tyr Lys Phe Leu Val Lys Gln Ala Asp Gly Arg Glu Val Met
          85          90          95
Lys Ile Asp Pro Met Ala Phe Glu Leu Glu Pro Arg Pro Gly Ser Ala
          100          105          110
Ala Val Ile Val Lys Leu Pro Asn Lys Lys Trp Leu Asp Gly Ala Trp
          115          120          125
Met Gly Arg Asn Lys Arg Ser Asn His Phe Ala Arg Pro Ile Asn Ile
          130          135          140
Tyr Glu Val His Ala Ser Ser Trp Lys Arg His Thr Asp Gly Ser Leu
          145          150          155          160
Tyr Thr Leu Lys Asp Leu Gln Lys Glu Leu Ile Pro Tyr Val Lys Glu
          165          170          175
Gln Gly Phe Asn Tyr Ile Glu Phe Leu Pro Leu Thr Ala His Pro Leu
          180          185          190
Asp Ala Ser Trp Gly Tyr Gln Thr Ile Gly Tyr Tyr Ala Leu Glu Arg
          195          200          205
Thr Tyr Gly Thr Pro Arg Glu Leu Gln Asp Phe Val Glu Ala Cys His
          210          215          220
Lys Glu Asn Ile Gly Val Leu Ala Asp Trp Val Pro Gly His Phe Cys
225          230          235          240
Ile Asn Asp Asp Ala Leu Ala Tyr Tyr Asp Gly Thr Pro Cys Tyr Glu
          245          250          255
Phe Ser Glu Lys Trp Arg Ala Glu Asn Lys Gly Trp Gly Ala Leu Asn
          260          265          270
Phe Asp Leu Gly Lys Pro Glu Val Gln Ser Phe Leu Leu Ser Ser Ala
          275          280          285
Leu Phe Trp Leu Glu Phe Tyr His Leu Asp Gly Leu Arg Val Asp Ala
          290          295          300
Val Ser Asn Met Ile Tyr Arg Asp Tyr Asp Arg Ser Asp Gly Glu Trp
305          310          315          320
Lys Thr Asp Lys Phe Gly Gly Asn Arg Asn Leu Glu Gly Ile Glu Phe
          325          330          335
Leu Gln Lys Leu Asn Arg Thr Ile Lys Gly Lys His Pro Glu Cys Leu
          340          345          350
Met Ile Ala Glu Glu Ser Ser Ala Gln Val Lys Ile Thr Gly Arg Ile
          355          360          365
Glu Asp Gly Gly Leu Gly Phe Asp Phe Lys Trp Asn Met Gly Trp Met
          370          375          380
Asn Asp Ile Leu Arg Phe Tyr Glu Met Asp Pro Leu Phe Arg Lys Phe
385          390          395          400
Asn Phe Asn Leu Ala Thr Phe Ser Phe Met Tyr Arg Met Ser Glu Asn
          405          410          415
Phe Ile Leu Pro Leu Ser His Asp Glu Val Val His Gly Lys Arg Ser
          420          425          430
Leu Met Asn Lys Met Phe Gly Asp Arg Asp Lys Gln Phe Ala Gln Leu

```

```

      435      440      445
Arg Asn Leu Leu Thr Leu Gln Met Thr Tyr Pro Gly Lys Lys Leu Leu
  450      455      460
Phe Met Gly Ser Glu Phe Gly Gln Tyr Leu Glu Trp Arg Tyr Asn Asp
  465      470      475      480
Gly Leu Asp Trp Ala Glu Leu Lys Asp Glu Leu Asn Ala Lys Met Lys
      485      490      495
His Phe Asp Gln Asp Leu Asn Ser Phe Tyr Leu Asn Glu Pro Ala Leu
      500      505      510
Trp Gln Leu Glu Gln Arg Glu Asp Ser Val Gln Ile Ile Asp Ala Asp
      515      520      525
Asn Lys Asp Glu Ser Val Leu Ser Phe Ile Arg Gln Gly Lys Thr Arg
      530      535      540
His Asp Phe Leu Ile Val Ile Leu Asn Phe Thr Pro Val Asp Arg Lys
  545      550      555      560
Lys Ile Thr Ile Gly Val Pro Tyr Ala Gly Lys Tyr Cys Glu Val Phe
      565      570      575
Asn Ser Ala Arg Lys Glu Tyr Gly Gly Ser Trp Asn Gln Glu Lys Gln
      580      585      590
Asn Leu Lys Thr Gln Asn Asn Ser Phe Lys Asn Phe Asn Tyr Gln Val
      595      600      605
Gln Leu Asp Ile Pro Gly Phe Ser Ala Val Ile Leu Lys Pro Val Asp
  610      615      620
Val His Ile Lys Arg Arg Ile Asn Arg Lys Thr Lys Thr Lys
  625      630      635

```

```

<210> 273
<211> 1719
<212> DNA
<213> Lactobacillus acidophilus

```

```

<220>
<221> misc_feature
<222> (0)...(0)
<223> ORF 1871 - neopullulanase

```

```

<220>
<221> CDS
<222> (1)...(1719)

```

```

<400> 273
atg caa tta gcc gct tta aga cac aga aca gaa agt gaa gat agt ttt 48
Met Gln Leu Ala Ala Leu Arg His Arg Thr Glu Ser Glu Asp Ser Phe
  1          5          10          15

gta gtt gat cca aaa cat gtt cgt gtt cgt ttt cac act gca aaa aat 96
Val Val Asp Pro Lys His Val Arg Val Arg Phe His Thr Ala Lys Asn
      20          25          30

gat gtt gaa aaa gta att gtt cat tac tgt gat aat tat tta cca tta 144
Asp Val Glu Lys Val Ile Val His Tyr Cys Asp Asn Tyr Leu Pro Leu
      35          40          45

aaa ttt gca gaa act act gaa atg gaa aag atc ggt gag ggt caa gtt 192
Lys Phe Ala Glu Thr Thr Glu Met Glu Lys Ile Gly Glu Gly Gln Val

```

50	55	60	
gaa gac tat tgg ggt att aca ctt gat gca cca tat cat cgt tta aag			240
Glu Asp Tyr Trp Gly Ile Thr Leu Asp Ala Pro Tyr His Arg Leu Lys			
65	70	75	80
tac act ttt gaa gtt att ggt aag gac ggt aca agt gta gtt tat ggt			288
Tyr Thr Phe Glu Val Ile Gly Lys Asp Gly Thr Ser Val Val Tyr Gly			
	85	90	95
gac cgt gcg att agc gat gat att aaa gac gca atc aat gaa gat gga			336
Asp Arg Ala Ile Ser Asp Asp Ile Lys Asp Ala Ile Asn Glu Asp Gly			
	100	105	110
tca tat ttt aaa att cca tat tgt cat gaa att gat atg gtc aaa aca			384
Ser Tyr Phe Lys Ile Pro Tyr Cys His Glu Ile Asp Met Val Lys Thr			
	115	120	125
cca gac tgg gtt aag aat acc gtt tgg tat cag ata ttc cct gaa cgt			432
Pro Asp Trp Val Lys Asn Thr Val Trp Tyr Gln Ile Phe Pro Glu Arg			
	130	135	140
tat gct aat ggg gat aaa tca aac gat cct aag aat att aag cca tgg			480
Tyr Ala Asn Gly Asp Lys Ser Asn Asp Pro Lys Asn Ile Lys Pro Trp			
	145	150	155
aat cca act gat cat cct ggt aga gag gat tat tat ggc ggt gat ttg			528
Asn Pro Thr Asp His Pro Gly Arg Glu Asp Tyr Tyr Gly Gly Asp Leu			
	165	170	175
caa ggt gtc tta gat cat tta gat tat tta caa aag cta ggc gtt aat			576
Gln Gly Val Leu Asp His Leu Asp Tyr Leu Gln Lys Leu Gly Val Asn			
	180	185	190
ggg tta tac ttt tgt cca att ttt aaa gcg agc tct aat cat aaa tat			624
Gly Leu Tyr Phe Cys Pro Ile Phe Lys Ala Ser Ser Asn His Lys Tyr			
	195	200	205
gac acg att gat tat tta caa gta gat ccg gaa ttt ggt gat aaa gat			672
Asp Thr Ile Asp Tyr Leu Gln Val Asp Pro Glu Phe Gly Asp Lys Asp			
	210	215	220
tta ttt gct aaa gtg gtt aac gaa gca cat gca cgt ggt atg aag att			720
Leu Phe Ala Lys Val Val Asn Glu Ala His Ala Arg Gly Met Lys Ile			
	225	230	235
atg ctc gat gcc gta ttt aat cac tta ggt gat caa tca atg caa tgg			768
Met Leu Asp Ala Val Phe Asn His Leu Gly Asp Gln Ser Met Gln Trp			
	245	250	255
caa gat gta gtg caa aat gga tct aag tca cgt ttt gca gat tgg ttc			816
Gln Asp Val Val Gln Asn Gly Ser Lys Ser Arg Phe Ala Asp Trp Phe			
	260	265	270
cat att aat gag tat cca gtt gaa cca tat cgt aat cca tta aaa ggc			864
His Ile Asn Glu Tyr Pro Val Glu Pro Tyr Arg Asn Pro Leu Lys Gly			
	275	280	285

gaa aag aat ccg caa tat gat act ttt gcc ttt gaa gaa cat atg cca	912
Glu Lys Asn Pro Gln Tyr Asp Thr Phe Ala Phe Glu Glu His Met Pro	
290 295 300	
aag ttg aat act gct aat cct gag gtt caa gat ttc ttg tta gaa att	960
Lys Leu Asn Thr Ala Asn Pro Glu Val Gln Asp Phe Leu Leu Glu Ile	
305 310 315 320	
gct aca tac tgg gtg aag tat ttt gat atc gat gca tgg cgt ctt gat	1008
Ala Thr Tyr Trp Val Lys Tyr Phe Asp Ile Asp Ala Trp Arg Leu Asp	
325 330 335	
gtg gca aat gaa gtt gat cat cac ttc tgg aag aag ttc cat aaa gca	1056
Val Ala Asn Glu Val Asp His His Phe Trp Lys Lys Phe His Lys Ala	
340 345 350	
gtc act gat att aag cca gac ttt tac att gta ggt gaa gtt tgg cat	1104
Val Thr Asp Ile Lys Pro Asp Phe Tyr Ile Val Gly Glu Val Trp His	
355 360 365	
tcg gct cgt cca tgg ctt aat ggc gat gaa ttt aca ggt gta atg aac	1152
Ser Ala Arg Pro Trp Leu Asn Gly Asp Glu Phe Thr Gly Val Met Asn	
370 375 380	
tat ccg tat act ttg caa att gaa gac cac ttt ttc aag cat aag tta	1200
Tyr Pro Tyr Thr Leu Gln Ile Glu Asp His Phe Phe Lys His Lys Leu	
385 390 395 400	
act gct gat caa atg act aca cgc ttg act gat caa ctt atg aaa tat	1248
Thr Ala Asp Gln Met Thr Thr Arg Leu Thr Asp Gln Leu Met Lys Tyr	
405 410 415	
cgt gat tct act aat gaa gca atg atg aat atg ctc gat tca cat gat	1296
Arg Asp Ser Thr Asn Glu Ala Met Met Asn Met Leu Asp Ser His Asp	
420 425 430	
act gcc aga att ttg aca gtt gca aaa ggt gat caa gac ttg gcg ctt	1344
Thr Ala Arg Ile Leu Thr Val Ala Lys Gly Asp Gln Asp Leu Ala Leu	
435 440 445	
caa gca tta act ttt gaa ttc atg caa aaa ggt agt cca tgt att tat	1392
Gln Ala Leu Thr Phe Glu Phe Met Gln Lys Gly Ser Pro Cys Ile Tyr	
450 455 460	
tac gga act gaa atg ggg atg gct gga gat aat gat cca gat tgt cgt	1440
Tyr Gly Thr Glu Met Gly Met Ala Gly Asp Asn Asp Pro Asp Cys Arg	
465 470 475 480	
aag cca atg gat tgg tca aaa gaa gat gga cct gta tgg caa agg gtt	1488
Lys Pro Met Asp Trp Ser Lys Glu Asp Gly Pro Val Trp Gln Arg Val	
485 490 495	
cat aag cta att aaa ttc cgt tta gct cat gat aaa acg ctc agt gaa	1536
His Lys Leu Ile Lys Phe Arg Leu Ala His Asp Lys Thr Leu Ser Glu	
500 505 510	

```

ggt aaa atc aag tta agc gta aca gaa aat agg cta att gaa gtt att 1584
Gly Lys Ile Lys Leu Ser Val Thr Glu Asn Arg Leu Ile Glu Val Ile
      515                      520                      525

aga gag ggc aaa gaa agt att cat gct tac ttt aat aca act aaa aat 1632
Arg Glu Gly Lys Glu Ser Ile His Ala Tyr Phe Asn Thr Thr Lys Asn
      530                      535                      540

gat gta aaa ctt gat ggt aaa gct gaa tta agt caa gat ttt gaa aaa 1680
Asp Val Lys Leu Asp Gly Lys Ala Glu Leu Ser Gln Asp Phe Glu Lys
545                      550                      555                      560

gga ata ctc gct cca aaa ggc ttt gta atc atg gtt gat 1719
Gly Ile Leu Ala Pro Lys Gly Phe Val Ile Met Val Asp
      565                      570

```

<210> 274

<211> 573

<212> PRT

<213> Lactobacillus acidophilus

<400> 274

```

Met Gln Leu Ala Ala Leu Arg His Arg Thr Glu Ser Glu Asp Ser Phe
 1                      5                      10                      15
Val Val Asp Pro Lys His Val Arg Val Arg Phe His Thr Ala Lys Asn
      20                      25                      30
Asp Val Glu Lys Val Ile Val His Tyr Cys Asp Asn Tyr Leu Pro Leu
      35                      40                      45
Lys Phe Ala Glu Thr Thr Glu Met Glu Lys Ile Gly Glu Gly Gln Val
      50                      55                      60
Glu Asp Tyr Trp Gly Ile Thr Leu Asp Ala Pro Tyr His Arg Leu Lys
65                      70                      75                      80
Tyr Thr Phe Glu Val Ile Gly Lys Asp Gly Thr Ser Val Val Tyr Gly
      85                      90                      95
Asp Arg Ala Ile Ser Asp Asp Ile Lys Asp Ala Ile Asn Glu Asp Gly
      100                      105                      110
Ser Tyr Phe Lys Ile Pro Tyr Cys His Glu Ile Asp Met Val Lys Thr
      115                      120                      125
Pro Asp Trp Val Lys Asn Thr Val Trp Tyr Gln Ile Phe Pro Glu Arg
      130                      135                      140
Tyr Ala Asn Gly Asp Lys Ser Asn Asp Pro Lys Asn Ile Lys Pro Trp
145                      150                      155                      160
Asn Pro Thr Asp His Pro Gly Arg Glu Asp Tyr Tyr Gly Gly Asp Leu
      165                      170                      175
Gln Gly Val Leu Asp His Leu Asp Tyr Leu Gln Lys Leu Gly Val Asn
      180                      185                      190
Gly Leu Tyr Phe Cys Pro Ile Phe Lys Ala Ser Ser Asn His Lys Tyr
      195                      200                      205
Asp Thr Ile Asp Tyr Leu Gln Val Asp Pro Glu Phe Gly Asp Lys Asp
      210                      215                      220
Leu Phe Ala Lys Val Val Asn Glu Ala His Ala Arg Gly Met Lys Ile
225                      230                      235                      240
Met Leu Asp Ala Val Phe Asn His Leu Gly Asp Gln Ser Met Gln Trp
      245                      250                      255
Gln Asp Val Val Gln Asn Gly Ser Lys Ser Arg Phe Ala Asp Trp Phe
      260                      265                      270

```

```

His Ile Asn Glu Tyr Pro Val Glu Pro Tyr Arg Asn Pro Leu Lys Gly
      275                      280                      285
Glu Lys Asn Pro Gln Tyr Asp Thr Phe Ala Phe Glu Glu His Met Pro
      290                      295                      300
Lys Leu Asn Thr Ala Asn Pro Glu Val Gln Asp Phe Leu Leu Glu Ile
      305                      310                      315                      320
Ala Thr Tyr Trp Val Lys Tyr Phe Asp Ile Asp Ala Trp Arg Leu Asp
      325                      330                      335
Val Ala Asn Glu Val Asp His His Phe Trp Lys Lys Phe His Lys Ala
      340                      345                      350
Val Thr Asp Ile Lys Pro Asp Phe Tyr Ile Val Gly Glu Val Trp His
      355                      360                      365
Ser Ala Arg Pro Trp Leu Asn Gly Asp Glu Phe Thr Gly Val Met Asn
      370                      375                      380
Tyr Pro Tyr Thr Leu Gln Ile Glu Asp His Phe Phe Lys His Lys Leu
      385                      390                      395                      400
Thr Ala Asp Gln Met Thr Thr Arg Leu Thr Asp Gln Leu Met Lys Tyr
      405                      410                      415
Arg Asp Ser Thr Asn Glu Ala Met Met Asn Met Leu Asp Ser His Asp
      420                      425                      430
Thr Ala Arg Ile Leu Thr Val Ala Lys Gly Asp Gln Asp Leu Ala Leu
      435                      440                      445
Gln Ala Leu Thr Phe Glu Phe Met Gln Lys Gly Ser Pro Cys Ile Tyr
      450                      455                      460
Tyr Gly Thr Glu Met Gly Met Ala Gly Asp Asn Asp Pro Asp Cys Arg
      465                      470                      475                      480
Lys Pro Met Asp Trp Ser Lys Glu Asp Gly Pro Val Trp Gln Arg Val
      485                      490                      495
His Lys Leu Ile Lys Phe Arg Leu Ala His Asp Lys Thr Leu Ser Glu
      500                      505                      510
Gly Lys Ile Lys Leu Ser Val Thr Glu Asn Arg Leu Ile Glu Val Ile
      515                      520                      525
Arg Glu Gly Lys Glu Ser Ile His Ala Tyr Phe Asn Thr Thr Lys Asn
      530                      535                      540
Asp Val Lys Leu Asp Gly Lys Ala Glu Leu Ser Gln Asp Phe Glu Lys
      545                      550                      555                      560
Gly Ile Leu Ala Pro Lys Gly Phe Val Ile Met Val Asp
      565                      570

```

<210> 275

<211> 3555

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1710 - pullulanase

<220>

<221> CDS

<222> (1)...(3555)

<400> 275

atg aaa aaa tat aat aaa tgg gga aca aaa ggt gtt ttt att tgt gct 48

Met	Lys	Lys	Tyr	Asn	Lys	Trp	Gly	Thr	Lys	Gly	Val	Phe	Ile	Cys	Ala		
1				5					10					15			
tca	gca	ctt	tta	agt	gtt	tgg	cta	gga	gca	aca	tgg	act	gat	ggc	aat	96	
Ser	Ala	Leu	Leu	Ser	Val	Trp	Leu	Gly	Ala	Thr	Trp	Thr	Asp	Gly	Asn		
			20					25					30				
gtg	caa	gca	gca	gaa	aca	cca	gat	gct	gga	aat	caa	gca	tct	act	gaa	144	
Val	Gln	Ala	Ala	Glu	Thr	Pro	Asp	Ala	Gly	Asn	Gln	Ala	Ser	Thr	Glu		
		35					40					45					
gtg	agt	cag	aga	gtt	atc	act	gaa	aat	gag	aaa	aag	act	gtt	gta	cag	192	
Val	Ser	Gln	Arg	Val	Ile	Thr	Glu	Asn	Glu	Lys	Lys	Thr	Val	Val	Gln		
	50					55					60						
cca	gct	aag	gat	act	caa	act	gat	gag	aag	gat	aca	gat	aat	act	caa	240	
Pro	Ala	Lys	Asp	Thr			Asp	Glu	Lys	Asp	Thr	Asp	Asn	Thr	Gln		
65					70					75					80		
tta	gct	agt	gca	act	cca	tcg	gaa	gaa	act	act	caa	gtt	gaa	gaa	gct	288	
Leu	Ala	Ser	Ala	Thr	Pro	Ser	Glu	Glu	Thr	Thr	Gln	Val	Glu	Glu	Ala		
				85					90					95			
aag	caa	caa	gca	tta	aaa	gat	acg	act	aaa	gtt	gta	gtc	cat	tat	cag	336	
Lys	Gln	Gln	Ala	Leu	Lys	Asp	Thr	Thr	Lys	Val	Val	Val	His	Tyr	Gln		
			100					105					110				
ggg	gat	ggg	tct	aag	tgg	gtt	ccg	tat	att	tgg	ggg	aaa	aaa	cca	aat	384	
Gly	Asp	Gly	Ser	Lys	Trp	Val	Pro	Tyr	Ile	Trp	Gly	Lys	Lys	Pro	Asn		
		115					120					125					
ggc	aat	ggg	aat	caa	tac	aag	tgg	gat	ggg	aaa	gat	gac	tat	ggc	tac	432	
Gly	Asn	Gly	Asn	Gln	Tyr	Lys	Trp	Asp	Gly	Lys	Asp	Asp	Tyr	Gly	Tyr		
	130					135					140						
tat	tcc	aac	att	aca	gtt	gat	ggg	aat	gaa	caa	gaa	atg	ggg	gtt	tta	480	
Tyr	Ser	Asn	Ile	Thr	Val	Asp	Gly	Asn	Glu	Gln	Glu	Met	Gly	Val	Leu		
145					150					155					160		
att	aag	ggc	aaa	gat	tct	tgg	gat	aaa	gat	ggg	caa	gga	aac	gac	aga	528	
Ile	Lys	Gly	Lys	Asp	Ser	Trp	Asp	Lys	Asp	Gly	Gln	Gly	Asn	Asp	Arg		
				165					170					175			
atc	gta	aaa	gtt	ggg	gat	aat	ggg	aaa	gct	gaa	gtt	tgg	tat	aaa	gaa	576	
Ile	Val	Lys	Val	Gly	Asp	Asn	Gly	Lys	Ala	Glu	Val	Trp	Tyr	Lys	Glu		
			180					185					190				
ggg	agc	gat	gaa	gca	caa	gat	gta	aag	cca	aca	tat	gat	tcg	gct	aaa	624	
Gly	Ser	Asp	Glu	Ala	Gln	Asp	Val	Lys	Pro	Thr	Tyr	Asp	Ser	Ala	Lys		
		195					200					205					
gtt	aat	att	cat	tat	cag	ggg	aat	gat	gac	gta	aca	tct	att	agt	tat	672	
Val	Asn	Ile	His	Tyr	Gln	Gly	Asn	Asp	Asp	Val	Thr	Ser	Ile	Ser	Tyr		
	210					215					220						
tgg	act	aat	aca	gat	cct	caa	aat	aag	aaa	att	atc	gat	tta	tcg	aaa	720	
Trp	Thr	Asn	Thr	Asp	Pro	Gln	Asn	Lys	Lys	Ile	Ile	Asp	Leu	Ser	Lys		

225	230	235	240	
tct gac gtt caa gaa aaa gag gga tgc ttc gat tta tca aat act aaa				768
Ser Asp Val Gln Glu Lys Glu Gly Ser Phe Asp Leu Ser Asn Thr Lys	245	250	255	
ttc aat agt atc ttt gta gca cct att ggt act gat aca gaa gta aga				816
Phe Asn Ser Ile Phe Val Ala Pro Ile Gly Thr Asp Thr Glu Val Arg	260	265	270	
gaa ttt act cca cta cct ggt aaa agt gct aca gat att tac cta gtg				864
Glu Phe Thr Pro Leu Pro Gly Lys Ser Ala Thr Asp Ile Tyr Leu Val	275	280	285	
act aaa gat cca act gtt tat tat act aag agt ttt gct tta gct act				912
Thr Lys Asp Pro Thr Val Tyr Tyr Thr Lys Ser Phe Ala Leu Ala Thr	290	295	300	
caa agc tta act tca gcc tca atg gat tca ggc aag act gtt aat att				960
Gln Ser Leu Thr Ser Ala Ser Met Asp Ser Gly Lys Thr Val Asn Ile	305	310	315	320
caa act ggt aag gaa atg aca gct gct gaa gca aaa aag aac ctt tca				1008
Gln Thr Gly Lys Glu Met Thr Ala Ala Glu Ala Lys Lys Asn Leu Ser	325	330	335	
ata aag gat aat tct att gtg aat gta gtt gca gtt aat cca gat caa				1056
Ile Lys Asp Asn Ser Ile Val Asn Val Val Ala Val Asn Pro Asp Gln	340	345	350	
gat ggt aag agt aag caa ttc aca att acc aca gca caa gat ttg agt				1104
Asp Gly Lys Ser Lys Gln Phe Thr Ile Thr Thr Ala Gln Asp Leu Ser	355	360	365	
att tta gat aat aat caa att ggt att tat ggt aac tac aag tct att				1152
Ile Leu Asp Asn Asn Gln Ile Gly Ile Tyr Gly Asn Tyr Lys Ser Ile	370	375	380	
gat att ggt agt tat gta aga tcc aaa gac ttt gat acg aaa tat tac				1200
Asp Ile Gly Ser Tyr Val Arg Ser Lys Asp Phe Asp Thr Lys Tyr Tyr	385	390	395	400
tat aat ggt gat gat tta ggt gct act tac act gaa aag caa agt caa				1248
Tyr Asn Gly Asp Asp Leu Gly Ala Thr Tyr Thr Glu Lys Gln Ser Gln	405	410	415	
att aag tta tgg gca cca acc gct aag aaa gtt gtt tta aat ctt tat				1296
Ile Lys Leu Trp Ala Pro Thr Ala Lys Lys Val Val Leu Asn Leu Tyr	420	425	430	
gat tca cta aac aac gat gct tca gct aca aag act ttt gta atg aac				1344
Asp Ser Leu Asn Asn Asp Ala Ser Ala Thr Lys Thr Phe Val Met Asn	435	440	445	
aga gga gac aaa ggt gtg tgg tca gtt att ctt cca ggt gat tac aag				1392
Arg Gly Asp Lys Gly Val Trp Ser Val Ile Leu Pro Gly Asp Tyr Lys	450	455	460	

aac tgg gca tac gat tat agt tta tcc ttc ggt aac ggc aca act acc	1440
Asn Trp Ala Tyr Asp Tyr Ser Leu Ser Phe Gly Asn Gly Thr Thr Thr	
465 470 475 480	
caa acc aac gat cca tat tct aaa gcc gtg act att aac ggt gat cgt	1488
Gln Thr Asn Asp Pro Tyr Ser Lys Ala Val Thr Ile Asn Gly Asp Arg	
485 490 495	
tct gtt att gaa gac gtt gat gca att aaa cca aat gat ttc tca aga	1536
Ser Val Ile Glu Asp Val Asp Ala Ile Lys Pro Asn Asp Phe Ser Arg	
500 505 510	
ttg cca caa ttt tct gca cca act aat gca att atc tat gaa acc agc	1584
Leu Pro Gln Phe Ser Ala Pro Thr Asn Ala Ile Ile Tyr Glu Thr Ser	
515 520 525	
att aga gac ttc act agt gac aag aat tct gga atc aaa gat aaa ggc	1632
Ile Arg Asp Phe Thr Ser Asp Lys Asn Ser Gly Ile Lys Asp Lys Gly	
530 535 540	
aag tat ttg ggc atg att gaa tct ggc gta act cca gat ggt caa att	1680
Lys Tyr Leu Gly Met Ile Glu Ser Gly Val Thr Pro Asp Gly Gln Ile	
545 550 555 560	
acg ggc ttg gat tac ttg aag tca tta ggc gta acc cat gta caa att	1728
Thr Gly Leu Asp Tyr Leu Lys Ser Leu Gly Val Thr His Val Gln Ile	
565 570 575	
atg cca atg ttt gac ttt gca agt att aat gaa agt aag gca gat gat	1776
Met Pro Met Phe Asp Phe Ala Ser Ile Asn Glu Ser Lys Ala Asp Asp	
580 585 590	
agc tat aat tgg ggt tat gat cct aag aat tat aat gtt cct gag ggt	1824
Ser Tyr Asn Trp Gly Tyr Asp Pro Lys Asn Tyr Asn Val Pro Glu Gly	
595 600 605	
agc tat tca agc aat gca gct gat cct act acc aga att atg gaa atg	1872
Ser Tyr Ser Ser Asn Ala Ala Asp Pro Thr Thr Arg Ile Met Glu Met	
610 615 620	
aag gaa atg atc aat ggc ctt cat aaa gcc ggc att aga gta gtg atg	1920
Lys Glu Met Ile Asn Gly Leu His Lys Ala Gly Ile Arg Val Val Met	
625 630 635 640	
gac gta gtt tat aac cac gtt tac aat acg gac gag caa tca ttg aat	1968
Asp Val Val Tyr Asn His Val Tyr Asn Thr Asp Glu Gln Ser Leu Asn	
645 650 655	
aag act gtt cca gga tat tat ttc caa tat gat tct gaa ggt cat aca	2016
Lys Thr Val Pro Gly Tyr Tyr Phe Gln Tyr Asp Ser Glu Gly His Thr	
660 665 670	
act aac ggt act ggt tgt ggt aat gat atg gct agt gaa cgc ttg atg	2064
Thr Asn Gly Thr Gly Cys Gly Asn Asp Met Ala Ser Glu Arg Leu Met	
675 680 685	

gca cgt aag tat att gtt gat tct gtt aaa tac tgg gct aaa aac tac	2112
Ala Arg Lys Tyr Ile Val Asp Ser Val Lys Tyr Trp Ala Lys Asn Tyr	
690 695 700	
aat atc gat ggc ttt aga ttc gat tta atg ggt att cta gat gtt gat	2160
Asn Ile Asp Gly Phe Arg Phe Asp Leu Met Gly Ile Leu Asp Val Asp	
705 710 715 720	
acg atg aat gaa gtt aga tct gaa ctt aat aag att gat ccg agc atc	2208
Thr Met Asn Glu Val Arg Ser Glu Leu Asn Lys Ile Asp Pro Ser Ile	
725 730 735	
tta gtt tat ggt gaa ggc tgg gat atg aga aag acc gat cat gat att	2256
Leu Val Tyr Gly Glu Gly Trp Asp Met Arg Lys Thr Asp His Asp Ile	
740 745 750	
ggg gca ggt cag tat aat gcc gac aag gtt gat aaa tca att ggc ttc	2304
Gly Ala Gly Gln Tyr Asn Ala Asp Lys Val Asp Lys Ser Ile Gly Phe	
755 760 765	
ttc tca gat gat att cgt aac gca atc aaa ggt gcc gaa ttt ggt gga	2352
Phe Ser Asp Asp Ile Arg Asn Ala Ile Lys Gly Ala Glu Phe Gly Gly	
770 775 780	
gta act cca ggt ttg gtt gaa gga aac ggt aaa gaa gag aac tat aag	2400
Val Thr Pro Gly Leu Val Glu Gly Asn Gly Lys Glu Glu Asn Tyr Lys	
785 790 795 800	
gaa gat gct aag aag ttt ata gat ggt ttc tta ggc ggt cag aat tat	2448
Glu Asp Ala Lys Lys Phe Ile Asp Gly Phe Leu Gly Gly Gln Asn Tyr	
805 810 815	
ggc aag gat gct aag cac cca tat caa gca cca gaa caa aca att aat	2496
Gly Lys Asp Ala Lys His Pro Tyr Gln Ala Pro Glu Gln Thr Ile Asn	
820 825 830	
tat gta gct tgc cat gat aac cgt aca ttg tac gat atg ttg aag act	2544
Tyr Val Ala Cys His Asp Asn Arg Thr Leu Tyr Asp Met Leu Lys Thr	
835 840 845	
tta atg cct gat gaa tct gaa gct aat att atc aag cgt gat aaa tta	2592
Leu Met Pro Asp Glu Ser Glu Ala Asn Ile Ile Lys Arg Asp Lys Leu	
850 855 860	
gct aca tca atg atg atg cta tct caa ggt att ccg ttt atc cat gcg	2640
Ala Thr Ser Met Met Met Leu Ser Gln Gly Ile Pro Phe Ile His Ala	
865 870 875 880	
gga caa gaa agt ctt ggt act aaa gat ggt aat gaa aat agt tac aat	2688
Gly Gln Glu Ser Leu Gly Thr Lys Asp Gly Asn Glu Asn Ser Tyr Asn	
885 890 895	
gct tcc gta gaa gta aat gag att aac tgg ggc cgg gta aaa gaa aac	2736
Ala Ser Val Glu Val Asn Glu Ile Asn Trp Gly Arg Val Lys Glu Asn	
900 905 910	
aaa gat atg gtt gac tac ttt aag aag tta gta aac ctt cgt aag agt	2784

Lys	Asp	Met	Val	Asp	Tyr	Phe	Lys	Lys	Leu	Val	Asn	Leu	Arg	Lys	Ser		
		915					920					925					
caa	tca	gta	ttt	aga	caa	aat	gat	tac	agt	caa	atc	aat	aag	aat	gta	2832	
Gln	Ser	Val	Phe	Arg	Gln	Asn	Asp	Tyr	Ser	Gln	Ile	Asn	Lys	Asn	Val		
		930				935					940						
aaa	gtt	ctt	aat	gac	ggg	caa	aat	ggg	gta	ttt	gca	ttt	gaa	tat	aat	2880	
Lys	Val	Leu	Asn	Asp	Gly	Gln	Asn	Gly	Val	Phe	Ala	Phe	Glu	Tyr	Asn		
		945			950					955					960		
act	aat	ggg	aag	aaa	cta	tat	gta	gca	ttt	aat	gtt	aat	gat	aaa	gat	2928	
Thr	Asn	Gly	Lys	Lys	Leu	Tyr	Val	Ala	Phe	Asn	Val	Asn	Asp	Lys	Asp		
				965					970					975			
gct	aaa	ttg	gaa	aac	gtt	gat	tta	tcg	gta	gct	act	aag	tta	ctg	gat	2976	
Ala	Lys	Leu	Glu	Asn	Val	Asp	Leu	Ser	Val	Ala	Thr	Lys	Leu	Leu	Asp		
			980					985					990				
agt	gat	ggg	aat	act	cag	att	ggc	aaa	gaa	agt	gtt	ttg	aaa	cca	ttg	3024	
Ser	Asp	Gly	Asn	Thr	Gln	Ile	Gly	Lys	Glu	Ser	Val	Leu	Lys	Pro	Leu		
		995					1000					1005					
agt	aca	tta	gtt	gct	gaa	gtt	tca	act	aaa	gaa	gcg	aag	cca	gat	gat	3072	
Ser	Thr	Leu	Val	Ala	Glu	Val	Ser	Thr	Lys	Glu	Ala	Lys	Pro	Asp	Asp		
		1010				1015					1020						
agt	tca	agc	ata	atc	aat	ccg	cca	gta	aac	acc	aat	att	gga	gat	aat	3120	
Ser	Ser	Ser	Ile	Ile	Asn	Pro	Pro	Val	Asn	Thr	Asn	Ile	Gly	Asp	Asn		
					1030					1035					1040		
aat	aca	gat	act	tta	ttg	tct	act	gtt	gat	att	gtt	ctt	act	cat	aat	3168	
Asn	Thr	Asp	Thr	Leu	Leu	Ser	Thr	Val	Asp	Ile	Val	Leu	Thr	His	Asn		
				1045					1050					1055			
gct	tat	att	tat	gaa	aat	gat	ggg	att	aca	acg	gtt	aaa	gct	aat	gat	3216	
Ala	Tyr	Ile	Tyr	Glu	Asn	Asp	Gly	Ile	Thr	Thr	Val	Lys	Ala	Asn	Asp		
			1060					1065					1070				
ggg	aag	aac	gtg	aca	tta	aag	gta	gga	caa	aca	att	cat	gca	ctt	aat	3264	
Gly	Lys	Asn	Val	Thr	Leu	Lys	Val	Gly	Gln	Thr	Ile	His	Ala	Leu	Asn		
		1075				1080						1085					
aag	gca	caa	ata	gta	att	ctt	aat	aat	aaa	gaa	ttc	tat	caa	att	ggc	3312	
Lys	Ala	Gln	Ile	Val	Ile	Leu	Asn	Asn	Lys	Glu	Phe	Tyr	Gln	Ile	Gly		
		1090				1095					1100						
gat	aac	caa	tat	gtt	aaa	gta	aac	aat	act	ttg	aat	tgg	aat	ata	ttg	3360	
Asp	Asn	Gln	Tyr	Val	Lys	Val	Asn	Asn	Thr	Leu	Asn	Trp	Asn	Ile	Leu		
				1105		1110				1115					1120		
aag	cat	aat	tca	ttt	gta	tac	tct	aag	agt	ggg	aaa	gcc	tta	aag	aaa	3408	
Lys	His	Asn	Ser	Phe	Val	Tyr	Ser	Lys	Ser	Gly	Lys	Ala	Leu	Lys	Lys		
				1125				1130						1135			
aat	cac	aag	cgg	att	ttg	ctc	aag	aaa	ggg	cac	aaa	gtt	ttg	ctt	ttg	3456	
Asn	His	Lys	Arg	Ile	Leu	Leu	Lys	Lys	Gly	His	Lys	Val	Leu	Leu	Leu		

1140	1145	1150	
gat aat gct tgt ttg act aag att cat ggt aag caa ttc tac aga att			3504
Asp Asn Ala Cys Leu Thr Lys Ile His Gly Lys Gln Phe Tyr Arg Ile			
1155	1160	1165	
gga aat aat aaa tat gta aaa gca gtg aat gtt gtt att gaa gta aaa			3552
Gly Asn Asn Lys Tyr Val Lys Ala Val Asn Val Val Ile Glu Val Lys			
1170	1175	1180	
gct			3555
Ala			
1185			

<210> 276

<211> 1185

<212> PRT

<213> Lactobacillus acidophilus

<400> 276

Met Lys Lys Tyr Asn Lys Trp Gly Thr Lys Gly Val Phe Ile Cys Ala		
1 5 10 15		
Ser Ala Leu Leu Ser Val Trp Leu Gly Ala Thr Trp Thr Asp Gly Asn		
20 25 30		
Val Gln Ala Ala Glu Thr Pro Asp Ala Gly Asn Gln Ala Ser Thr Glu		
35 40 45		
Val Ser Gln Arg Val Ile Thr Glu Asn Glu Lys Lys Thr Val Val Gln		
50 55 60		
Pro Ala Lys Asp Thr Gln Thr Asp Glu Lys Asp Thr Asp Asn Thr Gln		
65 70 75 80		
Leu Ala Ser Ala Thr Pro Ser Glu Glu Thr Thr Gln Val Glu Glu Ala		
85 90 95		
Lys Gln Gln Ala Leu Lys Asp Thr Thr Lys Val Val Val His Tyr Gln		
100 105 110		
Gly Asp Gly Ser Lys Trp Val Pro Tyr Ile Trp Gly Lys Lys Pro Asn		
115 120 125		
Gly Asn Gly Asn Gln Tyr Lys Trp Asp Gly Lys Asp Asp Tyr Gly Tyr		
130 135 140		
Tyr Ser Asn Ile Thr Val Asp Gly Asn Glu Gln Glu Met Gly Val Leu		
145 150 155 160		
Ile Lys Gly Lys Asp Ser Trp Asp Lys Asp Gly Gln Gly Asn Asp Arg		
165 170 175		
Ile Val Lys Val Gly Asp Asn Gly Lys Ala Glu Val Trp Tyr Lys Glu		
180 185 190		
Gly Ser Asp Glu Ala Gln Asp Val Lys Pro Thr Tyr Asp Ser Ala Lys		
195 200 205		
Val Asn Ile His Tyr Gln Gly Asn Asp Asp Val Thr Ser Ile Ser Tyr		
210 215 220		
Trp Thr Asn Thr Asp Pro Gln Asn Lys Lys Ile Ile Asp Leu Ser Lys		
225 230 235 240		
Ser Asp Val Gln Glu Lys Glu Gly Ser Phe Asp Leu Ser Asn Thr Lys		
245 250 255		
Phe Asn Ser Ile Phe Val Ala Pro Ile Gly Thr Asp Thr Glu Val Arg		
260 265 270		
Glu Phe Thr Pro Leu Pro Gly Lys Ser Ala Thr Asp Ile Tyr Leu Val		
275 280 285		

```

Thr Lys Asp Pro Thr Val Tyr Tyr Thr Lys Ser Phe Ala Leu Ala Thr
290                295                300
Gln Ser Leu Thr Ser Ala Ser Met Asp Ser Gly Lys Thr Val Asn Ile
305                310                315                320
Gln Thr Gly Lys Glu Met Thr Ala Ala Glu Ala Lys Lys Asn Leu Ser
325                330                335
Ile Lys Asp Asn Ser Ile Val Asn Val Val Ala Val Asn Pro Asp Gln
340                345                350
Asp Gly Lys Ser Lys Gln Phe Thr Ile Thr Thr Ala Gln Asp Leu Ser
355                360                365
Ile Leu Asp Asn Asn Gln Ile Gly Ile Tyr Gly Asn Tyr Lys Ser Ile
370                375                380
Asp Ile Gly Ser Tyr Val Arg Ser Lys Asp Phe Asp Thr Lys Tyr Tyr
385                390                395                400
Tyr Asn Gly Asp Asp Leu Gly Ala Thr Tyr Thr Glu Lys Gln Ser Gln
405                410                415
Ile Lys Leu Trp Ala Pro Thr Ala Lys Lys Val Val Leu Asn Leu Tyr
420                425                430
Asp Ser Leu Asn Asn Asp Ala Ser Ala Thr Lys Thr Phe Val Met Asn
435                440                445
Arg Gly Asp Lys Gly Val Trp Ser Val Ile Leu Pro Gly Asp Tyr Lys
450                455                460
Asn Trp Ala Tyr Asp Tyr Ser Leu Ser Phe Gly Asn Gly Thr Thr Thr
465                470                475                480
Gln Thr Asn Asp Pro Tyr Ser Lys Ala Val Thr Ile Asn Gly Asp Arg
485                490                495
Ser Val Ile Glu Asp Val Asp Ala Ile Lys Pro Asn Asp Phe Ser Arg
500                505                510
Leu Pro Gln Phe Ser Ala Pro Thr Asn Ala Ile Ile Tyr Glu Thr Ser
515                520                525
Ile Arg Asp Phe Thr Ser Asp Lys Asn Ser Gly Ile Lys Asp Lys Gly
530                535                540
Lys Tyr Leu Gly Met Ile Glu Ser Gly Val Thr Pro Asp Gly Gln Ile
545                550                555                560
Thr Gly Leu Asp Tyr Leu Lys Ser Leu Gly Val Thr His Val Gln Ile
565                570                575
Met Pro Met Phe Asp Phe Ala Ser Ile Asn Glu Ser Lys Ala Asp Asp
580                585                590
Ser Tyr Asn Trp Gly Tyr Asp Pro Lys Asn Tyr Asn Val Pro Glu Gly
595                600                605
Ser Tyr Ser Ser Asn Ala Ala Asp Pro Thr Thr Arg Ile Met Glu Met
610                615                620
Lys Glu Met Ile Asn Gly Leu His Lys Ala Gly Ile Arg Val Val Met
625                630                635                640
Asp Val Val Tyr Asn His Val Tyr Asn Thr Asp Glu Gln Ser Leu Asn
645                650                655
Lys Thr Val Pro Gly Tyr Tyr Phe Gln Tyr Asp Ser Glu Gly His Thr
660                665                670
Thr Asn Gly Thr Gly Cys Gly Asn Asp Met Ala Ser Glu Arg Leu Met
675                680                685
Ala Arg Lys Tyr Ile Val Asp Ser Val Lys Tyr Trp Ala Lys Asn Tyr
690                695                700
Asn Ile Asp Gly Phe Arg Phe Asp Leu Met Gly Ile Leu Asp Val Asp
705                710                715                720
Thr Met Asn Glu Val Arg Ser Glu Leu Asn Lys Ile Asp Pro Ser Ile
725                730                735
Leu Val Tyr Gly Glu Gly Trp Asp Met Arg Lys Thr Asp His Asp Ile

```

- 509 -

<210> 277
 <211> 1767
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 686 - amylopullulanase

<220>
 <221> CDS
 <222> (1)...(1767)

<400> 277
 atg aaa ata act tat gat tct tgg caa gag cag tat aaa aac cct ttt 48
 Met Lys Ile Thr Tyr Asp Ser Trp Gln Glu Gln Tyr Lys Asn Pro Phe
 1 5 10 15
 ggt gct gtt aaa gct ggt aat aca gtt aaa tgg tca atc aaa ata gat 96
 Gly Ala Val Lys Ala Gly Asn Thr Val Lys Trp Ser Ile Lys Ile Asp
 20 25 30
 caa gta ata caa gga gct gtc ttg tgg ttg act aaa agt cga gaa aca 144
 Gln Val Ile Gln Gly Ala Val Leu Trp Leu Thr Lys Ser Arg Glu Thr
 35 40 45
 cca gtg gct tat ccg atg aac tat gat gaa cag act aaa atg tat acc 192
 Pro Val Ala Tyr Pro Met Asn Tyr Asp Glu Gln Thr Lys Met Tyr Thr
 50 55 60
 aca cag gta aaa att ggt aca tct ggt tta tac aat tac tac ttt gct 240
 Thr Gln Val Lys Ile Gly Thr Ser Gly Leu Tyr Asn Tyr Tyr Phe Ala
 65 70 75 80
 ttg caa caa aat aat caa ata gtt tat ata gat caa gga ctt ttt ggt 288
 Leu Gln Gln Asn Asn Gln Ile Val Tyr Ile Asp Gln Gly Leu Phe Gly
 85 90 95
 aaa gga cac gta act aaa agt gat cat gat tta aga cag ttt caa tta 336
 Lys Gly His Val Thr Lys Ser Asp His Asp Leu Arg Gln Phe Gln Leu
 100 105 110
 act tgt tat gat att gca act cca cga atc gat tgg tat caa aag ggc 384
 Thr Cys Tyr Asp Ile Ala Thr Pro Arg Ile Asp Trp Tyr Gln Lys Gly
 115 120 125
 att gtt tat caa att ttt ccg gat cgc ttt gct aat gga aat cca tat 432
 Ile Val Tyr Gln Ile Phe Pro Asp Arg Phe Ala Asn Gly Asn Pro Tyr
 130 135 140
 gaa gaa gtt ata ggt aaa aaa agg aat agt ttt atc tat gct act aaa 480
 Glu Glu Val Ile Gly Lys Lys Arg Asn Ser Phe Ile Tyr Ala Thr Lys
 145 150 155 160

gaa gat att cca tat tat ata aaa aat agt gaa ggt gct ata gtg cgg	528
Glu Asp Ile Pro Tyr Tyr Ile Lys Asn Ser Glu Gly Ala Ile Val Arg	
165 170 175	
tgg gac ttt ttt ggc ggt aat tta act gga att aga aaa aag atc cct	576
Trp Asp Phe Phe Gly Gly Asn Leu Thr Gly Ile Arg Lys Lys Ile Pro	
180 185 190	
tat tta aaa caa cta ggt gtt aca gtc ctt tat ctt aat cca att ttt	624
Tyr Leu Lys Gln Leu Gly Val Thr Val Leu Tyr Leu Asn Pro Ile Phe	
195 200 205	
tta gct aaa agt aat cat cgc tat gat aca aca gat ttt atg aaa atc	672
Leu Ala Lys Ser Asn His Arg Tyr Asp Thr Thr Asp Phe Met Lys Ile	
210 215 220	
gat cca atg ttg ggt gat gaa aaa gat tta gct gac tta att agg gaa	720
Asp Pro Met Leu Gly Asp Glu Lys Asp Leu Ala Asp Leu Ile Arg Glu	
225 230 235 240	
tta cat gag aat aat atg cat cta ata tta gat gga gta ttt aat cat	768
Leu His Glu Asn Asn Met His Leu Ile Leu Asp Gly Val Phe Asn His	
245 250 255	
gta ggt ttt gat agc att tat ttt caa gga gcg att act gac aaa aat	816
Val Gly Phe Asp Ser Ile Tyr Phe Gln Gly Ala Ile Thr Asp Lys Asn	
260 265 270	
agt aat tat cgt tct tgg ttc aac ttt caa gac tat cca aat aaa tat	864
Ser Asn Tyr Arg Ser Trp Phe Asn Phe Gln Asp Tyr Pro Asn Lys Tyr	
275 280 285	
cag tct tgg tgg ggt gta aag tct tta ccg act gtt aat aaa gat aat	912
Gln Ser Trp Trp Gly Val Lys Ser Leu Pro Thr Val Asn Lys Asp Asn	
290 295 300	
tct gaa tat caa aat ctt gtt tat ggc gat cat ggt gta tta gct aag	960
Ser Glu Tyr Gln Asn Leu Val Tyr Gly Asp His Gly Val Leu Ala Lys	
305 310 315 320	
tgg aaa gtt gat ggt tgg cga ctt gat gta gct gat gag tta ccg atg	1008
Trp Lys Val Asp Gly Trp Arg Leu Asp Val Ala Asp Glu Leu Pro Met	
325 330 335	
gat ttc ttg cgt aat att cgt aac cgt ttg ata aag gaa aat tgt cca	1056
Asp Phe Leu Arg Asn Ile Arg Asn Arg Leu Ile Lys Glu Asn Cys Pro	
340 345 350	
att ttg att ggg gaa gtt tgg gaa gat gct tca aat aaa ttt gta aat	1104
Ile Leu Ile Gly Glu Val Trp Glu Asp Ala Ser Asn Lys Phe Val Asn	
355 360 365	
ggg gaa tat cga act tat aca gct ggt gat aat tta atg ggg gtt atg	1152
Gly Glu Tyr Arg Thr Tyr Thr Ala Gly Asp Asn Leu Met Gly Val Met	
370 375 380	

```

aat tat ccg ata cgc aat ttt att atc agt ttg tta tca gct caa gat 1200
Asn Tyr Pro Ile Arg Asn Phe Ile Ile Ser Leu Leu Ser Ala Gln Asp
385 390 395 400

agt act ata gag ata gaa gca atg aat gac ctg gct tta ctg att gaa 1248
Ser Thr Ile Glu Ile Glu Ala Met Asn Asp Leu Ala Leu Leu Ile Glu
405 410 415

aat tat cca act gac ttt ttg cat aat tgt tta aat aat atc ggt acc 1296
Asn Tyr Pro Thr Asp Phe Leu His Asn Cys Leu Asn Asn Ile Gly Thr
420 425 430

cat gat acg gta aga att aaa acc gtt ttg aat aaa aat gat aat tta 1344
His Asp Thr Val Arg Ile Lys Thr Val Leu Asn Lys Asn Asp Asn Leu
435 440 445

gtc atg atg gct ttt ggc tta tta ttt atg atg ccc gga gtt cca tgt 1392
Val Met Met Ala Phe Gly Leu Leu Phe Met Met Pro Gly Val Pro Cys
450 455 460

att tat tat ggc gat gag gct ggc tta att ggt aaa gaa gat cca gat 1440
Ile Tyr Tyr Gly Asp Glu Ala Gly Leu Ile Gly Lys Glu Asp Pro Asp
465 470 475 480

aat cga cgt tac ttt cta tgg gga cat gaa gat aaa aag cta ata gat 1488
Asn Arg Arg Tyr Phe Leu Trp Gly His Glu Asp Lys Lys Leu Ile Asp
485 490 495

tgt gtt agc agt tgg acc aaa ata cgc aag caa aat cca gta ttg gta 1536
Cys Val Ser Ser Trp Thr Lys Ile Arg Lys Gln Asn Pro Val Leu Val
500 505 510

aat ggc aaa atc ggt ttt gta cat ttg tcg gct ggg gtt aat agt ata 1584
Asn Gly Lys Ile Gly Phe Val His Leu Ser Ala Gly Val Asn Ser Ile
515 520 525

gtt aga tat aat gat caa gag atg att atg tat tgc gtt aat tgt act 1632
Val Arg Tyr Asn Asp Gln Glu Met Ile Met Tyr Cys Val Asn Cys Thr
530 535 540

aac gaa gat gtg ata ccg ttg cgt gaa aag tat tca ttt tat tgg ttg 1680
Asn Glu Asp Val Ile Pro Leu Arg Glu Lys Tyr Ser Phe Tyr Trp Leu
545 550 555 560

ccg agc ata att att gat aaa atc aag gat act ttg gac caa att caa 1728
Pro Ser Ile Ile Ile Asp Lys Ile Lys Asp Thr Leu Asp Gln Ile Gln
565 570 575

ctt aaa gca caa aca gat ttt att aag aaa ata tcg cta 1767
Leu Lys Ala Gln Thr Asp Phe Ile Lys Lys Ile Ser Leu
580 585

```

<210> 278

<211> 589

<212> PRT

<213> Lactobacillus acidophilus

<400> 278

```

Met Lys Ile Thr Tyr Asp Ser Trp Gln Glu Gln Tyr Lys Asn Pro Phe
 1          5          10          15
Gly Ala Val Lys Ala Gly Asn Thr Val Lys Trp Ser Ile Lys Ile Asp
          20          25          30
Gln Val Ile Gln Gly Ala Val Leu Trp Leu Thr Lys Ser Arg Glu Thr
          35          40          45
Pro Val Ala Tyr Pro Met Asn Tyr Asp Glu Gln Thr Lys Met Tyr Thr
          50          55          60
Thr Gln Val Lys Ile Gly Thr Ser Gly Leu Tyr Asn Tyr Tyr Phe Ala
          65          70          75          80
Leu Gln Gln Asn Asn Gln Ile Val Tyr Ile Asp Gln Gly Leu Phe Gly
          85          90          95
Lys Gly His Val Thr Lys Ser Asp His Asp Leu Arg Gln Phe Gln Leu
          100          105          110
Thr Cys Tyr Asp Ile Ala Thr Pro Arg Ile Asp Trp Tyr Gln Lys Gly
          115          120          125
Ile Val Tyr Gln Ile Phe Pro Asp Arg Phe Ala Asn Gly Asn Pro Tyr
          130          135          140
Glu Glu Val Ile Gly Lys Lys Arg Asn Ser Phe Ile Tyr Ala Thr Lys
          145          150          155          160
Glu Asp Ile Pro Tyr Tyr Ile Lys Asn Ser Glu Gly Ala Ile Val Arg
          165          170          175
Trp Asp Phe Phe Gly Gly Asn Leu Thr Gly Ile Arg Lys Lys Ile Pro
          180          185          190
Tyr Leu Lys Gln Leu Gly Val Thr Val Leu Tyr Leu Asn Pro Ile Phe
          195          200          205
Leu Ala Lys Ser Asn His Arg Tyr Asp Thr Thr Asp Phe Met Lys Ile
          210          215          220
Asp Pro Met Leu Gly Asp Glu Lys Asp Leu Ala Asp Leu Ile Arg Glu
          225          230          235          240
Leu His Glu Asn Asn Met His Leu Ile Leu Asp Gly Val Phe Asn His
          245          250          255
Val Gly Phe Asp Ser Ile Tyr Phe Gln Gly Ala Ile Thr Asp Lys Asn
          260          265          270
Ser Asn Tyr Arg Ser Trp Phe Asn Phe Gln Asp Tyr Pro Asn Lys Tyr
          275          280          285
Gln Ser Trp Trp Gly Val Lys Ser Leu Pro Thr Val Asn Lys Asp Asn
          290          295          300
Ser Glu Tyr Gln Asn Leu Val Tyr Gly Asp His Gly Val Leu Ala Lys
          305          310          315          320
Trp Lys Val Asp Gly Trp Arg Leu Asp Val Ala Asp Glu Leu Pro Met
          325          330          335
Asp Phe Leu Arg Asn Ile Arg Asn Arg Leu Ile Lys Glu Asn Cys Pro
          340          345          350
Ile Leu Ile Gly Glu Val Trp Glu Asp Ala Ser Asn Lys Phe Val Asn
          355          360          365
Gly Glu Tyr Arg Thr Tyr Thr Ala Gly Asp Asn Leu Met Gly Val Met
          370          375          380
Asn Tyr Pro Ile Arg Asn Phe Ile Ile Ser Leu Leu Ser Ala Gln Asp
          385          390          395          400
Ser Thr Ile Glu Ile Glu Ala Met Asn Asp Leu Ala Leu Leu Ile Glu
          405          410          415
Asn Tyr Pro Thr Asp Phe Leu His Asn Cys Leu Asn Asn Ile Gly Thr
          420          425          430
His Asp Thr Val Arg Ile Lys Thr Val Leu Asn Lys Asn Asp Asn Leu

```

```

      435              440              445
Val Met Met Ala Phe Gly Leu Leu Phe Met Met Pro Gly Val Pro Cys
      450              455              460
Ile Tyr Tyr Gly Asp Glu Ala Gly Leu Ile Gly Lys Glu Asp Pro Asp
465              470              475
Asn Arg Arg Tyr Phe Leu Trp Gly His Glu Asp Lys Lys Leu Ile Asp
      485              490              495
Cys Val Ser Ser Trp Thr Lys Ile Arg Lys Gln Asn Pro Val Leu Val
      500              505              510
Asn Gly Lys Ile Gly Phe Val His Leu Ser Ala Gly Val Asn Ser Ile
      515              520              525
Val Arg Tyr Asn Asp Gln Glu Met Ile Met Tyr Cys Val Asn Cys Thr
      530              535              540
Asn Glu Asp Val Ile Pro Leu Arg Glu Lys Tyr Ser Phe Tyr Trp Leu
545              550              555
Pro Ser Ile Ile Ile Asp Lys Ile Lys Asp Thr Leu Asp Gln Ile Gln
      565              570              575
Leu Lys Ala Gln Thr Asp Phe Ile Lys Lys Ile Ser Leu
      580              585

```

<210> 279

<211> 1305

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 36 - cyclomaltodextrin transport membrane protein

<220>

<221> CDS

<222> (1)...(1305)

<400> 279

```

gtg aaa aag ttt tta ata ggt atc gta ttt gga att gct ttg ttt ttg   48
Met Lys Lys Phe Leu Ile Gly Ile Val Phe Gly Ile Ala Leu Phe Leu
  1              5              10              15

act caa aaa aca aat att aca tat gcg gca aat tta agt gat aat ttt   96
Thr Gln Lys Thr Asn Ile Thr Tyr Ala Ala Asn Leu Ser Asp Asn Phe
      20              25              30

acg caa att ttg att gat aat gac cag aat aat ttg ctt aat aat agc   144
Thr Gln Ile Leu Ile Asp Asn Asp Gln Asn Asn Leu Leu Asn Asn Ser
      35              40              45

gaa att gct cac att agt gtt aaa ttt aat gat caa aaa aat aaa ttt   192
Glu Ile Ala His Ile Ser Val Lys Phe Asn Asp Gln Lys Asn Lys Phe
      50              55              60

aca aaa gat agc act atg ttt atc tta tta aat tcg aat aaa aag gat   240
Thr Lys Asp Ser Thr Met Phe Ile Leu Leu Asn Ser Asn Lys Lys Asp
      65              70              75              80

```

ggt cat gta caa gca tta aat gaa gtg aaa aaa tta ata att aaa gac	288
Val His Val Gln Ala Leu Asn Glu Val Lys Lys Leu Ile Ile Lys Asp	
85 90 95	
gat act ggt gag gct tat caa gtt ggc aaa tat att gtt aaa aat aat	336
Asp Thr Gly Glu Ala Tyr Gln Val Gly Lys Tyr Ile Val Lys Asn Asn	
100 105 110	
caa gta caa gta att ttt gat aaa aat att gaa aag ttt gaa aat ata	384
Gln Val Gln Val Ile Phe Asp Lys Asn Ile Glu Lys Phe Glu Asn Ile	
115 120 125	
tcc ggt caa att gat ttt gat ata caa ata agt aat gaa act act tct	432
Ser Gly Gln Ile Asp Phe Asp Ile Gln Ile Ser Asn Glu Thr Thr Ser	
130 135 140	
aat caa ttt att caa ata gaa gca ggc gaa att aat gaa aaa att tat	480
Asn Gln Phe Ile Gln Ile Glu Ala Gly Glu Ile Asn Glu Lys Ile Tyr	
145 150 155 160	
ggt tca tct cgt cca caa gtt aat aaa aat gtc gta acc gaa att agt	528
Val Ser Ser Arg Pro Gln Val Asn Lys Asn Val Val Thr Glu Ile Ser	
165 170 175	
ggc aaa tat aac tca gat aaa aat aaa att gct tgg gaa ata aag ata	576
Gly Lys Tyr Asn Ser Asp Lys Asn Lys Ile Ala Trp Glu Ile Lys Ile	
180 185 190	
aac tct gag aat aaa agc gag cta caa att ttt aat act att gaa aat	624
Asn Ser Glu Asn Lys Ser Glu Leu Gln Ile Phe Asn Thr Ile Glu Asn	
195 200 205	
caa aat att gat caa gat acg tta aaa ata aaa ata gac ggt aat tta	672
Gln Asn Ile Asp Gln Asp Thr Leu Lys Ile Lys Ile Asp Gly Asn Leu	
210 215 220	
att aaa ctc aat aaa aat aat att gaa ttt aat aaa gga tta aag ctg	720
Ile Lys Leu Asn Lys Asn Asn Ile Glu Phe Asn Lys Gly Leu Lys Leu	
225 230 235 240	
aag ttg gta ggt aaa gat att gtt att aca tat att act agt gca agt	768
Lys Leu Val Gly Lys Asp Ile Val Ile Thr Tyr Ile Thr Ser Ala Ser	
245 250 255	
gaa gtt agt tct gta ctt aat ata gtc cgt gta att gaa gat aat gaa	816
Glu Val Ser Ser Val Leu Asn Ile Val Arg Val Ile Glu Asp Asn Glu	
260 265 270	
aat caa aat gtt act agt gca aaa gta caa gta aat gat atc gtt aac	864
Asn Gln Asn Val Thr Ser Ala Lys Val Gln Val Asn Asp Ile Val Asn	
275 280 285	
att gat gga aaa ttt aat cag aca tct acg aat aag aaa caa aga gag	912
Ile Asp Gly Lys Phe Asn Gln Thr Ser Thr Asn Lys Lys Gln Arg Glu	
290 295 300	

```

aaa aaa att tct aaa ttt ttt tct aat tta gct aaa tta att att gat 960
Lys Lys Ile Ser Lys Phe Phe Ser Asn Leu Ala Lys Leu Ile Ile Asp
305 310 315 320

aaa aag caa gaa aaa act gat caa aat aat gat gaa aaa agt caa ttt 1008
Lys Lys Gln Glu Lys Thr Asp Gln Asn Asn Asp Glu Lys Ser Gln Phe
325 330 335

gaa tta gct caa tct act gct tta gct aat gcc aag tca aca aaa cat 1056
Glu Leu Ala Gln Ser Thr Ala Leu Ala Asn Ala Lys Ser Thr Lys His
340 345 350

gac atg gtc gtt tca agt aaa aca ccg tca tta gat gat act ttt gag 1104
Asp Met Val Val Ser Ser Lys Thr Pro Ser Leu Asp Asp Thr Phe Glu
355 360 365

cat aat att gat gat aaa gaa gtt aaa gaa act ata aat gag agt att 1152
His Asn Ile Asp Asp Lys Glu Val Lys Glu Thr Ile Asn Glu Ser Ile
370 375 380

cct aat act aaa aag gct cat tca aaa aag cat tcc gca aat aaa agt 1200
Pro Asn Thr Lys Lys Ala His Ser Lys Lys His Ser Ala Asn Lys Ser
385 390 395 400

aac tta cct aaa acg gga gaa gat aat ata gaa tta ttt ttc agt ata 1248
Asn Leu Pro Lys Thr Gly Glu Asp Asn Ile Glu Leu Phe Phe Ser Ile
405 410 415

gta gga act att ttt ttg agt atc tca gct ata ttt ttt tat aaa aaa 1296
Val Gly Thr Ile Phe Leu Ser Ile Ser Ala Ile Phe Phe Tyr Lys Lys
420 425 430

tcc aga aaa 1305
Ser Arg Lys
435

```

<210> 280

<211> 435

<212> PRT

<213> Lactobacillus acidophilus

<400> 280

```

Met Lys Lys Phe Leu Ile Gly Ile Val Phe Gly Ile Ala Leu Phe Leu
1 5 10 15
Thr Gln Lys Thr Asn Ile Thr Tyr Ala Ala Asn Leu Ser Asp Asn Phe
20 25 30
Thr Gln Ile Leu Ile Asp Asn Asp Gln Asn Asn Leu Leu Asn Asn Ser
35 40 45
Glu Ile Ala His Ile Ser Val Lys Phe Asn Asp Gln Lys Asn Lys Phe
50 55 60
Thr Lys Asp Ser Thr Met Phe Ile Leu Leu Asn Ser Asn Lys Lys Asp
65 70 75 80
Val His Val Gln Ala Leu Asn Glu Val Lys Lys Leu Ile Ile Lys Asp
85 90 95
Asp Thr Gly Glu Ala Tyr Gln Val Gly Lys Tyr Ile Val Lys Asn Asn
100 105 110

```

Gln Val Gln Val Ile Phe Asp Lys Asn Ile Glu Lys Phe Glu Asn Ile
 115 120 125
 Ser Gly Gln Ile Asp Phe Asp Ile Gln Ile Ser Asn Glu Thr Thr Ser
 130 135 140
 Asn Gln Phe Ile Gln Ile Glu Ala Gly Glu Ile Asn Glu Lys Ile Tyr
 145 150 155 160
 Val Ser Ser Arg Pro Gln Val Asn Lys Asn Val Val Thr Glu Ile Ser
 165 170 175
 Gly Lys Tyr Asn Ser Asp Lys Asn Lys Ile Ala Trp Glu Ile Lys Ile
 180 185 190
 Asn Ser Glu Asn Lys Ser Glu Leu Gln Ile Phe Asn Thr Ile Glu Asn
 195 200 205
 Gln Asn Ile Asp Gln Asp Thr Leu Lys Ile Lys Ile Asp Gly Asn Leu
 210 215 220
 Ile Lys Leu Asn Lys Asn Asn Ile Glu Phe Asn Lys Gly Leu Lys Leu
 225 230 235 240
 Lys Leu Val Gly Lys Asp Ile Val Ile Thr Tyr Ile Thr Ser Ala Ser
 245 250 255
 Glu Val Ser Ser Val Leu Asn Ile Val Arg Val Ile Glu Asp Asn Glu
 260 265 270
 Asn Gln Asn Val Thr Ser Ala Lys Val Gln Val Asn Asp Ile Val Asn
 275 280 285
 Ile Asp Gly Lys Phe Asn Gln Thr Ser Thr Asn Lys Lys Gln Arg Glu
 290 295 300
 Lys Lys Ile Ser Lys Phe Phe Ser Asn Leu Ala Lys Leu Ile Ile Asp
 305 310 315 320
 Lys Lys Gln Glu Lys Thr Asp Gln Asn Asn Asp Glu Lys Ser Gln Phe
 325 330 335
 Glu Leu Ala Gln Ser Thr Ala Leu Ala Asn Ala Lys Ser Thr Lys His
 340 345 350
 Asp Met Val Val Ser Ser Lys Thr Pro Ser Leu Asp Asp Thr Phe Glu
 355 360 365
 His Asn Ile Asp Asp Lys Glu Val Lys Glu Thr Ile Asn Glu Ser Ile
 370 375 380
 Pro Asn Thr Lys Lys Ala His Ser Lys Lys His Ser Ala Asn Lys Ser
 385 390 395 400
 Asn Leu Pro Lys Thr Gly Glu Asp Asn Ile Glu Leu Phe Phe Ser Ile
 405 410 415
 Val Gly Thr Ile Phe Leu Ser Ile Ser Ala Ile Phe Phe Tyr Lys Lys
 420 425 430
 Ser Arg Lys
 435

<210> 281

<211> 1146

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 530

<220>

<221> CDS

<222> (1)...(1146)

<400> 281

gtg	aaa	aaa	tat	ttg	caa	att	atg	gct	tta	gca	ggg	ata	gcc	att	act	48
Met	Lys	Lys	Tyr	Leu	Gln	Ile	Met	Ala	Leu	Ala	Gly	Ile	Ala	Ile	Thr	
1				5					10					15		
tta	act	ggg	tgt	ggg	aga	ttg	aaa	gac	tct	agt	tta	gcg	aat	aat	gca	96
Leu	Thr	Gly	Cys	Gly	Arg	Leu	Lys	Asp	Ser	Ser	Leu	Ala	Asn	Asn	Ala	
			20					25					30			
act	act	act	tca	aca	act	aag	aaa	aag	agt	tat	caa	aca	act	aat	acc	144
Thr	Thr	Thr	Ser	Thr	Thr	Lys	Lys	Lys	Ser	Tyr	Gln	Thr	Thr	Asn	Thr	
			35					40				45				
ggg	aat	agt	ggc	tat	tct	gtt	tta	ttg	aaa	aat	gga	cgc	tat	gta	gtt	192
Gly	Asn	Ser	Gly	Tyr	Ser	Val	Leu	Leu	Lys	Asn	Gly	Arg	Tyr	Val	Val	
	50					55					60					
agt	cca	att	gct	ggg	tta	aca	gca	acc	gat	aat	gat	aat	tca	gtt	gat	240
Ser	Pro	Ile	Ala	Gly	Leu	Thr	Ala	Thr	Asp	Asn	Asp	Asn	Ser	Val	Asp	
	65					70				75					80	
aca	aga	gaa	tta	gaa	cgt	ggc	ttg	att	caa	att	tct	aag	aat	caa	ttc	288
Thr	Arg	Glu	Leu	Glu	Arg	Gly	Leu	Ile	Gln	Ile	Ser	Lys	Asn	Gln	Phe	
				85					90					95		
tca	act	aat	cag	tat	gtt	ttc	caa	gaa	gga	caa	caa	ctg	gat	act	tca	336
Ser	Thr	Asn	Gln	Tyr	Val	Phe	Gln	Glu	Gly	Gln	Gln	Leu	Asp	Thr	Ser	
			100					105					110			
act	gta	act	gat	tgg	tta	acc	aga	aaa	tca	aag	act	aat	cct	caa	gga	384
Thr	Val	Thr	Asp	Trp	Leu	Thr	Arg	Lys	Ser	Lys	Thr	Asn	Pro	Gln	Gly	
			115				120					125				
tta	aat	cca	gtc	aat	aat	ggg	aag	act	gga	act	gat	act	aga	aat	cca	432
Leu	Asn	Pro	Val	Asn	Asn	Gly	Lys	Thr	Gly	Thr	Asp	Thr	Arg	Asn	Pro	
	130					135					140					
att	tat	tta	gaa	gaa	att	gtt	gag	caa	gat	tat	tta	act	ggg	tca	ggg	480
Ile	Tyr	Leu	Glu	Glu	Ile	Val	Glu	Gln	Asp	Tyr	Leu	Thr	Gly	Ser	Gly	
	145				150					155				160		
tct	aag	tat	caa	tta	ggg	ggg	atg	agt	ctt	ggc	tta	gca	atg	aat	tcc	528
Ser	Lys	Tyr	Gln	Leu	Gly	Gly	Met	Ser	Leu	Gly	Leu	Ala	Met	Asn	Ser	
				165					170					175		
gtt	gac	tat	tac	caa	aaa	aag	cgt	gat	ggg	gca	gaa	ttt	caa	act	gat	576
Val	Asp	Tyr	Tyr	Gln	Lys	Lys	Arg	Asp	Gly	Ala	Glu	Phe	Gln	Thr	Asp	
			180					185					190			
att	tcc	aaa	gct	acc	cag	cgt	gct	caa	ggg	gag	aaa	ata	gct	aat	gaa	624
Ile	Ser	Lys	Ala	Thr	Gln	Arg	Ala	Gln	Gly	Glu	Lys	Ile	Ala	Asn	Glu	
		195					200					205				
att	gtg	gct	cgt	ttg	cgt	aag	cgt	aag	agc	ttg	aag	aat	att	cca	att	672
Ile	Val	Ala	Arg	Leu	Arg	Lys	Arg	Lys	Ser	Leu	Lys	Asn	Ile	Pro	Ile	

210	215	220	
acc att gga tta ttc tct aaa aca gga aaa gat tca tta gtt ggc gga			720
Thr Ile Gly Leu Phe Ser Lys Thr Gly Lys Asp Ser Leu Val Gly Gly			
225	230	235	240
act tac ttt gct tac ggg aca gcg gcc gct aat agt agt aaa ata act			768
Thr Tyr Phe Ala Tyr Gly Thr Ala Ala Ala Asn Ser Ser Lys Ile Thr			
	245	250	255
aaa tgg aaa tcc atg tcg gaa aaa atg caa gtt tta ccg aca act ggt			816
Lys Trp Lys Ser Met Ser Glu Lys Met Gln Val Leu Pro Thr Thr Gly			
	260	265	270
aat gaa aaa gca att aat agc gac gac gca tct cat ttc aat gat ttt			864
Asn Glu Lys Ala Ile Asn Ser Asp Asp Ala Ser His Phe Asn Asp Phe			
	275	280	285
aag acg gca att caa aat tac ttc cct aat att agt gga gta acg gca			912
Lys Thr Ala Ile Gln Asn Tyr Phe Pro Asn Ile Ser Gly Val Thr Ala			
	290	295	300
act ttg cgt tat gat aat ggc aag ctg gct caa gaa aat att tca att			960
Thr Leu Arg Tyr Asp Asn Gly Lys Leu Ala Gln Glu Asn Ile Ser Ile			
305	310	315	320
acg acc cag ttt tat ggt tat gag caa att caa agt ttt act cgt tta			1008
Thr Thr Gln Phe Tyr Gly Tyr Glu Gln Ile Gln Ser Phe Thr Arg Leu			
	325	330	335
acc tta tca aca gcg aag aaa tat ttg ccg aac aat att cca att gaa			1056
Thr Leu Ser Thr Ala Lys Lys Tyr Leu Pro Asn Asn Ile Pro Ile Glu			
	340	345	350
atc aag att gga tca gtt gat gac gta caa gca tta att gca aaa gaa			1104
Ile Lys Ile Gly Ser Val Asp Asp Val Gln Ala Leu Ile Ala Lys Glu			
	355	360	365
acc ggc gat agt gat tat caa gtc cat gtt tat ggc ggc gaa			1146
Thr Gly Asp Ser Asp Tyr Gln Val His Val Tyr Gly Gly Glu			
370	375	380	

<210> 282

<211> 382

<212> PRT

<213> Lactobacillus acidophilus

<400> 282

Met Lys Lys Tyr Leu Gln Ile Met Ala Leu Ala Gly Ile Ala Ile Thr	
1	5 10 15
Leu Thr Gly Cys Gly Arg Leu Lys Asp Ser Ser Leu Ala Asn Asn Ala	
	20 25 30
Thr Thr Thr Ser Thr Thr Lys Lys Lys Ser Tyr Gln Thr Asn Thr	
	35 40 45
Gly Asn Ser Gly Tyr Ser Val Leu Leu Lys Asn Gly Arg Tyr Val Val	

50	55	60
Ser Pro Ile Ala Gly	Leu Thr Ala Thr Asp	Asn Asp Asn Ser Val Asp
65	70	75
Thr Arg Glu Leu Glu	Arg Gly Leu Ile Gln	Ile Ser Lys Asn Gln Phe
	85	90
Ser Thr Asn Gln Tyr	Val Phe Gln Glu Gly	Gln Gln Leu Asp Thr Ser
	100	105
Thr Val Thr Asp Trp	Leu Thr Arg Lys Ser	Lys Thr Asn Pro Gln Gly
	115	120
Leu Asn Pro Val Asn	Asn Gly Lys Thr Gly	Thr Asp Thr Arg Asn Pro
	130	135
Ile Tyr Leu Glu Glu	Ile Val Glu Gln Asp	Tyr Leu Thr Gly Ser Gly
145	150	155
Ser Lys Tyr Gln Leu	Gly Gly Met Ser Leu	Gly Leu Ala Met Asn Ser
	165	170
Val Asp Tyr Tyr Gln	Lys Lys Arg Asp Gly	Ala Glu Phe Gln Thr Asp
	180	185
Ile Ser Lys Ala Thr	Gln Arg Ala Gln Gly	Glu Lys Ile Ala Asn Glu
	195	200
Ile Val Ala Arg Leu	Arg Lys Arg Lys Ser	Leu Lys Asn Ile Pro Ile
	210	215
Thr Ile Gly Leu Phe	Ser Lys Thr Gly Lys	Asp Ser Leu Val Gly Gly
225	230	235
Thr Tyr Phe Ala Tyr	Gly Thr Ala Ala Ala	Asn Ser Ser Lys Ile Thr
	245	250
Lys Trp Lys Ser Met	Ser Glu Lys Met Gln	Val Leu Pro Thr Thr Gly
	260	265
Asn Glu Lys Ala Ile	Asn Ser Asp Asp Ala	Ser His Phe Asn Asp Phe
	275	280
Lys Thr Ala Ile Gln	Asn Tyr Phe Pro Asn	Ile Ser Gly Val Thr Ala
	290	295
Thr Leu Arg Tyr Asp	Asn Gly Lys Leu Ala	Gln Glu Asn Ile Ser Ile
305	310	315
Thr Thr Gln Phe Tyr	Gly Tyr Glu Gln Ile	Gln Ser Phe Thr Arg Leu
	325	330
Thr Leu Ser Thr Ala	Lys Lys Tyr Leu Pro	Asn Asn Ile Pro Ile Glu
	340	345
Ile Lys Ile Gly Ser	Val Asp Asp Val Gln	Ala Leu Ile Ala Lys Glu
	355	360
Thr Gly Asp Ser Asp	Tyr Gln Val His Val	Tyr Gly Gly Glu
	370	375
		380

<210> 283

<211> 519

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 701 - cell surface protein

<220>

<221> CDS

<222> (1)...(519)

<400> 283

```

atg att ttt tgg cta gaa ctc aat caa gat aaa gat tat ggt caa atc 48
Met Ile Phe Trp Leu Glu Leu Asn Gln Asp Lys Asp Tyr Gly Gln Ile
  1             5             10             15

cct gtt att ggt gaa gac gga caa att caa ttt atc ata caa ggc aat 96
Pro Val Ile Gly Glu Asp Gly Gln Ile Gln Phe Ile Ile Gln Gly Asn
          20             25             30

ctc gat aat cca aat cat act ttg tat cta gat aac act aat aaa gaa 144
Leu Asp Asn Pro Asn His Thr Leu Tyr Leu Asp Asn Thr Asn Lys Glu
          35             40             45

gaa att gga cgt ttg ttt tct gat gga gca gga ctc att gct tct ttt 192
Glu Ile Gly Arg Leu Phe Ser Asp Gly Ala Gly Leu Ile Ala Ser Phe
          50             55             60

act atc gac gtc gta aat cat tct cta gta ggt gta aaa aaa tta aac 240
Thr Ile Asp Val Val Asn His Ser Leu Val Gly Val Lys Lys Leu Asn
          65             70             75             80

aca cct aat acc aat ata ttt tat ata acc aaa tta aaa tat att gtt 288
Thr Pro Asn Thr Asn Ile Phe Tyr Ile Thr Lys Leu Lys Tyr Ile Val
          85             90             95

aca ggt agt att aaa cat ggt acc tat acc ttt aga tcc gga att aaa 336
Thr Gly Ser Ile Lys His Gly Thr Tyr Thr Phe Arg Ser Gly Ile Lys
          100            105            110

aat gta gcc agt gta aaa act atg atg ggt gat cat ggt gtg gtt ttg 384
Asn Val Ala Ser Val Lys Thr Met Met Gly Asp His Gly Val Val Leu
          115            120            125

gta tgt gat att agt aag ccc gaa gat atc cca ttt att ctt tta agc 432
Val Cys Asp Ile Ser Lys Pro Glu Asp Ile Pro Phe Ile Leu Leu Ser
          130            135            140

tct gta tta ttt act cag tgg cat gta act cct tta aaa ttg cca att 480
Ser Val Leu Phe Thr Gln Trp His Val Thr Pro Leu Lys Leu Pro Ile
          145            150            155            160

ttt cca cct att ggc aac aag ttt gga gta aat cct aat 519
Phe Pro Pro Ile Gly Asn Lys Phe Gly Val Asn Pro Asn
          165            170

```

<210> 284

<211> 173

<212> PRT

<213> *Lactobacillus acidophilus*

<400> 284

```

Met Ile Phe Trp Leu Glu Leu Asn Gln Asp Lys Asp Tyr Gly Gln Ile
  1             5             10             15
Pro Val Ile Gly Glu Asp Gly Gln Ile Gln Phe Ile Ile Gln Gly Asn
          20             25             30

```

```

Leu Asp Asn Pro Asn His Thr Leu Tyr Leu Asp Asn Thr Asn Lys Glu
      35              40              45
Glu Ile Gly Arg Leu Phe Ser Asp Gly Ala Gly Leu Ile Ala Ser Phe
      50              55              60
Thr Ile Asp Val Val Asn His Ser Leu Val Gly Val Lys Lys Leu Asn
      65              70              75              80
Thr Pro Asn Thr Asn Ile Phe Tyr Ile Thr Lys Leu Lys Tyr Ile Val
      85              90              95
Thr Gly Ser Ile Lys His Gly Thr Tyr Thr Phe Arg Ser Gly Ile Lys
      100             105             110
Asn Val Ala Ser Val Lys Thr Met Met Gly Asp His Gly Val Val Leu
      115             120             125
Val Cys Asp Ile Ser Lys Pro Glu Asp Ile Pro Phe Ile Leu Leu Ser
      130             135             140
Ser Val Leu Phe Thr Gln Trp His Val Thr Pro Leu Lys Leu Pro Ile
      145             150             155             160
Phe Pro Pro Ile Gly Asn Lys Phe Gly Val Asn Pro Asn
      165             170

```

<210> 285

<211> 1242

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 833 ~ cell division protein

<220>

<221> CDS

<222> (1)...(1242)

<400> 285

```

gtg gtg act ttt ttg ttt tat aat gaa aaa agt att att tca cat aaa   48
Met Val Thr Phe Leu Phe Tyr Asn Glu Lys Ser Ile Ile Ser His Lys
  1              5              10              15

ggg gca acg ctc gtg cgt cga aaa tta aga tat ctt aat tac cga att   96
Gly Ala Thr Leu Val Arg Arg Lys Leu Arg Tyr Leu Asn Tyr Arg Ile
      20              25              30

tta atc cca tac tta att tta gta gtt gta gga ata att ttg gta tat   144
Leu Ile Pro Tyr Leu Ile Leu Val Val Val Gly Ile Ile Leu Val Tyr
      35              40              45

tca gca agt tca gac att tta tta gtt aat gga ttt aag cca gat gtt   192
Ser Ala Ser Ser Asp Ile Leu Leu Val Asn Gly Phe Lys Pro Asp Val
      50              55              60

tat gga att cgt caa gca atc tat gct gct gta gca ttt ttt gga ttt   240
Tyr Gly Ile Arg Gln Ala Ile Tyr Ala Ala Val Ala Phe Phe Gly Phe
      65              70              75              80

ggt att cct ttt ttt gca tta agg cta aag gtt att aaa aat cca aaa   288

```

Gly	Ile	Pro	Phe	Phe	Ala	Leu	Arg	Leu	Lys	Val	Ile	Lys	Asn	Pro	Lys	
				85					90					95		
ttt	gta	gct	ggt	ttt	tta	ata	atc	tgt	att	tta	atg	ctg	cta	tgg	ttg	336
Phe	Val	Ala	Gly	Phe	Leu	Ile	Ile	Cys	Ile	Leu	Met	Leu	Leu	Trp	Leu	
			100					105					110			
gtc	ttt	tta	aga	ttt	gct	cat	ggt	agt	gca	gca	gcc	ggt	aat	ggg	gct	384
Val	Phe	Leu	Arg	Phe	Ala	His	Gly	Ser	Ala	Ala	Ala	Val	Asn	Gly	Ala	
		115					120					125				
ggt	ggt	tgg	att	aac	ttg	ggt	ttc	att	aat	ctt	cag	ccg	tta	gaa	gtt	432
Val	Gly	Trp	Ile	Asn	Leu	Gly	Phe	Ile	Asn	Leu	Gln	Pro	Leu	Glu	Val	
	130					135					140					
act	aaa	ttg	gct	tta	gta	att	tat	tta	gct	tat	ggt	ttg	gat	cga	aga	480
Thr	Lys	Leu	Ala	Leu	Val	Ile	Tyr	Leu	Ala	Tyr	Val	Leu	Asp	Arg	Arg	
145					150					155					160	
gac	gga	aaa	tta	gta	agg	gga	aaa	att	aaa	gat	aat	cta	tct	cat	cct	528
Asp	Gly	Lys	Leu	Val	Arg	Gly	Lys	Ile	Lys	Asp	Asn	Leu	Ser	His	Pro	
			165					170						175		
gct	atg	cta	gct	ggt	ttc	tta	atg	tgt	tta	ggt	att	gta	gag	cct	gac	576
Ala	Met	Leu	Ala	Gly	Phe	Leu	Met	Cys	Leu	Val	Ile	Val	Glu	Pro	Asp	
			180					185					190			
ttt	ggt	ggt	acc	gca	att	tta	ttc	atg	att	acg	tta	gta	atg	ttt	tcc	624
Phe	Gly	Gly	Thr	Ala	Ile	Leu	Phe	Met	Ile	Thr	Leu	Val	Met	Phe	Ser	
	195					200						205				
gta	tct	ggt	gta	cca	ggt	agg	tta	gca	cta	act	tgg	cta	ctc	gga	atc	672
Val	Ser	Gly	Val	Pro	Val	Arg	Leu	Ala	Leu	Thr	Trp	Leu	Leu	Gly	Ile	
	210					215					220					
ata	cta	tta	ggt	ggg	gca	ggt	ttt	att	tta	gta	ggt	ctt	tgg	aat	cct	720
Ile	Leu	Leu	Val	Gly	Ala	Val	Phe	Ile	Leu	Val	Val	Leu	Trp	Asn	Pro	
225					230					235					240	
aaa	ttt	ttg	cag	gat	agt	tat	caa	ttt	caa	cga	ttg	atg	tca	ttt	tta	768
Lys	Phe	Leu	Gln	Asp	Ser	Tyr	Gln	Phe	Gln	Arg	Leu	Met	Ser	Phe	Leu	
			245					250						255		
cat	ccc	ttt	caa	ctt	gaa	aga	aaa	ggt	gga	gcc	caa	tta	ggt	aat	tct	816
His	Pro	Phe	Gln	Leu	Glu	Arg	Lys	Gly	Gly	Ala	Gln	Leu	Val	Asn	Ser	
			260					265					270			
tac	tat	gca	atc	cat	aat	gga	gga	ttg	ttt	ggt	gta	gga	tta	ggg	aac	864
Tyr	Tyr	Ala	Ile	His	Asn	Gly	Gly	Leu	Phe	Gly	Val	Gly	Leu	Gly	Asn	
		275				280					285					
agt	atg	caa	aaa	cga	gga	tat	ttg	cca	gaa	cca	tat	act	gat	ttt	att	912
Ser	Met	Gln	Lys	Arg	Gly	Tyr	Leu	Pro	Glu	Pro	Tyr	Thr	Asp	Phe	Ile	
	290					295					300					
tta	tct	att	aca	gcc	gaa	gaa	att	ggc	ggt	atc	ttc	acg	att	gta	ctg	960
Leu	Ser	Ile	Thr	Ala	Glu	Glu	Ile	Gly	Val	Ile	Phe	Thr	Ile	Val	Leu	

305	310	315	320	
gtt ggt cta tta ttt tat tta atg tgg caa att atg gaa gta ggt att				1008
Val Gly Leu Leu Phe Tyr Leu Met Trp Gln Ile Met Glu Val Gly Ile				
	325	330	335	
aat gcc gtc tca caa ttt gat gca tta att tgc ttt ggc gtg aca aca				1056
Asn Ala Val Ser Gln Phe Asp Ala Leu Ile Cys Phe Gly Val Thr Thr				
	340	345	350	
att att ttt act gaa gca ttg ttt aat atc ggt gct gta tta ggt cta				1104
Ile Ile Phe Thr Glu Ala Leu Phe Asn Ile Gly Ala Val Leu Gly Leu				
	355	360	365	
tta cca att act ggt gtt acg ctg cca ttt att tcg tat ggt ggt tct				1152
Leu Pro Ile Thr Gly Val Thr Leu Pro Phe Ile Ser Tyr Gly Gly Ser				
	370	375	380	
tct atg atc gtt tta act gct gca att ggg tta gtg ctg aat gta tct				1200
Ser Met Ile Val Leu Thr Ala Ala Ile Gly Leu Val Leu Asn Val Ser				
	385	390	400	
gct aat gaa aaa atg tta aaa gaa aag gat gaa aca att gca				1242
Ala Asn Glu Lys Met Leu Lys Glu Lys Asp Glu Thr Ile Ala				
	405	410		

<210> 286

<211> 414

<212> PRT

<213> Lactobacillus acidophilus

<400> 286

Met Val Thr Phe Leu Phe Tyr Asn Glu Lys Ser Ile Ile Ser His Lys				
1 5 10 15				
Gly Ala Thr Leu Val Arg Arg Lys Leu Arg Tyr Leu Asn Tyr Arg Ile				
20 25 30				
Leu Ile Pro Tyr Leu Ile Leu Val Val Gly Ile Ile Leu Val Tyr				
35 40 45				
Ser Ala Ser Ser Asp Ile Leu Leu Val Asn Gly Phe Lys Pro Asp Val				
50 55 60				
Tyr Gly Ile Arg Gln Ala Ile Tyr Ala Ala Val Ala Phe Phe Gly Phe				
65 70 75 80				
Gly Ile Pro Phe Phe Ala Leu Arg Leu Lys Val Ile Lys Asn Pro Lys				
85 90 95				
Phe Val Ala Gly Phe Leu Ile Ile Cys Ile Leu Met Leu Leu Trp Leu				
100 105 110				
Val Phe Leu Arg Phe Ala His Gly Ser Ala Ala Ala Val Asn Gly Ala				
115 120 125				
Val Gly Trp Ile Asn Leu Gly Phe Ile Asn Leu Gln Pro Leu Glu Val				
130 135 140				
Thr Lys Leu Ala Leu Val Ile Tyr Leu Ala Tyr Val Leu Asp Arg Arg				
145 150 155 160				
Asp Gly Lys Leu Val Arg Gly Lys Ile Lys Asp Asn Leu Ser His Pro				
165 170 175				
Ala Met Leu Ala Gly Phe Leu Met Cys Leu Val Ile Val Glu Pro Asp				

```

      180      185      190
Phe Gly Gly Thr Ala Ile Leu Phe Met Ile Thr Leu Val Met Phe Ser
      195      200      205
Val Ser Gly Val Pro Val Arg Leu Ala Leu Thr Trp Leu Leu Gly Ile
      210      215      220
Ile Leu Leu Val Gly Ala Val Phe Ile Leu Val Val Leu Trp Asn Pro
      225      230      235      240
Lys Phe Leu Gln Asp Ser Tyr Gln Phe Gln Arg Leu Met Ser Phe Leu
      245      250      255
His Pro Phe Gln Leu Glu Arg Lys Gly Gly Ala Gln Leu Val Asn Ser
      260      265      270
Tyr Tyr Ala Ile His Asn Gly Gly Leu Phe Gly Val Gly Leu Gly Asn
      275      280      285
Ser Met Gln Lys Arg Gly Tyr Leu Pro Glu Pro Tyr Thr Asp Phe Ile
      290      295      300
Leu Ser Ile Thr Ala Glu Glu Ile Gly Val Ile Phe Thr Ile Val Leu
      305      310      315      320
Val Gly Leu Leu Phe Tyr Leu Met Trp Gln Ile Met Glu Val Gly Ile
      325      330      335
Asn Ala Val Ser Gln Phe Asp Ala Leu Ile Cys Phe Gly Val Thr Thr
      340      345      350
Ile Ile Phe Thr Glu Ala Leu Phe Asn Ile Gly Ala Val Leu Gly Leu
      355      360      365
Leu Pro Ile Thr Gly Val Thr Leu Pro Phe Ile Ser Tyr Gly Gly Ser
      370      375      380
Ser Met Ile Val Leu Thr Ala Ala Ile Gly Leu Val Leu Asn Val Ser
      385      390      395      400
Ala Asn Glu Lys Met Leu Lys Glu Lys Asp Glu Thr Ile Ala
      405      410

```

<210> 287

<211> 453

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 919

<220>

<221> CDS

<222> (1)...(453)

<400> 287

atg gaa agt tgg tta ttt ctt gca ttg att ttg gtt gta gca tta tta 48

Met Glu Ser Trp Leu Phe Leu Ala Leu Ile Leu Val Val Ala Leu Leu

1 5 10 15

ggc aag aac atg tct ttg att att gct aca gca gta gtt atg ctt ttt 96

Gly Lys Asn Met Ser Leu Ile Ile Ala Thr Ala Val Val Met Leu Phe

20 25 30

aaa tta tta cca ttt act gga aag tgg cta cct act att cag gct aaa 144

Lys Leu Leu Pro Phe Thr Gly Lys Trp Leu Pro Thr Ile Gln Ala Lys

35	40	45	
gga ata aat tgg gga gta act att att tct gtg gct att tta att ccg			192
Gly Ile Asn Trp Gly Val Thr Ile Ile Ser Val Ala Ile Leu Ile Pro			
50	55	60	
att gct act ggt caa ata ggt ttt aaa gat tta att aga aca ttc aaa			240
Ile Ala Thr Gly Gln Ile Gly Phe Lys Asp Leu Ile Arg Thr Phe Lys			
65	70	75	80
aca cca gct ggg tgg ata gct att ttg gct ggt ata gca gtt gct gtt			288
Thr Pro Ala Gly Trp Ile Ala Ile Leu Ala Gly Ile Ala Val Ala Val			
85	90	95	
tta tca aga tat ggt gtt aat caa ctt gct gca gtt cct caa gta acc			336
Leu Ser Arg Tyr Gly Val Asn Gln Leu Ala Ala Val Pro Gln Val Thr			
100	105	110	
gtt gct tta gta ctt gga acg att att ggg gtt gta gca ttt aaa ggc			384
Val Ala Leu Val Leu Gly Thr Ile Ile Gly Val Val Ala Phe Lys Gly			
115	120	125	
gta gct gct ggg cct gta att gcg agt gga atg aca tat tta gta gtt			432
Val Ala Ala Gly Pro Val Ile Ala Ser Gly Met Thr Tyr Leu Val Val			
130	135	140	
act ttg ttt aac ctg cat ttt			453
Thr Leu Phe Asn Leu His Phe			
145	150		

<210> 288

<211> 151

<212> PRT

<213> Lactobacillus acidophilus

<400> 288

Met Glu Ser Trp Leu Phe Leu Ala Leu Ile Leu Val Val Ala Leu Leu			
1	5	10	15
Gly Lys Asn Met Ser Leu Ile Ile Ala Thr Ala Val Val Met Leu Phe			
20	25	30	
Lys Leu Leu Pro Phe Thr Gly Lys Trp Leu Pro Thr Ile Gln Ala Lys			
35	40	45	
Gly Ile Asn Trp Gly Val Thr Ile Ile Ser Val Ala Ile Leu Ile Pro			
50	55	60	
Ile Ala Thr Gly Gln Ile Gly Phe Lys Asp Leu Ile Arg Thr Phe Lys			
65	70	75	80
Thr Pro Ala Gly Trp Ile Ala Ile Leu Ala Gly Ile Ala Val Ala Val			
85	90	95	
Leu Ser Arg Tyr Gly Val Asn Gln Leu Ala Ala Val Pro Gln Val Thr			
100	105	110	
Val Ala Leu Val Leu Gly Thr Ile Ile Gly Val Val Ala Phe Lys Gly			
115	120	125	
Val Ala Ala Gly Pro Val Ile Ala Ser Gly Met Thr Tyr Leu Val Val			
130	135	140	
Thr Leu Phe Asn Leu His Phe			
145	150		

<210> 289
 <211> 1353
 <212> DNA
 <213> *Lactobacillus acidophilus*

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 927 - membrane protein

<220>
 <221> CDS
 <222> (1)...(1353)

<400> 289
 ttg att tta cca atg gaa aat gaa cag gca cgt cga tta tca caa aaa 48
 Met Ile Leu Pro Met Glu Asn Glu Gln Ala Arg Arg Leu Ser Gln Lys
 1 5 10 15
 cat cat atg aag atc ctt tgg gag gat ttt ttt aaa agt gac gat gat 96
 His His Met Lys Ile Leu Trp Glu Asp Phe Phe Lys Ser Asp Asp Asp
 20 25 30
 acg ata gct caa gat gct act ttg gtt gaa aag aca tct att gtt gga 144
 Thr Ile Ala Gln Asp Ala Thr Leu Val Glu Lys Thr Ser Ile Val Gly
 35 40 45
 cga ata gga att atg ttg ctt agt tgc ggt act ggt gca tgg aga gtc 192
 Arg Ile Gly Ile Met Leu Leu Ser Cys Gly Thr Gly Ala Trp Arg Val
 50 55 60
 cgt gac tca atg gat aca gtt gct aga acg ctt ggt ata act tgt tca 240
 Arg Asp Ser Met Asp Thr Val Ala Arg Thr Leu Gly Ile Thr Cys Ser
 65 70 75 80
 aca gac att ggt ctg gtt tcg att gaa tat act tgc ttt gac gtt gat 288
 Thr Asp Ile Gly Leu Val Ser Ile Glu Tyr Thr Cys Phe Asp Val Asp
 85 90 95
 aat gaa tcc tat tca caa act ttg tct tta cca tct acc ggt gta aat 336
 Asn Glu Ser Tyr Ser Gln Thr Leu Ser Leu Pro Ser Thr Gly Val Asn
 100 105 110
 atg act aaa tta aat gaa tta gaa aaa tta att cgt caa ttt gaa aaa 384
 Met Thr Lys Leu Asn Glu Leu Glu Lys Leu Ile Arg Gln Phe Glu Lys
 115 120 125
 gaa cgt gga aat tgg aca ata ggt caa atc cat aaa aaa ttg cgt gag 432
 Glu Arg Gly Asn Trp Thr Ile Gly Gln Ile His Lys Lys Leu Arg Glu
 130 135 140
 att gaa aat caa aag tct gca tat ccg tct ata ata gca gta tta agc 480
 Ile Glu Asn Gln Lys Ser Ala Tyr Pro Ser Ile Ile Ala Val Leu Ser
 145 150 155 160

gca gga ctg gca tgt gct gga ttt atc ttt tta ttg ggt gga ggc cta	528
Ala Gly Leu Ala Cys Ala Gly Phe Ile Phe Leu Leu Gly Gly Gly Leu	
165 170 175	
ccc aag gtt atc tgt gca ttt ttt gga gcg ggt gtc ggt aac tat gtt	576
Pro Lys Val Ile Cys Ala Phe Phe Gly Ala Gly Val Gly Asn Tyr Val	
180 185 190	
cgc tca att atg gga aaa cga aaa att aca tta gtt gcc aag att gca	624
Arg Ser Ile Met Gly Lys Arg Lys Ile Thr Leu Val Ala Lys Ile Ala	
195 200 205	
gta gca gta gca ata gca tgg gct gtt tat ttt att tgt ttt cat att	672
Val Ala Val Ala Ile Ala Trp Ala Val Tyr Phe Ile Cys Phe His Ile	
210 215 220	
ggc atg ata tta ttt cac ttg gat tat cat cat gca tat ggc tat atc	720
Gly Met Ile Leu Phe His Leu Asp Tyr His His Ala Tyr Gly Tyr Ile	
225 230 235 240	
ggt gct atg ctg ttt gtt att cca ggt ttt cca ttt att aca tct ggt	768
Gly Ala Met Leu Phe Val Ile Pro Gly Phe Pro Phe Ile Thr Ser Gly	
245 250 255	
cta gat atg tct aaa tta gat atg aga tcg gga ctt gag cgt tta acg	816
Leu Asp Met Ser Lys Leu Asp Met Arg Ser Gly Leu Glu Arg Leu Thr	
260 265 270	
tat gca att tta gtc att att att gct act atg gct ggc tgg gct gta	864
Tyr Ala Ile Leu Val Ile Ile Ile Ala Thr Met Ala Gly Trp Ala Val	
275 280 285	
gca aca att ttg aat tta cat cca ggt tca atg cta aga ttg aaa att	912
Ala Thr Ile Leu Asn Leu His Pro Gly Ser Met Leu Arg Leu Lys Ile	
290 295 300	
gat ccc ggt atg tta acc ttt ttg agg tta att gca agc ttt tgt gga	960
Asp Pro Gly Met Leu Thr Phe Leu Arg Leu Ile Ala Ser Phe Cys Gly	
305 310 315 320	
gta ttt gga ttt tct att atg ttt aat agt cgt cct cca atg gca gca	1008
Val Phe Gly Phe Ser Ile Met Phe Asn Ser Arg Pro Pro Met Ala Ala	
325 330 335	
act gca gct att atg ggg gcg atg gct aat act ttg cgc tta agt tta	1056
Thr Ala Ala Ile Met Gly Ala Met Ala Asn Thr Leu Arg Leu Ser Leu	
340 345 350	
gtt gat tat gca cat atg gca cct gct ctt gca gca ttt att ggt gct	1104
Val Asp Tyr Ala His Met Ala Pro Ala Leu Ala Ala Phe Ile Gly Ala	
355 360 365	
tta acc gcg ggg ctg tta gca agt gtt gtt cgc caa aaa gtg gga ttt	1152
Leu Thr Ala Gly Leu Leu Ala Ser Val Val Arg Gln Lys Val Gly Phe	
370 375 380	

```

cct aga att gcc att aca gtt cca tca att gta att atg gta cca ggg 1200
Pro Arg Ile Ala Ile Thr Val Pro Ser Ile Val Ile Met Val Pro Gly
385                      390                      395                      400

ctt tat atg tat aga gct gtc ttt aat ttc gga gtc act aat att aat 1248
Leu Tyr Met Tyr Arg Ala Val Phe Asn Phe Gly Val Thr Asn Ile Asn
405                      410                      415

att ggt gct ttt tgg att act gaa gca ttg atg att gtt att gct ttg 1296
Ile Gly Ala Phe Trp Ile Thr Glu Ala Leu Met Ile Val Ile Ala Leu
420                      425                      430

cca ttg gga ctt tta gcg gca cgt ata ttg act gat aag aaa tgg cgt 1344
Pro Leu Gly Leu Leu Ala Ala Arg Ile Leu Thr Asp Lys Lys Trp Arg
435                      440                      445

cat gct gat 1353
His Ala Asp
450

```

<210> 290

<211> 451

<212> PRT

<213> Lactobacillus acidophilus

<400> 290

```

Met Ile Leu Pro Met Glu Asn Glu Gln Ala Arg Arg Leu Ser Gln Lys
1          5          10          15
His His Met Lys Ile Leu Trp Glu Asp Phe Phe Lys Ser Asp Asp Asp
20          25          30
Thr Ile Ala Gln Asp Ala Thr Leu Val Glu Lys Thr Ser Ile Val Gly
35          40          45
Arg Ile Gly Ile Met Leu Leu Ser Cys Gly Thr Gly Ala Trp Arg Val
50          55          60
Arg Asp Ser Met Asp Thr Val Ala Arg Thr Leu Gly Ile Thr Cys Ser
65          70          75          80
Thr Asp Ile Gly Leu Val Ser Ile Glu Tyr Thr Cys Phe Asp Val Asp
85          90          95
Asn Glu Ser Tyr Ser Gln Thr Leu Ser Leu Pro Ser Thr Gly Val Asn
100         105         110
Met Thr Lys Leu Asn Glu Leu Glu Lys Leu Ile Arg Gln Phe Glu Lys
115         120         125
Glu Arg Gly Asn Trp Thr Ile Gly Gln Ile His Lys Lys Leu Arg Glu
130         135         140
Ile Glu Asn Gln Lys Ser Ala Tyr Pro Ser Ile Ile Ala Val Leu Ser
145         150         155         160
Ala Gly Leu Ala Cys Ala Gly Phe Ile Phe Leu Leu Gly Gly Gly Leu
165         170         175
Pro Lys Val Ile Cys Ala Phe Phe Gly Ala Gly Val Gly Asn Tyr Val
180         185         190
Arg Ser Ile Met Gly Lys Arg Lys Ile Thr Leu Val Ala Lys Ile Ala
195         200         205
Val Ala Val Ala Ile Ala Trp Ala Val Tyr Phe Ile Cys Phe His Ile
210         215         220
Gly Met Ile Leu Phe His Leu Asp Tyr His His Ala Tyr Gly Tyr Ile
225         230         235         240

```

<400> 291																	
atg	aaa	aaa	tat	caa	ctt	tac	gca	aca	atg	ggc	gca	ggg	ttc	gaa	agc	48	
Met	Lys	Lys	Tyr	Gln	Leu	Tyr	Ala	Thr	Met	Gly	Ala	Gly	Phe	Glu	Ser		
1				5					10					15			
gtc	gta	aat	aaa	gaa	tta	caa	agt	atg	ggg	tat	aaa	acc	aag	gtt	gaa	96	
Val	Val	Asn	Lys	Glu	Leu	Gln	Ser	Met	Gly	Tyr	Lys	Thr	Lys	Val	Glu		
			20					25					30				
aat	ggg	cgt	gta	ttt	ttt	gaa	ggg	aca	caa	gaa	gac	att	gta	aaa	gta	144	
Asn	Gly	Arg	Val	Phe	Phe	Glu	Gly	Thr	Gln	Glu	Asp	Ile	Val	Lys	Val		
		35					40					45					

aat cta tgg tca aga aca gct gat cga atc aag att tta tta aag gaa	192
Asn Leu Trp Ser Arg Thr Ala Asp Arg Ile Lys Ile Leu Leu Lys Glu	
50 55 60	
ttt aag gca aca gat ttt agc act ttg ttt gat gaa gtt tat gct tat	240
Phe Lys Ala Thr Asp Phe Ser Thr Leu Phe Asp Glu Val Tyr Ala Tyr	
65 70 75 80	
gat tgg gca gaa tta ttg cca gtt gat gca aaa ttt cca gtt caa ggt	288
Asp Trp Ala Glu Leu Leu Pro Val Asp Ala Lys Phe Pro Val Gln Gly	
85 90 95	
aga gca gta aaa tcc aag ttg cat tca gag cct gat gta caa tct atc	336
Arg Ala Val Lys Ser Lys Leu His Ser Glu Pro Asp Val Gln Ser Ile	
100 105 110	
gta aaa aaa gca att gtt aat aag atg att gat caa tat cat cgc cgt	384
Val Lys Lys Ala Ile Val Asn Lys Met Ile Asp Gln Tyr His Arg Arg	
115 120 125	
ggg ttt tta cca gaa act ggt aac gaa tat cca tta gat atc cat att	432
Gly Phe Leu Pro Glu Thr Gly Asn Glu Tyr Pro Leu Asp Ile His Ile	
130 135 140	
tac aaa aat tta gct aga tta tca ttg gat act act gga gct agt tta	480
Tyr Lys Asn Leu Ala Arg Leu Ser Leu Asp Thr Thr Gly Ala Ser Leu	
145 150 155 160	
ttt aag cgt ggt tat aga att gaa cat ggt gga gct ccg atg aaa gaa	528
Phe Lys Arg Gly Tyr Arg Ile Glu His Gly Gly Ala Pro Met Lys Glu	
165 170 175	
aat ttt gct gca agt tta tta aag ctc act cct tat aac ggc acg cat	576
Asn Phe Ala Ala Ser Leu Leu Lys Leu Thr Pro Tyr Asn Gly Thr His	
180 185 190	
ccc ttg ata gat cca atg act gga tca ggt act tta gca att gag gct	624
Pro Leu Ile Asp Pro Met Thr Gly Ser Gly Thr Leu Ala Ile Glu Ala	
195 200 205	
gca ttg att gcc aaa aat att gca cct ggt acc tgg cgc aaa ttt gct	672
Ala Leu Ile Ala Lys Asn Ile Ala Pro Gly Thr Trp Arg Lys Phe Ala	
210 215 220	
ttt gat ggc ttc gat tgg ttt aat acc aat ctt cat aaa gaa gca tta	720
Phe Asp Gly Phe Asp Trp Phe Asn Thr Asn Leu His Lys Glu Ala Leu	
225 230 235 240	
gct aaa gca aaa gca gag gtc aaa tct tta gag gca ccc att tgg gct	768
Ala Lys Ala Lys Ala Glu Val Lys Ser Leu Glu Ala Pro Ile Trp Ala	
245 250 255	
agt gat att gat caa tca gtt ctt gaa att gct aaa ctt aat gca cat	816
Ser Asp Ile Asp Gln Ser Val Leu Glu Ile Ala Lys Leu Asn Ala His	
260 265 270	

```

aat gct gga gtt tta caa gat atc cgc ttt aaa caa gtt gca gta aaa      864
Asn Ala Gly Val Leu Gln Asp Ile Arg Phe Lys Gln Val Ala Val Lys
      275                      280                      285

gat ttc acc act gat tta gaa aat ggg att att ata gcc aat cca cca      912
Asp Phe Thr Thr Asp Leu Glu Asn Gly Ile Ile Ala Asn Pro Pro
      290                      295                      300

tat ggt aaa aga ctg aaa gat cgt gaa tct gcg gaa gaa ttg tat aaa      960
Tyr Gly Lys Arg Leu Lys Asp Arg Glu Ser Ala Glu Glu Leu Tyr Lys
      305                      310                      315                      320

caa atg gga gag gct tta aga ccg tta gat tca ttt agt caa tat tat      1008
Gln Met Gly Glu Ala Leu Arg Pro Leu Asp Ser Phe Ser Gln Tyr Tyr
      325                      330                      335

tta act gca gat cct aat ttt gaa aaa tac ttt ggt gct aaa gcc aca      1056
Leu Thr Ala Asp Pro Asn Phe Glu Lys Tyr Phe Gly Ala Lys Ala Thr
      340                      345                      350

aag aaa cgt aaa tta ttt aat ggt aat tta aga gtt gat ttc tat caa      1104
Lys Lys Arg Lys Leu Phe Asn Gly Asn Leu Arg Val Asp Phe Tyr Gln
      355                      360                      365

tat tgg gct aac aga agg                                          1122
Tyr Trp Ala Asn Arg Arg
      370

```

<210> 292

<211> 374

<212> PRT

<213> Lactobacillus acidophilus

<400> 292

```

Met Lys Lys Tyr Gln Leu Tyr Ala Thr Met Gly Ala Gly Phe Glu Ser
 1          5          10          15
Val Val Asn Lys Glu Leu Gln Ser Met Gly Tyr Lys Thr Lys Val Glu
      20          25          30
Asn Gly Arg Val Phe Phe Glu Gly Thr Gln Glu Asp Ile Val Lys Val
      35          40          45
Asn Leu Trp Ser Arg Thr Ala Asp Arg Ile Lys Ile Leu Leu Lys Glu
      50          55          60
Phe Lys Ala Thr Asp Phe Ser Thr Leu Phe Asp Glu Val Tyr Ala Tyr
      65          70          75          80
Asp Trp Ala Glu Leu Pro Val Asp Ala Lys Phe Pro Val Gln Ser Gly
      85          90          95
Arg Ala Val Lys Ser Lys Leu His Ser Glu Pro Asp Val Gln Ser Ile
      100         105         110
Val Lys Lys Ala Ile Val Asn Lys Met Ile Asp Gln Tyr His Arg Arg
      115         120         125
Gly Phe Leu Pro Glu Thr Gly Asn Glu Tyr Pro Leu Asp Ile His Ile
      130         135         140
Tyr Lys Asn Leu Ala Arg Leu Ser Leu Asp Thr Thr Gly Ala Ser Leu
      145         150         155         160
Phe Lys Arg Gly Tyr Arg Ile Glu His Gly Gly Ala Pro Met Lys Glu
      165         170         175

```

```
<210> 293
<211> 726
<212> DNA
<213> Lactobacillus acidophilus
```

```
<220>
<221> misc_feature
<222> (0)...(0)
<223> ORF 1287 - tRNA (guanine-N1)-methyltransferase
```

```
<220>  
<221> CDS  
<222> (1) ... (726)
```

<400> 293																	
atg	aag	att	aat	atc	ctg	acc	ctt	ttt	cct	gat	atg	ttt	acg	cca	ttg	48	
Met	Lys	Ile	Asn	Ile	Leu	Thr	Leu	Phe	Pro	Asp	Met	Phe	Thr	Pro	Leu		
1				5					10					15			
caa	gtt	tct	atg	ctg	gga	cgt	ggc	ctt	gaa	gat	ggc	aag	tgg	gat	ctc	96	
Gln	Val	Ser	Met	Leu	Gly	Arg	Gly	Leu	Glu	Asp	Gly	Lys	Trp	Asp	Leu		
			20					25					30				
aat	ttg	gtt	aat	ttc	cgt	gat	ttc	act	aca	gac	ctg	cat	cac	cat	gtt	144	
Asn	Leu	Val	Asn	Phe	Arg	Asp	Phe	Thr	Thr	Asp	Leu	His	His	His	Val		
		35					40					45					
gat	gat	acg	cca	tat	ggt	ggc	gga	gcg	gga	atg	gtg	ctt	caa	ata	atg	192	

Asp	Asp	Thr	Pro	Tyr	Gly	Gly	Gly	Ala	Gly	Met	Val	Leu	Gln	Ile	Met	
50						55					60					
ccg	att	aag	aaa	gca	ctt	gat	tca	ctt	cct	tct	act	ggc	aag	att	att	240
Pro	Ile	Lys	Lys	Ala	Leu	Asp	Ser	Leu	Pro	Ser	Thr	Gly	Lys	Ile	Ile	
65					70				75					80		
att	act	gca	cca	caa	ggc	aag	aca	ttt	aat	gaa	aaa	atg	gca	caa	gaa	288
Ile	Thr	Ala	Pro	Gln	Gly	Lys	Thr	Phe	Asn	Glu	Lys	Met	Ala	Gln	Glu	
				85					90					95		
tgg	gct	aag	gaa	gat	gaa	tta	act	ttt	att	tgt	ggc	cac	tac	gaa	ggg	336
Trp	Ala	Lys	Glu	Asp	Glu	Leu	Thr	Phe	Ile	Cys	Gly	His	Tyr	Glu	Gly	
			100					105					110			
ttt	gat	caa	cgt	gtt	tat	gat	ttg	gct	gat	gaa	act	gtt	tca	att	gga	384
Phe	Asp	Gln	Arg	Val	Tyr	Asp	Leu	Ala	Asp	Glu	Thr	Val	Ser	Ile	Gly	
		115					120					125				
gat	tat	gtt	tta	acc	ggc	gga	gaa	tta	cct	aca	atg	agt	atg	gtt	gat	432
Asp	Tyr	Val	Leu	Thr	Gly	Gly	Glu	Leu	Pro	Thr	Met	Ser	Met	Val	Asp	
		130				135					140					
gca	aca	gtt	aga	tta	tta	cca	ggc	att	tta	ggc	aat	tct	gct	tca	tca	480
Ala	Thr	Val	Arg	Leu	Leu	Pro	Gly	Ile	Leu	Gly	Asn	Ser	Ala	Ser	Ser	
145					150					155					160	
gtt	gaa	gaa	agt	ttc	tca	cat	ggc	tta	ctt	gag	tat	ccg	caa	tat	act	528
Val	Glu	Glu	Ser	Phe	Ser	His	Gly	Leu	Leu	Glu	Tyr	Pro	Gln	Tyr	Thr	
				165				170						175		
cgt	cca	gct	gat	ttc	gaa	gga	aaa	aaa	agt	gcc	aga	agt	ttt	aag	cca	576
Arg	Pro	Ala	Asp	Phe	Glu	Gly	Lys	Lys	Ser	Ala	Arg	Ser	Phe	Lys	Pro	
			180					185					190			
gtg	gta	atc	atc	aaa	aga	ttg	ctg	aat	ggc	gac	act	atc	agg	ctt	tta	624
Val	Val	Ile	Ile	Lys	Arg	Leu	Leu	Asn	Gly	Asp	Thr	Ile	Arg	Leu	Leu	
		195					200					205				
aag	gca	aca	tat	tta	cat	aga	cct	gat	atg	ctt	gaa	aat	cgc	aat	ctt	672
Lys	Ala	Thr	Tyr	Leu	His	Arg	Pro	Asp	Met	Leu	Glu	Asn	Arg	Asn	Leu	
		210				215					220					
tct	gat	gaa	gaa	aag	aaa	atg	ctg	caa	gaa	ata	aag	aat	gaa	atg	aat	720
Ser	Asp	Glu	Glu	Lys	Lys	Met	Leu	Gln	Glu	Ile	Lys	Asn	Glu	Met	Asn	
225					230				235					240		
gag	gat															726
Glu	Asp															

<210> 294

<211> 242

<212> PRT

<213> Lactobacillus acidophilus

<400> 294

```

Met Lys Ile Asn Ile Leu Thr Leu Phe Pro Asp Met Phe Thr Pro Leu
 1           5           10           15
Gln Val Ser Met Leu Gly Arg Gly Leu Glu Asp Gly Lys Trp Asp Leu
          20           25           30
Asn Leu Val Asn Phe Arg Asp Phe Thr Thr Asp Leu His His His Val
          35           40           45
Asp Asp Thr Pro Tyr Gly Gly Gly Ala Gly Met Val Leu Gln Ile Met
 50           55           60
Pro Ile Lys Lys Ala Leu Asp Ser Leu Pro Ser Thr Gly Lys Ile Ile
 65           70           75           80
Ile Thr Ala Pro Gln Gly Lys Thr Phe Asn Glu Lys Met Ala Gln Glu
          85           90           95
Trp Ala Lys Glu Asp Glu Leu Thr Phe Ile Cys Gly His Tyr Glu Gly
          100          105          110
Phe Asp Gln Arg Val Tyr Asp Leu Ala Asp Glu Thr Val Ser Ile Gly
          115          120          125
Asp Tyr Val Leu Thr Gly Gly Glu Leu Pro Thr Met Ser Met Val Asp
          130          135          140
Ala Thr Val Arg Leu Leu Pro Gly Ile Leu Gly Asn Ser Ala Ser Ser
 145          150          155          160
Val Glu Glu Ser Phe Ser His Gly Leu Leu Glu Tyr Pro Gln Tyr Thr
          165          170          175
Arg Pro Ala Asp Phe Glu Gly Lys Lys Ser Ala Arg Ser Phe Lys Pro
          180          185          190
Val Val Ile Ile Lys Arg Leu Leu Asn Gly Asp Thr Ile Arg Leu Leu
          195          200          205
Lys Ala Thr Tyr Leu His Arg Pro Asp Met Leu Glu Asn Arg Asn Leu
          210          215          220
Ser Asp Glu Glu Lys Lys Met Leu Gln Glu Ile Lys Asn Glu Met Asn
 225          230          235          240
Glu Asp

```

<210> 295

<211> 2001

<212> DNA

<213> *Lactobacillus acidophilus*

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1543 - theronyl-tRNA synthetase (EC 6.1.1.3)

<220>

<221> CDS

<222> (1)...(2001)

<400> 295

```

ttg ggt gga acc acg caa tta acg tcc cag tgc att gtc gca ctg gga   48
Met Gly Gly Thr Thr Gln Leu Thr Ser Gln Cys Ile Val Ala Leu Gly
 1           5           10           15

ttt ttt ttt gga ggt aat ttt atg agt ttt tca gtt act ttg cca gat   96
Phe Phe Phe Gly Gly Asn Phe Met Ser Phe Ser Val Thr Leu Pro Asp

```

20	25	30	
ggc tca aag aaa gaa ttc gac aag gct gtt tca gtt aaa gaa gta gct Gly Ser Lys Lys Glu Phe Asp Lys Ala Val Ser Val Lys Glu Val Ala 35 40 45			144
tca tca atc gct act tct ctt gga aag gct gct gtt ggt gct aag gta Ser Ser Ile Ala Thr Ser Leu Gly Lys Ala Ala Val Gly Ala Lys Val 50 55 60			192
aat ggt caa gtt aag cca ctt gat tac gaa att gat agt gat gtt gaa Asn Gly Gln Val Lys Pro Leu Asp Tyr Glu Ile Asp Ser Asp Val Glu 65 70 75 80			240
att gct atc att act gat aag gat gaa gaa gga tta gat atc tta aga Ile Ala Ile Ile Thr Asp Lys Asp Glu Gly Leu Asp Ile Leu Arg 85 90 95			288
gca act gca gct ttt gca ttt gaa gct gtt gct aag aag aag tac cca Ala Thr Ala Ala Phe Ala Phe Glu Ala Val Ala Lys Lys Lys Tyr Pro 100 105 110			336
gaa ctt cgt tta ggt caa cac gta gct gat gaa ggt ggc ttc tat gtt Glu Leu Arg Leu Gly Gln His Val Ala Asp Glu Gly Gly Phe Tyr Val 115 120 125			384
gat act gac aag aag gac caa att aag gtt act gaa ttg cca gaa ctt Asp Thr Asp Lys Lys Asp Gln Ile Lys Val Thr Glu Leu Pro Glu Leu 130 135 140			432
gaa aag gca atg gaa aag ctt att aag agt ggt caa cct att gaa cat Glu Lys Ala Met Glu Lys Leu Ile Lys Ser Gly Gln Pro Ile Glu His 145 150 155 160			480
gtt gta atg gac aag tca gaa ctt gaa gaa atg ttc aag gat gat cca Val Val Met Asp Lys Ser Glu Leu Glu Glu Met Phe Lys Asp Asp Pro 165 170 175			528
ttc aag agc gat ctt tta aag aag att gac tct gac aag gtt gat gct Phe Lys Ser Asp Leu Leu Lys Lys Ile Asp Ser Asp Lys Val Asp Ala 180 185 190			576
tac aaa tta ggt gac ttt gtg gac ttt ggc ttt gat gca tta tta cca Tyr Lys Leu Gly Asp Phe Val Asp Phe Gly Phe Asp Ala Leu Leu Pro 195 200 205			624
aac act ggt aaa att aag cac ttt aag ctt tta tca gta gct ggt gct Asn Thr Gly Lys Ile Lys His Phe Lys Leu Leu Ser Val Ala Gly Ala 210 215 220			672
tac tgg ctt ggt aag tca tca aac cct atg ctt caa aga att ttt ggt Tyr Trp Leu Gly Lys Ser Ser Asn Pro Met Leu Gln Arg Ile Phe Gly 225 230 235 240			720
act gca ttc ttc aag gaa gct gct tta aag gaa gac ttg aag cgt cgt Thr Ala Phe Phe Lys Glu Ala Ala Leu Lys Glu Asp Leu Lys Arg Arg 245 250 255			768

gct gaa att aag gaa cgt gac cac cgt act atc ggt cgt gac ctt gat	816
Ala Glu Ile Lys Glu Arg Asp His Arg Thr Ile Gly Arg Asp Leu Asp	
260 265 270	
ctc ttc ttc gta gat cct aag gtt ggt gca ggt ctt cct tac tgg atg	864
Leu Phe Phe Val Asp Pro Lys Val Gly Ala Gly Leu Pro Tyr Trp Met	
275 280 285	
cca aag ggt gct act att cgt cgt gtt gtt gaa cgt tac atc atc gat	912
Pro Lys Gly Ala Thr Ile Arg Arg Val Val Glu Arg Tyr Ile Ile Asp	
290 295 300	
cgt gaa gta gct gac ggt tac aag cac gtt tac act cca gta ctt atg	960
Arg Glu Val Ala Asp Gly Tyr Lys His Val Tyr Thr Pro Val Leu Met	
305 310 315 320	
aac ctt gat gct tac aag acg tca ggt cac tgg gca cac tat cgt gat	1008
Asn Leu Asp Ala Tyr Lys Thr Ser Gly His Trp Ala His Tyr Arg Asp	
325 330 335	
gac atg ttc cca cca atg gac atg ggt gat ggc gaa atg ctt gaa ctt	1056
Asp Met Phe Pro Pro Met Asp Met Gly Asp Gly Glu Met Leu Glu Leu	
340 345 350	
cgt cca atg aac tgc cca tca cat att caa att tac aag cac cac att	1104
Arg Pro Met Asn Cys Pro Ser His Ile Gln Ile Tyr Lys His His Ile	
355 360 365	
cgt tca tac cgt gat tta cca ctt cgt gtt gct gaa ctt ggt atg atg	1152
Arg Ser Tyr Arg Asp Leu Pro Leu Arg Val Ala Glu Leu Gly Met Met	
370 375 380	
cac aga tac gaa aaa tca ggt gct tta tct ggt ctt caa cgt gta cgt	1200
His Arg Tyr Glu Lys Ser Gly Ala Leu Ser Gly Leu Gln Arg Val Arg	
385 390 395 400	
gaa atg acc ttg aac gat ggt cac aca ttt gta gaa ctt gat caa gtt	1248
Glu Met Thr Leu Asn Asp Gly His Thr Phe Val Glu Leu Asp Gln Val	
405 410 415	
caa agc gaa ttt gct aag atc ttg aag ttg atc atg gac gta tac aga	1296
Gln Ser Glu Phe Ala Lys Ile Leu Lys Leu Ile Met Asp Val Tyr Arg	
420 425 430	
gac ttc gat att act gat tac tac ttc aga ctt tca tac cgt gat cca	1344
Asp Phe Asp Ile Thr Asp Tyr Tyr Phe Arg Leu Ser Tyr Arg Asp Pro	
435 440 445	
aag aac act gac aag tac ttt gca aat gat gaa atg tgg gaa aga agt	1392
Lys Asn Thr Asp Lys Tyr Phe Ala Asn Asp Glu Met Trp Glu Arg Ser	
450 455 460	
caa aag atg ctt aag ggt gct atg gat gac ctt ggc ctt gac tat gtt	1440
Gln Lys Met Leu Lys Gly Ala Met Asp Asp Leu Gly Leu Asp Tyr Val	
465 470 475 480	

gaa gct gaa ggt gaa gca gca ttc tat ggt cct aag ctt gat att caa 1488
 Glu Ala Glu Gly Glu Ala Ala Phe Tyr Gly Pro Lys Leu Asp Ile Gln
 485 490 495

act aag act gct ttg ggt aac gac gaa act atg tca act atc caa ctt 1536
 Thr Lys Thr Ala Leu Gly Asn Asp Glu Thr Met Ser Thr Ile Gln Leu
 500 505 510

gat ttc atg ctc cca gaa aga ttt ggc tta act tac gtt ggt aaa gat 1584
 Asp Phe Met Leu Pro Glu Arg Phe Gly Leu Thr Tyr Val Gly Lys Asp
 515 520 525

ggt gaa gaa cac cgt cca gtt atg gtt cac cgt ggt att gtt ggt act 1632
 Gly Glu Glu His Arg Pro Val Met Val His Arg Gly Ile Val Gly Thr
 530 535 540

atg gaa aga ttc att gct tac ctt act gaa atc tac aaa ggt gca ttc 1680
 Met Glu Arg Phe Ile Ala Tyr Leu Thr Glu Ile Tyr Lys Gly Ala Phe
 545 550 555 560

cca act tgg ctt gct cca gtt caa gct gaa atc atc cca gtt aac aat 1728
 Pro Thr Trp Leu Ala Pro Val Gln Ala Glu Ile Ile Pro Val Asn Asn
 565 570 575

gaa gct cat ggc gaa tat gca gaa aag gtt cgt caa gaa ctt gct aag 1776
 Glu Ala His Gly Glu Tyr Ala Glu Lys Val Arg Gln Glu Leu Ala Lys
 580 585 590

cgc ggc ttc aga gta gaa gtt gat gat aga aac gaa aag atg ggt tac 1824
 Arg Gly Phe Arg Val Glu Val Asp Asp Arg Asn Glu Lys Met Gly Tyr
 595 600 605

aag att cgt gaa tca caa act caa aaa gta cct tac act tta gta tta 1872
 Lys Ile Arg Glu Ser Gln Thr Gln Lys Val Pro Tyr Thr Leu Val Leu
 610 615 620

ggt gac gaa gaa atg aag aac ggt agc gtt aac gta cgt cgt tac ggt 1920
 Gly Asp Glu Glu Met Lys Asn Gly Ser Val Asn Val Arg Arg Tyr Gly
 625 630 635 640

act gat gaa gaa att tct aag agt ctt gat gac ttc att aat gaa att 1968
 Thr Asp Glu Glu Ile Ser Lys Ser Leu Asp Asp Phe Ile Asn Glu Ile
 645 650 655

gat gct gac gtt aag tca tac tca aga gaa aac 2001
 Asp Ala Asp Val Lys Ser Tyr Ser Arg Glu Asn
 660 665

<210> 296

<211> 667

<212> PRT

<213> Lactobacillus acidophilus

<400> 296

Met Gly Gly Thr Thr Gln Leu Thr Ser Gln Cys Ile Val Ala Leu Gly

1 5 10 15

Phe	Phe	Phe	Gly	Gly	Asn	Phe	Met	Ser	Phe	Ser	Val	Thr	Leu	Pro	Asp
			20					25					30		
Gly	Ser	Lys	Lys	Glu	Phe	Asp	Lys	Ala	Val	Ser	Val	Lys	Glu	Val	Ala
		35					40					45			
Ser	Ser	Ile	Ala	Thr	Ser	Leu	Gly	Lys	Ala	Ala	Val	Gly	Ala	Lys	Val
	50					55					60				
Asn	Gly	Gln	Val	Lys	Pro	Leu	Asp	Tyr	Glu	Ile	Asp	Ser	Asp	Val	Glu
65					70					75				80	
Ile	Ala	Ile	Ile	Thr	Asp	Lys	Asp	Glu	Glu	Gly	Leu	Asp	Ile	Leu	Arg
				85					90					95	
Ala	Thr	Ala	Ala	Phe	Ala	Phe	Glu	Ala	Val	Ala	Lys	Lys	Lys	Tyr	Pro
			100					105						110	
Glu	Leu	Arg	Leu	Gly	Gln	His	Val	Ala	Asp	Glu	Gly	Gly	Phe	Tyr	Val
		115				120						125			
Asp	Thr	Asp	Lys	Lys	Asp	Gln	Ile	Lys	Val	Thr	Glu	Leu	Pro	Glu	Leu
	130					135					140				
Glu	Lys	Ala	Met	Glu	Lys	Leu	Ile	Lys	Ser	Gly	Gln	Pro	Ile	Glu	His
145					150					155				160	
Val	Val	Met	Asp	Lys	Ser	Glu	Leu	Glu	Glu	Met	Phe	Lys	Asp	Asp	Pro
			165						170					175	
Phe	Lys	Ser	Asp	Leu	Leu	Lys	Lys	Ile	Asp	Ser	Asp	Lys	Val	Asp	Ala
			180					185					190		
Tyr	Lys	Leu	Gly	Asp	Phe	Val	Asp	Phe	Gly	Phe	Asp	Ala	Leu	Leu	Pro
		195					200					205			
Asn	Thr	Gly	Lys	Ile	Lys	His	Phe	Lys	Leu	Leu	Ser	Val	Ala	Gly	Ala
	210					215						220			
Tyr	Trp	Leu	Gly	Lys	Ser	Ser	Asn	Pro	Met	Leu	Gln	Arg	Ile	Phe	Gly
225					230					235				240	
Thr	Ala	Phe	Phe	Lys	Glu	Ala	Ala	Leu	Lys	Glu	Asp	Leu	Lys	Arg	Arg
			245						250					255	
Ala	Glu	Ile	Lys	Glu	Arg	Asp	His	Arg	Thr	Ile	Gly	Arg	Asp	Leu	Asp
			260					265					270		
Leu	Phe	Phe	Val	Asp	Pro	Lys	Val	Gly	Ala	Gly	Leu	Pro	Tyr	Trp	Met
	275						280					285			
Pro	Lys	Gly	Ala	Thr	Ile	Arg	Arg	Val	Val	Glu	Arg	Tyr	Ile	Ile	Asp
	290					295					300				
Arg	Glu	Val	Ala	Asp	Gly	Tyr	Lys	His	Val	Tyr	Thr	Pro	Val	Leu	Met
305					310					315				320	
Asn	Leu	Asp	Ala	Tyr	Lys	Thr	Ser	Gly	His	Trp	Ala	His	Tyr	Arg	Asp
			325						330					335	
Asp	Met	Phe	Pro	Pro	Met	Asp	Met	Gly	Asp	Gly	Glu	Met	Leu	Glu	Leu
			340					345					350		
Arg	Pro	Met	Asn	Cys	Pro	Ser	His	Ile	Gln	Ile	Tyr	Lys	His	His	Ile
		355					360					365			
Arg	Ser	Tyr	Arg	Asp	Leu	Pro	Leu	Arg	Val	Ala	Glu	Leu	Gly	Met	Met
	370					375					380				
His	Arg	Tyr	Glu	Lys	Ser	Gly	Ala	Leu	Ser	Gly	Leu	Gln	Arg	Val	Arg
385					390					395				400	
Glu	Met	Thr	Leu	Asn	Asp	Gly	His	Thr	Phe	Val	Glu	Leu	Asp	Gln	Val
			405						410					415	
Gln	Ser	Glu	Phe	Ala	Lys	Ile	Leu	Lys	Leu	Ile	Met	Asp	Val	Tyr	Arg
			420					425					430		
Asp	Phe	Asp	Ile	Thr	Asp	Tyr	Tyr	Phe	Arg	Leu	Ser	Tyr	Arg	Asp	Pro
		435					440					445			
Lys	Asn	Thr	Asp	Lys	Tyr	Phe	Ala	Asn	Asp	Glu	Met	Trp	Glu	Arg	Ser
	450					455					460				
Gln	Lys	Met	Leu	Lys	Gly	Ala	Met	Asp	Asp	Leu	Gly	Leu	Asp	Tyr	Val

```

465          470          475          480
Glu Ala Glu Gly Glu Ala Ala Phe Tyr Gly Pro Lys Leu Asp Ile Gln
          485          490          495
Thr Lys Thr Ala Leu Gly Asn Asp Glu Thr Met Ser Thr Ile Gln Leu
          500          505          510
Asp Phe Met Leu Pro Glu Arg Phe Gly Leu Thr Tyr Val Gly Lys Asp
          515          520          525
Gly Glu Glu His Arg Pro Val Met Val His Arg Gly Ile Val Gly Thr
          530          535          540
Met Glu Arg Phe Ile Ala Tyr Leu Thr Glu Ile Tyr Lys Gly Ala Phe
545          550          555          560
Pro Thr Trp Leu Ala Pro Val Gln Ala Glu Ile Ile Pro Val Asn Asn
          565          570          575
Glu Ala His Gly Glu Tyr Ala Glu Lys Val Arg Gln Glu Leu Ala Lys
          580          585          590
Arg Gly Phe Arg Val Glu Val Asp Asp Arg Asn Glu Lys Met Gly Tyr
          595          600          605
Lys Ile Arg Glu Ser Gln Thr Gln Lys Val Pro Tyr Thr Leu Val Leu
          610          615          620
Gly Asp Glu Glu Met Lys Asn Gly Ser Val Asn Val Arg Arg Tyr Gly
625          630          635          640
Thr Asp Glu Glu Ile Ser Lys Ser Leu Asp Asp Phe Ile Asn Glu Ile
          645          650          655
Asp Ala Asp Val Lys Ser Tyr Ser Arg Glu Asn
          660          665

```

<210> 297
 <211> 2118
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1654 - surface protein

<220>
 <221> CDS
 <222> (1)...(2118)

```

<400> 297
gtg tca tat aat gta tac aag gaa gga aaa gga tat att att atg tac   48
Met Ser Tyr Asn Val Tyr Lys Glu Gly Lys Gly Tyr Ile Ile Met Tyr
  1          5          10          15

tac gga ggt act aaa atg gtt aag aca aag aag acg caa ttt gct att   96
Tyr Gly Gly Thr Lys Met Val Lys Thr Lys Lys Thr Gln Phe Ala Ile
          20          25          30

cgc aaa ttg gct aag ggt gct gtt gca gtg tta tta agt ttc ggc ata   144
Arg Lys Leu Ala Lys Gly Ala Val Ala Val Leu Leu Ser Phe Gly Ile
          35          40          45

cta gct ggt cct agt gcg cca att gtc tca gca gcc tct gaa gca att   192
Leu Ala Gly Pro Ser Ala Pro Ile Val Ser Ala Ala Ser Glu Ala Ile

```

50	55	60	
caa aat gaa atg aca gat gat aca act tca gta gta gaa gaa agt gtc Gln Asn Glu Met Thr Asp Asp Thr Thr Ser Val Val Glu Glu Ser Val 65 70 75 80			240
cct gta gaa aat aat aca gca gac act tta act act gat aat act gga Pro Val Glu Asn Asn Thr Ala Asp Thr Leu Thr Thr Asp Asn Thr Gly 85 90 95			288
gtt tca gct aat tac tct gaa aat act gat gat agt act aca act act Val Ser Ala Asn Tyr Ser Glu Asn Thr Asp Asp Ser Thr Thr Thr Thr 100 105 110			336
gtg caa act gat aca gat gta tct act caa gaa aaa aca gat cca gta Val Gln Thr Asp Thr Asp Val Ser Thr Gln Glu Lys Thr Asp Pro Val 115 120 125			384
aca tct gtt aat act gag caa cca gtt caa aca gaa gaa gct gaa agt Thr Ser Val Asn Thr Glu Gln Pro Val Gln Thr Glu Glu Ala Glu Ser 130 135 140			432
act act cca gtt gaa gat gta aat tca aaa tct gaa gaa aat gta tct Thr Thr Pro Val Glu Asp Val Asn Ser Lys Ser Glu Glu Asn Val Ser 145 150 155 160			480
caa aat aat aat att aat act tct acc gaa gat aca aat tcg act aat Gln Asn Asn Asn Ile Asn Thr Ser Thr Glu Asp Thr Asn Ser Thr Asn 165 170 175			528
act gaa gca gaa gtg aac aaa aat act act tct aaa gaa gat aca aat Thr Glu Ala Glu Val Asn Lys Asn Thr Thr Ser Lys Glu Asp Thr Asn 180 185 190			576
aaa aaa gat aaa cca aat att aat gaa atg acc aag gaa gaa ttg gca Lys Lys Asp Lys Pro Asn Ile Asn Glu Met Thr Lys Glu Glu Leu Ala 195 200 205			624
aat cat att aaa gat ttg gca aat aaa cat cct tta ggt atc gct ggt Asn His Ile Lys Asp Leu Ala Asn Lys His Pro Leu Gly Ile Ala Gly 210 215 220			672
atc ttc cat att ttc ggt aat gaa gtg act caa aat ggt cgt att gca Ile Phe His Ile Phe Gly Asn Glu Val Thr Gln Asn Gly Arg Ile Ala 225 230 235 240			720
ggg aat att gct aca gat aaa ctt tct ggt aca aat ttt ggt acc aat Gly Asn Ile Ala Thr Asp Lys Leu Ser Gly Thr Asn Phe Gly Thr Asn 245 250 255			768
tca aat gca acc aat aat tta acc aac ggt gat atc cac tat gtt ggc Ser Asn Ala Thr Asn Asn Leu Thr Asn Gly Asp Ile His Tyr Val Gly 260 265 270			816
aat ctc aat gga ctt aac aaa atc gac ggt gac aac aaa gta gtc atc Asn Leu Asn Gly Leu Asn Lys Ile Asp Gly Asp Asn Lys Val Val Ile 275 280 285			864

ttt gga cca gac att gaa tac cgt tca ttt gag aat gat gga gca att	912
Phe Gly Pro Asp Ile Glu Tyr Arg Ser Phe Glu Asn Asp Gly Ala Ile	
290 295 300	
gaa gtt aac tat gga act gct gaa aaa cct gac tgg aga aaa gta gat	960
Glu Val Asn Tyr Gly Thr Ala Glu Lys Pro Asp Trp Arg Lys Val Asp	
305 310 315 320	
att cct tat aac cac att gtt caa gct gat caa aaa att aat att caa	1008
Ile Pro Tyr Asn His Ile Val Gln Ala Asp Gln Lys Ile Asn Ile Gln	
325 330 335	
ggc gaa cta gat aaa tta agt caa aag tca gat aac tgg gct agt caa	1056
Gly Glu Leu Asp Lys Leu Ser Gln Lys Ser Asp Asn Trp Ala Ser Gln	
340 345 350	
gca cag act gaa gga gtt aaa gcc gat ttt agt act gac aat agt tgg	1104
Ala Gln Thr Glu Gly Val Lys Ala Asp Phe Ser Thr Asp Asn Ser Trp	
355 360 365	
atc gat gtt tct gaa gct ata aag aat gct ggc gac aat aag gaa cct	1152
Ile Asp Val Ser Glu Ala Ile Lys Asn Ala Gly Asp Asn Lys Glu Pro	
370 375 380	
att tac gta aca att gat gcc gca cac ctt tca ggc gac aaa cgt aat	1200
Ile Tyr Val Thr Ile Asp Ala Ala His Leu Ser Gly Asp Lys Arg Asn	
385 390 395 400	
att acg atc aaa ggt att cct gct ggt gct gaa gct cca atg att att	1248
Ile Thr Ile Lys Gly Ile Pro Ala Gly Ala Glu Ala Pro Met Ile Ile	
405 410 415	
tta aat gta act aat att caa ggt gga gat tta aca gtt caa act cac	1296
Leu Asn Val Thr Asn Ile Gln Gly Gly Asp Leu Thr Val Gln Thr His	
420 425 430	
ctc gta ctg gaa tat gct gat ggt aat aat att ggt ggt tct tct gaa	1344
Leu Val Leu Glu Tyr Ala Asp Gly Asn Asn Ile Gly Gly Ser Ser Glu	
435 440 445	
act cca act caa ttt aat aaa ttg ctc tgg aac ttc ggt aca gat gtt	1392
Thr Pro Thr Gln Phe Asn Lys Leu Leu Trp Asn Phe Gly Thr Asp Val	
450 455 460	
aat aaa tta cat ttt gct aga gac tac cat ttg gga agt gtt cta gca	1440
Asn Lys Leu His Phe Ala Arg Asp Tyr His Leu Gly Ser Val Leu Ala	
465 470 475 480	
acc aac gct cat att aca aat gct gtt aat att gac ggt aat att att	1488
Thr Asn Ala His Ile Thr Asn Ala Val Asn Ile Asp Gly Asn Ile Ile	
485 490 495	
ggt aac aaa gtt act gtt agt ggt gaa aca cac cgt tgg gac tta aca	1536
Gly Asn Lys Val Thr Val Ser Gly Glu Thr His Arg Trp Asp Leu Thr	
500 505 510	

ccg cca ttc gta gaa att gaa gaa cct gaa aag cct aag cct gag cct	1584
Pro Pro Phe Val Glu Ile Glu Glu Pro Glu Lys Pro Lys Pro Glu Pro	
515 520 525	
aaa cca gat ccc gaa ccg aag ccg aag cct aag cct gac cct gag cca	1632
Lys Pro Asp Pro Glu Pro Lys Pro Lys Pro Lys Pro Asp Pro Glu Pro	
530 535 540	
gag cca gag cct gaa aat cca act cca gat act cct gct cca caa cct	1680
Glu Pro Glu Pro Glu Asn Pro Thr Pro Asp Thr Pro Ala Pro Gln Pro	
545 550 555 560	
aaa cca gag gaa act cct gac aat aca gaa gat ttt act cct cca tta	1728
Lys Pro Glu Glu Thr Pro Asp Asn Thr Glu Asp Phe Thr Pro Pro Leu	
565 570 575	
act gta gat gta ctg gat cca gat ggt aca gat gaa aat gaa aca cca	1776
Thr Val Asp Val Leu Asp Pro Asp Gly Thr Asp Glu Asn Glu Thr Pro	
580 585 590	
gct gga gaa gaa tca aca gaa gaa gaa gct att gct cca ctt cct gaa	1824
Ala Gly Glu Glu Ser Thr Glu Glu Glu Ala Ile Ala Pro Leu Pro Glu	
595 600 605	
aat gta atc gaa aaa aat caa aaa gaa gta act tct tcc aag tct acg	1872
Asn Val Ile Glu Lys Asn Gln Lys Glu Val Thr Ser Ser Lys Ser Thr	
610 615 620	
gta act cct act cct gta acc gag aaa tct ggt gaa aca aca act aaa	1920
Val Thr Pro Thr Pro Val Thr Glu Lys Ser Gly Glu Thr Thr Thr Lys	
625 630 635 640	
ccg aaa gca gaa gta aaa aat gaa act gta act gca act gaa acc aca	1968
Pro Lys Ala Glu Val Lys Asn Glu Thr Val Thr Ala Thr Glu Thr Thr	
645 650 655	
aaa gaa gtt gga ctt cca gaa acc ggt gaa gat aaa act aac ctc att	2016
Lys Glu Val Gly Leu Pro Glu Thr Gly Glu Asp Lys Thr Asn Leu Ile	
660 665 670	
act ata ggc att tgt ttt agc aag tat tgc tgc aac aat cac ggc att	2064
Thr Ile Gly Ile Cys Phe Ser Lys Tyr Cys Cys Asn Asn His Gly Ile	
675 680 685	
agg ctc att cat caa caa gaa aaa gaa aaa tta act aaa aat aag cat	2112
Arg Leu Ile His Gln Gln Glu Lys Glu Lys Leu Thr Lys Asn Lys His	
690 695 700	
cta aaa	2118
Leu Lys	
705	

<210> 298

<211> 706

<212> PRT

<213> Lactobacillus acidophilus

<400> 298

```

Met Ser Tyr Asn Val Tyr Lys Glu Gly Lys Gly Tyr Ile Ile Met Tyr
 1          5          10          15
Tyr Gly Gly Thr Lys Met Val Lys Thr Lys Lys Thr Gln Phe Ala Ile
          20          25          30
Arg Lys Leu Ala Lys Gly Ala Val Ala Val Leu Leu Ser Phe Gly Ile
          35          40          45
Leu Ala Gly Pro Ser Ala Pro Ile Val Ser Ala Ala Ser Glu Ala Ile
          50          55          60
Gln Asn Glu Met Thr Asp Asp Thr Thr Ser Val Val Glu Glu Ser Val
65          70          75          80
Pro Val Glu Asn Asn Thr Ala Asp Thr Leu Thr Thr Asp Asn Thr Gly
          85          90          95
Val Ser Ala Asn Tyr Ser Glu Asn Thr Asp Asp Ser Thr Thr Thr Thr
          100          105          110
Val Gln Thr Asp Thr Asp Val Ser Thr Gln Glu Lys Thr Asp Pro Val
          115          120          125
Thr Ser Val Asn Thr Glu Gln Pro Val Gln Thr Glu Glu Ala Glu Ser
130          135          140
Thr Thr Pro Val Glu Asp Val Asn Ser Lys Ser Glu Glu Asn Val Ser
145          150          155          160
Gln Asn Asn Asn Ile Asn Thr Ser Thr Glu Asp Thr Asn Ser Thr Asn
          165          170          175
Thr Glu Ala Glu Val Asn Lys Asn Thr Thr Ser Lys Glu Asp Thr Asn
          180          185          190
Lys Lys Asp Lys Pro Asn Ile Asn Glu Met Thr Lys Glu Glu Leu Ala
195          200          205
Asn His Ile Lys Asp Leu Ala Asn Lys His Pro Leu Gly Ile Ala Gly
210          215          220
Ile Phe His Ile Phe Gly Asn Glu Val Thr Gln Asn Gly Arg Ile Ala
225          230          235          240
Gly Asn Ile Ala Thr Asp Lys Leu Ser Gly Thr Asn Phe Gly Thr Asn
          245          250          255
Ser Asn Ala Thr Asn Asn Leu Thr Asn Gly Asp Ile His Tyr Val Gly
          260          265          270
Asn Leu Asn Gly Leu Asn Lys Ile Asp Gly Asp Asn Lys Val Val Ile
          275          280          285
Phe Gly Pro Asp Ile Glu Tyr Arg Ser Phe Glu Asn Asp Gly Ala Ile
290          295          300
Glu Val Asn Tyr Gly Thr Ala Glu Lys Pro Asp Trp Arg Lys Val Asp
305          310          315          320
Ile Pro Tyr Asn His Ile Val Gln Ala Asp Gln Lys Ile Asn Ile Gln
          325          330          335
Gly Glu Leu Asp Lys Leu Ser Gln Lys Ser Asp Asn Trp Ala Ser Gln
          340          345          350
Ala Gln Thr Glu Gly Val Lys Ala Asp Phe Ser Thr Asp Asn Ser Trp
          355          360          365
Ile Asp Val Ser Glu Ala Ile Lys Asn Ala Gly Asp Asn Lys Glu Pro
          370          375          380
Ile Tyr Val Thr Ile Asp Ala Ala His Leu Ser Gly Asp Lys Arg Asn
385          390          395          400
Ile Thr Ile Lys Gly Ile Pro Ala Gly Ala Glu Ala Pro Met Ile Ile
          405          410          415
Leu Asn Val Thr Asn Ile Gln Gly Gly Asp Leu Thr Val Gln Thr His
          420          425          430
Leu Val Leu Glu Tyr Ala Asp Gly Asn Asn Ile Gly Gly Ser Ser Glu

```

```

      435              440              445
Thr Pro Thr Gln Phe Asn Lys Leu Leu Trp Asn Phe Gly Thr Asp Val
      450              455              460
Asn Lys Leu His Phe Ala Arg Asp Tyr His Leu Gly Ser Val Leu Ala
465              470              475              480
Thr Asn Ala His Ile Thr Asn Ala Val Asn Ile Asp Gly Asn Ile Ile
      485              490              495
Gly Asn Lys Val Thr Val Ser Gly Glu Thr His Arg Trp Asp Leu Thr
      500              505              510
Pro Pro Phe Val Glu Ile Glu Glu Pro Glu Lys Pro Lys Pro Glu Pro
      515              520              525
Lys Pro Asp Pro Glu Pro Lys Pro Lys Pro Lys Pro Asp Pro Glu Pro
      530              535              540
Glu Pro Glu Pro Glu Asn Pro Thr Pro Asp Thr Pro Ala Pro Gln Pro
545              550              555              560
Lys Pro Glu Glu Thr Pro Asp Asn Thr Glu Asp Phe Thr Pro Pro Leu
      565              570              575
Thr Val Asp Val Leu Asp Pro Asp Gly Thr Asp Glu Asn Glu Thr Pro
      580              585              590
Ala Gly Glu Glu Ser Thr Glu Glu Glu Ala Ile Ala Pro Leu Pro Glu
      595              600              605
Asn Val Ile Glu Lys Asn Gln Lys Glu Val Thr Ser Ser Lys Ser Thr
      610              615              620
Val Thr Pro Thr Pro Val Thr Glu Lys Ser Gly Glu Thr Thr Thr Lys
625              630              635              640
Pro Lys Ala Glu Val Lys Asn Glu Thr Val Thr Ala Thr Glu Thr Thr
      645              650              655
Lys Glu Val Gly Leu Pro Glu Thr Gly Glu Asp Lys Thr Asn Leu Ile
      660              665              670
Thr Ile Gly Ile Cys Phe Ser Lys Tyr Cys Cys Asn Asn His Gly Ile
      675              680              685
Arg Leu Ile His Gln Gln Glu Lys Glu Lys Leu Thr Lys Asn Lys His
      690              695              700
Leu Lys
705

```

<210> 299

<211> 1314

<212> DNA

<213> Lactobacillus acidophilus

<220>

<221> misc_feature

<222> (0)...(0)

<223> ORF 1793 - transport accessory protein

<220>

<221> CDS

<222> (1)...(1314)

<400> 299

```

atg aat aag aaa aat gta tca atg cta atg tta agt cca gca atc tta 48
Met Asn Lys Lys Asn Val Ser Met Leu Met Leu Ser Pro Ala Ile Leu
  1              5              10              15

```

tta atg atg aat agt act att gtg cat gcg gat aaa ggt agt act tct	96
Leu Met Met Asn Ser Thr Ile Val His Ala Asp Lys Gly Ser Thr Ser	
20 25 30	
cat gag att agt agt aaa gta gta tct aaa aca aaa aat gat gat aaa	144
His Glu Ile Ser Ser Lys Val Val Ser Lys Thr Lys Asn Asp Asp Lys	
35 40 45	
aat gtt cct gaa tcc gag caa gaa act agt agt aat aac gaa att gat	192
Asn Val Pro Glu Ser Glu Gln Glu Thr Ser Ser Asn Asn Glu Ile Asp	
50 55 60	
caa tct caa gat aag cag gaa aaa gaa gaa caa gca att cct gaa gat	240
Gln Ser Gln Asp Lys Gln Glu Lys Glu Glu Gln Ala Ile Pro Glu Asp	
65 70 75 80	
caa aat gat caa tct cag aat aca aat aat caa gat cct aat gac gca	288
Gln Asn Asp Gln Ser Gln Asn Thr Asn Asn Gln Asp Pro Asn Asp Ala	
85 90 95	
agt gaa gaa gat gat gaa gat gaa gta tct gtt gaa gat tat gaa aac	336
Ser Glu Glu Asp Asp Glu Asp Glu Val Ser Val Glu Asp Tyr Glu Asn	
100 105 110	
aat gta aaa gat ttt cat aga gtg aaa atg caa gag gtg aaa gat ctt	384
Asn Val Lys Asp Phe His Arg Val Lys Met Gln Glu Val Lys Asp Leu	
115 120 125	
cta gca gag aaa aat aat caa gaa cat ctt atg tac att ggt cgc cca	432
Leu Ala Glu Lys Asn Asn Gln Glu His Leu Met Tyr Ile Gly Arg Pro	
130 135 140	
aca tgt tat tac tgc cga caa ttt tca cct gat tta aaa gat ttc aat	480
Thr Cys Tyr Tyr Cys Arg Gln Phe Ser Pro Asp Leu Lys Asp Phe Asn	
145 150 155 160	
gaa atc gtt aaa ggt aag ctg ctt tat ttc aat att gat gat gaa gaa	528
Glu Ile Val Lys Gly Lys Leu Leu Tyr Phe Asn Ile Asp Asp Glu Glu	
165 170 175	
gga gca cat gat tat gct ttt aag gtt att ggt att cca gga aca cct	576
Gly Ala His Asp Tyr Ala Phe Lys Val Ile Gly Ile Pro Gly Thr Pro	
180 185 190	
aca acg atg aga ttt atg aat gga aaa ttg ata agt gct tgg ata ggt	624
Thr Thr Met Arg Phe Met Asn Gly Lys Leu Ile Ser Ala Trp Ile Gly	
195 200 205	
gga gaa aaa aca gga caa gag cta cat gat ttt ttg tat tct gac aca	672
Gly Glu Lys Thr Gly Gln Glu Leu His Asp Phe Leu Tyr Ser Asp Thr	
210 215 220	
gct aat aaa tta gta gaa cag gtt gta att aaa aat caa tcg aat gat	720
Ala Asn Lys Leu Val Glu Gln Val Val Ile Lys Asn Gln Ser Asn Asp	
225 230 235 240	
acg gct act caa gca gat aat gat gtc gtt gca tct gag agc gat aaa	768

Thr	Ala	Thr	Gln	Ala	Asp	Asn	Asp	Val	Val	Ala	Ser	Glu	Ser	Asp	Lys	
				245					250					255		
aca	cct	gaa	gtg	act	gta	gag	gaa	aat	aat	caa	gcg	cag	tct	aat	aat	816
Thr	Pro	Glu	Val	Thr	Val	Glu	Glu	Asn	Asn	Gln	Ala	Gln	Ser	Asn	Asn	
			260					265					270			
gat	gtc	gct	att	act	aac	ttc	gct	gag	aat	agt	gta	ttt	gaa	aat	gct	864
Asp	Val	Ala	Ile	Thr	Asn	Phe	Ala	Glu	Asn	Ser	Val	Phe	Glu	Asn	Ala	
		275					280					285				
aaa	aat	gtt	gct	agt	tct	act	gcg	gat	tta	act	caa	gta	gcg	acg	ggc	912
Lys	Asn	Val	Ala	Ser	Ser	Thr	Ala	Asp	Leu	Thr	Gln	Val	Ala	Thr	Gly	
	290					295					300					
gat	caa	gat	gat	gta	gct	cct	aaa	gct	gaa	act	aaa	aat	aaa	act	gtg	960
Asp	Gln	Asp	Asp	Val	Ala	Pro	Lys	Ala	Glu	Thr	Lys	Asn	Lys	Thr	Val	
305				310						315					320	
aag	aaa	cca	ata	aaa	cat	aaa	att	gta	gcc	aat	aag	gtt	aag	aaa	caa	1008
Lys	Lys	Pro	Ile	Lys	His	Lys	Ile	Val	Ala	Asn	Lys	Val	Lys	Lys	Gln	
			325					330						335		
gct	aaa	ttg	cat	aag	acg	aat	att	att	ata	cct	atg	tcc	gct	aaa	aaa	1056
Ala	Lys	Leu	His	Lys	Thr	Asn	Ile	Ile	Ile	Pro	Met	Ser	Ala	Lys	Lys	
			340				345						350			
cgt	gaa	gat	gta	aaa	gaa	aat	aat	caa	tat	gat	acg	gta	aaa	gta	cac	1104
Arg	Glu	Asp	Val	Lys	Glu	Asn	Asn	Gln	Tyr	Asp	Thr	Val	Lys	Val	His	
	355					360						365				
ggc	aca	tct	cct	aat	gca	att	aag	gac	aaa	caa	gct	aga	att	act	atg	1152
Gly	Thr	Ser	Pro	Asn	Ala	Ile	Lys	Asp	Lys	Gln	Ala	Arg	Ile	Thr	Met	
	370				375					380						
ttg	aag	gaa	ctt	gag	aat	gat	act	tca	gat	act	att	tct	act	gtg	tct	1200
Leu	Lys	Glu	Leu	Glu	Asn	Asp	Thr	Ser	Asp	Thr	Ile	Ser	Thr	Val	Ser	
385				390					395						400	
ttg	ccg	tct	act	ggc	gag	aag	aaa	aat	atc	tgg	att	caa	tta	atg	gga	1248
Leu	Pro	Ser	Thr	Gly	Glu	Lys	Lys	Asn	Ile	Trp	Ile	Gln	Leu	Met	Gly	
			405					410						415		
atg	att	agt	gtt	cta	gtt	agt	gta	gtt	tta	ggc	att	tcg	tta	aga	aag	1296
Met	Ile	Ser	Val	Leu	Val	Ser	Val	Val	Leu	Gly	Ile	Ser	Leu	Arg	Lys	
			420				425						430			
aaa	act	aag	gag	gaa	aag											1314
Lys	Thr	Lys	Glu	Glu	Lys											
		435														

<210> 300

<211> 438

<212> PRT

<213> Lactobacillus acidophilus

<400> 300

```

Met Asn Lys Lys Asn Val Ser Met Leu Met Leu Ser Pro Ala Ile Leu
 1          5          10          15
Leu Met Met Asn Ser Thr Ile Val His Ala Asp Lys Gly Ser Thr Ser
          20          25          30
His Glu Ile Ser Ser Lys Val Val Ser Lys Thr Lys Asn Asp Asp Lys
          35          40          45
Asn Val Pro Glu Ser Glu Gln Glu Thr Ser Ser Asn Asn Glu Ile Asp
          50          55          60
Gln Ser Gln Asp Lys Gln Glu Lys Glu Glu Gln Ala Ile Pro Glu Asp
65          70          75          80
Gln Asn Asp Gln Ser Gln Asn Thr Asn Asn Gln Asp Pro Asn Asp Ala
          85          90          95
Ser Glu Glu Asp Asp Glu Asp Glu Val Ser Val Glu Asp Tyr Glu Asn
          100          105          110
Asn Val Lys Asp Phe His Arg Val Lys Met Gln Glu Val Lys Asp Leu
          115          120          125
Leu Ala Glu Lys Asn Asn Gln Glu His Leu Met Tyr Ile Gly Arg Pro
          130          135          140
Thr Cys Tyr Tyr Cys Arg Gln Phe Ser Pro Asp Leu Lys Asp Phe Asn
145          150          155          160
Glu Ile Val Lys Gly Lys Leu Leu Tyr Phe Asn Ile Asp Asp Glu Glu
          165          170          175
Gly Ala His Asp Tyr Ala Phe Lys Val Ile Gly Ile Pro Gly Thr Pro
          180          185          190
Thr Thr Met Arg Phe Met Asn Gly Lys Leu Ile Ser Ala Trp Ile Gly
          195          200          205
Gly Glu Lys Thr Gly Gln Glu Leu His Asp Phe Leu Tyr Ser Asp Thr
210          215          220
Ala Asn Lys Leu Val Glu Gln Val Val Ile Lys Asn Gln Ser Asn Asp
225          230          235          240
Thr Ala Thr Gln Ala Asp Asn Asp Val Val Ala Ser Glu Ser Asp Lys
          245          250          255
Thr Pro Glu Val Thr Val Glu Glu Asn Asn Gln Ala Gln Ser Asn Asn
          260          265          270
Asp Val Ala Ile Thr Asn Phe Ala Glu Asn Ser Val Phe Glu Asn Ala
          275          280          285
Lys Asn Val Ala Ser Ser Thr Ala Asp Leu Thr Gln Val Ala Thr Gly
290          295          300
Asp Gln Asp Asp Val Ala Pro Lys Ala Glu Thr Lys Asn Lys Thr Val
305          310          315          320
Lys Lys Pro Ile Lys His Lys Ile Val Ala Asn Lys Val Lys Lys Gln
          325          330          335
Ala Lys Leu His Lys Thr Asn Ile Ile Ile Pro Met Ser Ala Lys Lys
          340          345          350
Arg Glu Asp Val Lys Glu Asn Asn Gln Tyr Asp Thr Val Lys Val His
          355          360          365
Gly Thr Ser Pro Asn Ala Ile Lys Asp Lys Gln Ala Arg Ile Thr Met
          370          375          380
Leu Lys Glu Leu Glu Asn Asp Thr Ser Asp Thr Ile Ser Thr Val Ser
385          390          395          400
Leu Pro Ser Thr Gly Glu Lys Lys Asn Ile Trp Ile Gln Leu Met Gly
          405          410          415
Met Ile Ser Val Leu Val Ser Val Val Leu Gly Ile Ser Leu Arg Lys
          420          425          430
Lys Thr Lys Glu Glu Lys
          435

```

<210> 301
 <211> 1116
 <212> DNA
 <213> Lactobacillus acidophilus

<220>
 <221> CDS
 <222> (1)...(1116)

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1080: MetK - methionine synthase II

<400> 301
 atg agt aaa act tta gta cat tat gac att gtt ggt agt ttc tta aga 48
 Met Ser Lys Thr Leu Val His Tyr Asp Ile Val Gly Ser Phe Leu Arg
 1 5 10 15
 cca gaa gaa ttg aaa aag gca cgt gct gat ttt gca gcg ggt aac att 96
 Pro Glu Glu Leu Lys Lys Ala Arg Ala Asp Phe Ala Ala Gly Asn Ile
 20 25 30
 tca aaa act gac ttg aaa aag gtt gaa gat gaa gaa atc gct aaa tta 144
 Ser Lys Thr Asp Leu Lys Lys Val Glu Asp Glu Glu Ile Ala Lys Leu
 35 40 45
 gtt aaa aaa gaa gaa aaa gct ggt tta aag att gta act gat ggt gaa 192
 Val Lys Lys Glu Glu Lys Ala Gly Leu Lys Ile Val Thr Asp Gly Glu
 50 55 60
 ttc aga aga agt tat tgg cac ctt gat act ttt tgg ggc ttc ggt gga 240
 Phe Arg Arg Ser Tyr Trp His Leu Asp Thr Phe Trp Gly Phe Gly Gly
 65 70 75 80
 att aag cac act act caa gaa cat ggc tac ttc ttc cac gat gaa gaa 288
 Ile Lys His Thr Thr Gln Glu His Gly Tyr Phe Phe His Asp Glu Glu
 85 90 95
 act cgt aat gat tct gct caa gtt gag gga aag att aaa ttt aca ggt 336
 Thr Arg Asn Asp Ser Ala Gln Val Glu Gly Lys Ile Lys Phe Thr Gly
 100 105 110
 gat cat cca gat tta gaa gca ttt aag ttt ttg aag agt tta acc gat 384
 Asp His Pro Asp Leu Glu Ala Phe Lys Phe Leu Lys Ser Leu Thr Asp
 115 120 125
 ggc agt gat gta act cca cgt caa agc att cct tca cca gcc caa ttt 432
 Gly Ser Asp Val Thr Pro Arg Gln Ser Ile Pro Ser Pro Ala Gln Phe
 130 135 140
 tac gca gaa ctc gtc cgt ggc cca gaa aat gtt gca gca gtg aag aaa 480
 Tyr Ala Glu Leu Val Arg Gly Pro Glu Asn Val Ala Ala Val Lys Lys
 145 150 155 160

gtt tac gat acc gaa gac gaa ctt tta aac gat att tca aaa gca tat	528
Val Tyr Asp Thr Glu Asp Glu Leu Leu Asn Asp Ile Ser Lys Ala Tyr	
165 170 175	
tat gat tta atc atc gca ctt tac aaa gca ggt tgt cgc gat gtg aaa	576
Tyr Asp Leu Ile Ile Ala Leu Tyr Lys Ala Gly Cys Arg Asp Val Lys	
180 185 190	
ttg gat gac tgt act tgg gga atg gtc gta gat gat gat ttc tgg gca	624
Leu Asp Asp Cys Thr Trp Gly Met Val Val Asp Asp Asp Phe Trp Ala	
195 200 205	
aca atg gtt aaa caa ggt ttt gac cgt gac gaa ctt caa gaa aaa tac	672
Thr Met Val Lys Gln Gly Phe Asp Arg Asp Glu Leu Gln Glu Lys Tyr	
210 215 220	
ctt cgt gtt aac aat ggc gca ctt aaa gat cta cca gct gat tta aga	720
Leu Arg Val Asn Asn Gly Ala Leu Lys Asp Leu Pro Ala Asp Leu Arg	
225 230 235 240	
act tca act cat att tgt cga ggc aat tac cac tca act tgg gct gct	768
Thr Ser Thr His Ile Cys Arg Gly Asn Tyr His Ser Thr Trp Ala Ala	
245 250 255	
aaa ggt ggt tat gga cgg gtt gcc aaa tac gtt ttt gca caa gaa aat	816
Lys Gly Gly Tyr Gly Pro Val Ala Lys Tyr Val Phe Ala Gln Glu Asn	
260 265 270	
gtc gat gca ttc tat ctt gaa ttt gat aat gaa aga tca ggt aac ttc	864
Val Asp Ala Phe Tyr Leu Glu Phe Asp Asn Glu Arg Ser Gly Asn Phe	
275 280 285	
gat cca atc aag gaa att cct gct gat aaa gaa gta gta ctt ggt tta	912
Asp Pro Ile Lys Glu Ile Pro Ala Asp Lys Glu Val Val Leu Gly Leu	
290 295 300	
gta act agt aag aaa cct gaa ttg gaa aag cca gag gat ttg att gct	960
Val Thr Ser Lys Lys Pro Glu Leu Glu Lys Pro Glu Asp Leu Ile Ala	
305 310 315 320	
cgt atc aat gaa gca agt aag ttc cac gat tta gcc aac tta gcc tta	1008
Arg Ile Asn Glu Ala Ser Lys Phe His Asp Leu Ala Asn Leu Ala Leu	
325 330 335	
agc act caa tgt ggt ttt gca tca acc gag gaa gga aac caa ttg aca	1056
Ser Thr Gln Cys Gly Phe Ala Ser Thr Glu Glu Gly Asn Gln Leu Thr	
340 345 350	
gaa gac gat gaa tgg aaa aag att ggc tta gta atc gat act gct aag	1104
Glu Asp Asp Glu Trp Lys Lys Ile Gly Leu Val Ile Asp Thr Ala Lys	
355 360 365	
caa gtt tgg aag	1116
Gln Val Trp Lys	
370	

<210> 302

<211> 372

<212> PRT

<213> Lactobacillus acidophilus

<400> 302

```

Met Ser Lys Thr Leu Val His Tyr Asp Ile Val Gly Ser Phe Leu Arg
 1          5          10          15
Pro Glu Glu Leu Lys Lys Ala Arg Ala Asp Phe Ala Ala Gly Asn Ile
      20          25          30
Ser Lys Thr Asp Leu Lys Lys Val Glu Asp Glu Glu Ile Ala Lys Leu
      35          40          45
Val Lys Lys Glu Glu Lys Ala Gly Leu Lys Ile Val Thr Asp Gly Glu
 50          55          60
Phe Arg Arg Ser Tyr Trp His Leu Asp Thr Phe Trp Gly Phe Gly Gly
 65          70          75          80
Ile Lys His Thr Thr Gln Glu His Gly Tyr Phe Phe His Asp Glu Glu
      85          90          95
Thr Arg Asn Asp Ser Ala Gln Val Glu Gly Lys Ile Lys Phe Thr Gly
      100          105          110
Asp His Pro Asp Leu Glu Ala Phe Lys Phe Leu Lys Ser Leu Thr Asp
      115          120          125
Gly Ser Asp Val Thr Pro Arg Gln Ser Ile Pro Ser Pro Ala Gln Phe
      130          135          140
Tyr Ala Glu Leu Val Arg Gly Pro Glu Asn Val Ala Ala Val Lys Lys
      145          150          155          160
Val Tyr Asp Thr Glu Asp Glu Leu Leu Asn Asp Ile Ser Lys Ala Tyr
      165          170          175
Tyr Asp Leu Ile Ile Ala Leu Tyr Lys Ala Gly Cys Arg Asp Val Lys
      180          185          190
Leu Asp Asp Cys Thr Trp Gly Met Val Val Asp Asp Asp Phe Trp Ala
      195          200          205
Thr Met Val Lys Gln Gly Phe Asp Arg Asp Glu Leu Gln Glu Lys Tyr
      210          215          220
Leu Arg Val Asn Asn Gly Ala Leu Lys Asp Leu Pro Ala Asp Leu Arg
      225          230          235          240
Thr Ser Thr His Ile Cys Arg Gly Asn Tyr His Ser Thr Trp Ala Ala
      245          250          255
Lys Gly Gly Tyr Gly Pro Val Ala Lys Tyr Val Phe Ala Gln Glu Asn
      260          265          270
Val Asp Ala Phe Tyr Leu Glu Phe Asp Asn Glu Arg Ser Gly Asn Phe
      275          280          285
Asp Pro Ile Lys Glu Ile Pro Ala Asp Lys Glu Val Val Leu Gly Leu
      290          295          300
Val Thr Ser Lys Lys Pro Glu Leu Glu Lys Pro Glu Asp Leu Ile Ala
      305          310          315          320
Arg Ile Asn Glu Ala Ser Lys Phe His Asp Leu Ala Asn Leu Ala Leu
      325          330          335
Ser Thr Gln Cys Gly Phe Ala Ser Thr Glu Glu Gly Asn Gln Leu Thr
      340          345          350
Glu Asp Asp Glu Trp Lys Lys Ile Gly Leu Val Ile Asp Thr Ala Lys
      355          360          365
Gln Val Trp Lys
      370

```

<210> 303
 <211> 471
 <212> DNA
 <213> *Lactobacillus acidophilus*

<220>
 <221> CDS
 <222> (1)...(471)

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF 1081: LuxS - Autoinducer AII

<400> 303
 atg gca aaa gtt gaa agt ttt aca tta gac cac act aaa gtt aag gca 48
 Met Ala Lys Val Glu Ser Phe Thr Leu Asp His Thr Lys Val Lys Ala
 1 5 10 15
 cct tac gtt cgt tta att act gtt gaa gaa ggt cct aaa ggc gac aag 96
 Pro Tyr Val Arg Leu Ile Thr Val Glu Glu Gly Pro Lys Gly Asp Lys
 20 25 30
 att tct aac tat gac tta cgt tta gtt caa ccg aac gaa aat gca att 144
 Ile Ser Asn Tyr Asp Leu Arg Leu Val Gln Pro Asn Glu Asn Ala Ile
 35 40 45
 cct acc ggc gga ttg cat act att gaa cac tta ctt gcc agc tta ctt 192
 Pro Thr Gly Gly Leu His Thr Ile Glu His Leu Leu Ala Ser Leu Leu
 50 55 60
 cgt gac cgt ctt gat ggt gta atc gat tgt tca cca ttt ggt tgc cga 240
 Arg Asp Arg Leu Asp Gly Val Ile Asp Cys Ser Pro Phe Gly Cys Arg
 65 70 75 80
 aca gga ttc cac cta atc gtt tgg ggt gaa cat tca act act gaa gtt 288
 Thr Gly Phe His Leu Ile Val Trp Gly Glu His Ser Thr Thr Glu Val
 85 90 95
 gct aaa gca ttg aag tct tca tta gag gaa att cgt gac aca att act 336
 Ala Lys Ala Leu Lys Ser Ser Leu Glu Glu Ile Arg Asp Thr Ile Thr
 100 105 110
 tgg gaa gat gta cca ggt aca act att aag act tgt ggt aac tac cgt 384
 Trp Glu Asp Val Pro Gly Thr Thr Ile Lys Thr Cys Gly Asn Tyr Arg
 115 120 125
 gat cac tca ttg ttc acc gca aaa gaa tgg tgt cgt gat att ctt gaa 432
 Asp His Ser Leu Phe Thr Ala Lys Glu Trp Cys Arg Asp Ile Leu Glu
 130 135 140
 aaa gga att agt gat gac cca ttc gaa aga aat gtg att 471
 Lys Gly Ile Ser Asp Asp Pro Phe Glu Arg Asn Val Ile
 145 150 155

<210> 304

<211> 157
 <212> PRT
 <213> *Lactobacillus acidophilus*

<400> 304
 Met Ala Lys Val Glu Ser Phe Thr Leu Asp His Thr Lys Val Lys Ala
 1 5 10 15
 Pro Tyr Val Arg Leu Ile Thr Val Glu Glu Gly Pro Lys Gly Asp Lys
 20 25 30
 Ile Ser Asn Tyr Asp Leu Arg Leu Val Gln Pro Asn Glu Asn Ala Ile
 35 40 45
 Pro Thr Gly Gly Leu His Thr Ile Glu His Leu Leu Ala Ser Leu Leu
 50 55 60
 Arg Asp Arg Leu Asp Gly Val Ile Asp Cys Ser Pro Phe Gly Cys Arg
 65 70 75 80
 Thr Gly Phe His Leu Ile Val Trp Gly Glu His Ser Thr Thr Glu Val
 85 90 95
 Ala Lys Ala Leu Lys Ser Ser Leu Glu Glu Ile Arg Asp Thr Ile Thr
 100 105 110
 Trp Glu Asp Val Pro Gly Thr Thr Ile Lys Thr Cys Gly Asn Tyr Arg
 115 120 125
 Asp His Ser Leu Phe Thr Ala Lys Glu Trp Cys Arg Asp Ile Leu Glu
 130 135 140
 Lys Gly Ile Ser Asp Asp Pro Phe Glu Arg Asn Val Ile
 145 150 155

<210> 305
 <211> 1797
 <212> DNA
 <213> *Lactobacillus acidophilus*

<220>
 <221> CDS
 <222> (1)...(1797)

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> ORF - 223

<400> 305
 atg tct ttt cga tta aga aaa gat gtc ttt ttt tgt cct aaa att ggc 48
 Met Ser Phe Arg Leu Arg Lys Asp Val Phe Phe Cys Pro Lys Ile Gly
 1 5 10 15
 aaa ttt cca att tgg att tac aat aga gta gat gag ttt aaa tat agc 96
 Lys Phe Pro Ile Trp Ile Tyr Asn Arg Val Asp Glu Phe Lys Tyr Ser
 20 25 30
 atg cga ggt ata tta tcg atg aaa tta aat cat aag ttg att atg gta 144
 Met Arg Gly Ile Leu Ser Met Lys Leu Asn His Lys Leu Ile Met Val
 35 40 45
 tca gca gct gca tta atg agc gta agt cca ttt gta ggt act gtg caa 192
 Ser Ala Ala Ala Leu Met Ser Val Ser Pro Phe Val Gly Thr Val Gln
 50 55 60

aat gtt caa gct gct act act aaa tca tca agc aaa act act gct aag	240
Asn Val Gln Ala Ala Thr Thr Lys Ser Ser Ser Lys Thr Thr Ala Lys	
65 70 75 80	
aag act act tca gct tca aag act aag act aag tct tca tca aag aag	288
Lys Thr Thr Ser Ala Ser Lys Thr Lys Thr Lys Ser Ser Ser Lys Lys	
85 90 95	
gct act agt caa tct act tca act aag aag aca agt tca aca aaa tca	336
Ala Thr Ser Gln Ser Thr Ser Thr Lys Lys Thr Ser Ser Thr Lys Ser	
100 105 110	
agc tct aag act act tct tca act agt gca aag agt act tca act aag	384
Ser Ser Lys Thr Thr Ser Ser Ser Ala Lys Ser Thr Ser Thr Lys	
115 120 125	
aag gca gct tca aac act att aag tta gtt cac aat gct tat gtt tat	432
Lys Ala Ala Ser Asn Thr Ile Lys Leu Val His Asn Ala Tyr Val Tyr	
130 135 140	
gac aag aat ggt aag cgt ctt act aag tac atg ggc agt gca aag tac	480
Asp Lys Asn Gly Lys Arg Leu Thr Lys Tyr Met Gly Ser Ala Lys Tyr	
145 150 155 160	
act act att gct aaa ggt gta act ctt aag tct aat ggt aca gtg aag	528
Thr Thr Ile Ala Lys Gly Val Thr Leu Lys Ser Asn Gly Thr Val Lys	
165 170 175	
atc gat ggt gtt ctt tac tac agc ctc ggt aat aat gcc tat att aag	576
Ile Asp Gly Val Leu Tyr Tyr Ser Leu Gly Asn Asn Ala Tyr Ile Lys	
180 185 190	
gct gtt aac gta gat ggc cca tct gct tca gct tca tca act act aag	624
Ala Val Asn Val Asp Gly Pro Ser Ala Ser Ala Ser Ser Thr Thr Lys	
195 200 205	
aag cca tct tca agt act tct tca aca gta act gct gta agc att aag	672
Lys Pro Ser Ser Ser Thr Ser Ser Thr Val Thr Ala Val Ser Ile Lys	
210 215 220	
att gct cgt aat tca tac gtt tat gat gaa aat ggt aag cgt att aaa	720
Ile Ala Arg Asn Ser Tyr Val Tyr Asp Glu Asn Gly Lys Arg Ile Lys	
225 230 235 240	
aag tat gaa ggt aaa gat aaa ctt act aag ggt act act gtt gat tca	768
Lys Tyr Glu Gly Lys Asp Lys Leu Thr Lys Gly Thr Thr Val Asp Ser	
245 250 255	
tac ggt aca gaa act att gat ggt aag tta tac tac caa ctt aat aaa	816
Tyr Gly Thr Glu Thr Ile Asp Gly Lys Leu Tyr Tyr Gln Leu Asn Lys	
260 265 270	
aag ggt aca gct ttt gta aag gca agt aat gta gat aca aat gaa aca	864
Lys Gly Thr Ala Phe Val Lys Ala Ser Asn Val Asp Thr Asn Glu Thr	
275 280 285	

gct act att act tta aag aag aat gcc tac att tat gat ggc aat ggc	912
Ala Thr Ile Thr Leu Lys Lys Asn Ala Tyr Ile Tyr Asp Gly Asn Gly	
290 295 300	
gat act aag aaa aag aaa att aag aag ggc aag agt gta aag gct act	960
Asp Thr Lys Lys Lys Lys Ile Lys Lys Gly Lys Ser Val Lys Ala Thr	
305 310 315 320	
gaa gca aga tac att ggt act aag ctt tac tac aag att ggt gat gat	1008
Glu Ala Arg Tyr Ile Gly Thr Lys Leu Tyr Tyr Lys Ile Gly Asp Asp	
325 330 335	
caa ttt gta aag gct gct aat gtg ggt aaa gtt tca ggt gct aag ctt	1056
Gln Phe Val Lys Ala Ala Asn Val Gly Lys Val Ser Gly Ala Lys Leu	
340 345 350	
gat cct atc aat gaa cca gat gga gaa gca act gtt gat gat cca tcg	1104
Asp Pro Ile Asn Glu Pro Asp Gly Glu Ala Thr Val Asp Asp Pro Ser	
355 360 365	
act gat aat gtt aac cca gat gta act aag gta act acc att ggt gta	1152
Thr Asp Asn Val Asn Pro Asp Val Thr Lys Val Thr Thr Ile Gly Val	
370 375 380	
act cca ctt tac aat att aag ggt caa aaa gac gac acc aga tta ttt	1200
Thr Pro Leu Tyr Asn Ile Lys Gly Gln Lys Asp Asp Thr Arg Leu Phe	
385 390 395 400	
ggg gct ggt caa agt caa caa gtt tca gaa tta aga tat att gca act	1248
Gly Ala Gly Gln Ser Gln Gln Val Ser Glu Leu Arg Tyr Ile Ala Thr	
405 410 415	
tca gca aac ggt acc cca gac ttg ttc tac aaa tta gct agt ggt aga	1296
Ser Ala Asn Gly Thr Pro Asp Leu Phe Tyr Lys Leu Ala Ser Gly Arg	
420 425 430	
ggg tac ttg aag gct agt gat gta att gtt agt ggt aag act ttg tca	1344
Gly Tyr Leu Lys Ala Ser Asp Val Ile Val Ser Gly Lys Thr Leu Ser	
435 440 445	
cct gtt aat act cca gaa caa gct aag gct gat gta act gtt gca act	1392
Pro Val Asn Thr Pro Glu Gln Ala Lys Ala Asp Val Thr Val Ala Thr	
450 455 460	
gca gca gat aag act aag ttg tca gaa agt att aat aat tct aag aac	1440
Ala Ala Asp Lys Thr Lys Leu Ser Glu Ser Ile Asn Asn Ser Lys Asn	
465 470 475 480	
ggt aaa aat tct act act tac aag ctt tca tca tca gac tta aga aat	1488
Val Lys Asn Ser Thr Thr Tyr Lys Leu Ser Ser Ser Asp Leu Arg Asn	
485 490 495	
aac tat gat aag gct gtt tct gat gca act gct gtt aat aac aat gct	1536
Asn Tyr Asp Lys Ala Val Ser Asp Ala Thr Ala Val Asn Asn Asn Ala	
500 505 510	
tca gca act att gct caa gtt aat gaa gca gta gct aac att aat gaa	1584

Ser Ala Thr Ile Ala Gln Val Asn Glu Ala Val Ala Asn Ile Asn Glu
515 520 525

gct tac gct aag ctt aac ggt caa aaa ata gtt gta gct aac tta agt 1632
Ala Tyr Ala Lys Leu Asn Gly Gln Lys Ile Val Val Ala Asn Leu Ser
530 535 540

aat ctt act tta gat gaa gcc aac caa att gtt aag tta gtt gct agt 1680
Asn Leu Thr Leu Asp Glu Ala Asn Gln Ile Val Lys Leu Val Ala Ser
545 550 555 560

gta aga aac gtt cca gaa agt aat gtt caa ttc tca aat aac aac act 1728
Val Arg Asn Val Pro Glu Ser Asn Val Gln Phe Ser Asn Asn Asn Thr
565 570 575

act tta gca atc gtt tca tca aat ggc tac aat gaa cct ttg aat att 1776
Thr Leu Ala Ile Val Ser Ser Asn Gly Tyr Asn Glu Pro Leu Asn Ile
580 585 590

agc gac ttt gct caa caa aga 1797
Ser Asp Phe Ala Gln Gln Arg
595

<210> 306

<211> 599

<212> PRT

<213> Lactobacillus acidophilus

<400> 306

Met Ser Phe Arg Leu Arg Lys Asp Val Phe Phe Cys Pro Lys Ile Gly
1 5 10 15

Lys Phe Pro Ile Trp Ile Tyr Asn Arg Val Asp Glu Phe Lys Tyr Ser
20 25 30

Met Arg Gly Ile Leu Ser Met Lys Leu Asn His Lys Leu Ile Met Val
35 40 45

Ser Ala Ala Ala Leu Met Ser Val Ser Pro Phe Val Gly Thr Val Gln
50 55 60

Asn Val Gln Ala Ala Thr Thr Lys Ser Ser Ser Lys Thr Thr Ala Lys
65 70 75 80

Lys Thr Thr Ser Ala Ser Lys Thr Lys Thr Lys Ser Ser Ser Lys Lys
85 90 95

Ala Thr Ser Gln Ser Thr Ser Thr Lys Lys Thr Ser Ser Thr Lys Ser
100 105 110

Ser Ser Lys Lys Thr Thr Ser Ser Thr Ser Ala Lys Ser Thr Ser Thr Lys
115 120 125

Lys Ala Ala Ser Asn Thr Ile Lys Leu Val His Asn Ala Tyr Val Tyr
130 135 140

Asp Lys Asn Gly Lys Arg Leu Thr Lys Tyr Met Gly Ser Ala Lys Tyr
145 150 155 160

Thr Thr Ile Ala Lys Gly Val Thr Leu Lys Ser Asn Gly Thr Val Lys
165 170 175

Ile Asp Gly Val Leu Tyr Tyr Ser Leu Gly Asn Asn Ala Tyr Ile Lys
180 185 190

Ala Val Asn Val Asp Gly Pro Ser Ala Ser Ala Ser Ser Thr Thr Lys
195 200 205

Lys Pro Ser Ser Ser Thr Ser Ser Thr Val Thr Ala Val Ser Ile Lys

210	215	220
Ile Ala Arg Asn Ser Tyr Val Tyr Asp Glu Asn Gly Lys Arg Ile Lys		
225	230	235
Lys Tyr Glu Gly Lys Asp Lys Leu Thr Lys Gly Thr Thr Val Asp Ser		240
	245	250
Tyr Gly Thr Glu Thr Ile Asp Gly Lys Leu Tyr Tyr Gln Leu Asn Lys		255
	260	265
Lys Gly Thr Ala Phe Val Lys Ala Ser Asn Val Asp Thr Asn Glu Thr		270
	275	280
Ala Thr Ile Thr Leu Lys Lys Asn Ala Tyr Ile Tyr Asp Gly Asn Gly		285
	290	295
Asp Thr Lys Lys Lys Lys Ile Lys Lys Gly Lys Ser Val Lys Ala Thr		300
305	310	315
Glu Ala Arg Tyr Ile Gly Thr Lys Leu Tyr Tyr Lys Ile Gly Asp Asp		320
	325	330
Gln Phe Val Lys Ala Ala Asn Val Gly Lys Val Ser Gly Ala Lys Leu		335
	340	345
Asp Pro Ile Asn Glu Pro Asp Gly Glu Ala Thr Val Asp Asp Pro Ser		350
	355	360
Thr Asp Asn Val Asn Pro Asp Val Thr Lys Val Thr Thr Ile Gly Val		365
	370	375
Thr Pro Leu Tyr Asn Ile Lys Gly Gln Lys Asp Asp Thr Arg Leu Phe		380
385	390	395
Gly Ala Gly Gln Ser Gln Gln Val Ser Glu Leu Arg Tyr Ile Ala Thr		400
	405	410
Ser Ala Asn Gly Thr Pro Asp Leu Phe Tyr Lys Leu Ala Ser Gly Arg		415
	420	425
Gly Tyr Leu Lys Ala Ser Asp Val Ile Val Ser Gly Lys Thr Leu Ser		430
	435	440
Pro Val Asn Thr Pro Glu Gln Ala Lys Ala Asp Val Thr Val Ala Thr		445
	450	455
Ala Ala Asp Lys Thr Lys Leu Ser Glu Ser Ile Asn Asn Ser Lys Asn		460
465	470	475
Val Lys Asn Ser Thr Tyr Lys Leu Ser Ser Ser Asp Leu Arg Asn		480
	485	490
Asn Tyr Asp Lys Ala Val Ser Asp Ala Thr Ala Val Asn Asn Asn Ala		495
	500	505
Ser Ala Thr Ile Ala Gln Val Asn Glu Ala Val Ala Asn Ile Asn Glu		510
	515	520
Ala Tyr Ala Lys Leu Asn Gly Gln Lys Ile Val Val Ala Asn Leu Ser		525
	530	535
Asn Leu Thr Leu Asp Glu Ala Asn Gln Ile Val Lys Leu Val Ala Ser		540
545	550	555
Val Arg Asn Val Pro Glu Ser Asn Val Gln Phe Ser Asn Asn Asn Thr		560
	565	570
Thr Leu Ala Ile Val Ser Ser Asn Gly Tyr Asn Glu Pro Leu Asn Ile		575
	580	585
Ser Asp Phe Ala Gln Gln Arg		590
595		

<210> 307

<211> 3859

<212> DNA

<213> Lactobacillus acidophilus

<400> 307

```

atgaaattag cctatgacga ttggcgtaaa aataaagaaa agaattatcc ttttgcgggg 60
tacactgtag agattgattc attatcgaat gtcctattaa caaatggagg tacctacact 120
atcaatttgg gaaccgaaac tcgcctttat atggaacctat attgggtaat aacttcacgc 180
actatttcatt atgtaaaata tggctctaacc ggttctgata gtgttgcttc tccagatgtg 240
atccaggaag gtcattcaaa tgtaaccagt tctaaaaata atccagtggg aaataacttt 300
aatttagaaa aagatgggtca tcactatgtg agttatgaaa cggttcaaag atcgataaat 360
gtagcttctg gtattcctga tgggatgaca gataataaag gtaatatgaa ttctattatt 420
atctttgatg gacagataaa cccaactatt actgattggg ttactccaga tcctgatgta 480
actcaaacca aatcacccgg caagaatctt tctaataaaa ttccaacaaa tgggtgaatct 540
tacaattacc tctatagaaa gttctatcat cataactatt atgataaaga tggtaacttc 600
catcagaaga catatcttcc taataatgaa ggagagccaa ttactattac ttactaccac 660
aaccaacctg tagatctttc atttgaagat atttcaaaga ttgatcctca agattttaagt 720
gggagcaact attctgctac taacgaatta acgacaaaga acgatgatag taatcaatac 780
aatgtttacg atgcatcaaa tgggtactaaa agtttaagtc aagtaattag tgatattgaa 840
gcgaaagggt acaagcttgt ttcaattact acgatgacg atgattctca aaccgacttg 900
aagggcaaca gttcaattga tttaacttat aacaaagatg gtgtttggaa gagtgcact 960
ggtggggata atgctgataa cttgattcat aagcgctaca ctatcaagtt tgttcatgac 1020
gtaaaaccta caactaaaaa tacttctgta agccgtaaca ttactatgt ggctgacgaa 1080
ggcaatagca agtatgaagt attgaagaat cctgatactc aaactgttaa ctttgaacgt 1140
actgcttata ttgatcaagt tactaagcaa gaagttatta agaatgcaga tgggtacttac 1200
agtgaattac cagctgactt caagccaact tggaaagctg ttggaactga taactttgat 1260
aaaatccaaa aggatagatt taacaaggat gaaggtaagg ttcttggcgt ttgggaaatt 1320
gaacgtgcta actatgatga tccagaggga actcaattaa cggataactt tgctcctaaa 1380
gttgcaaatg ttgatgctgc taagacttat aatgatattt atcttgttta caaacaaaaa 1440
gctcaatata atattcacta cattgatgtt aatgggtgtag aagataaaaa cacttatact 1500
ccaactgacg gttatgaact taccgatcat ttagtctcta acgttgggtga aggtaaagg 1560
atctttattg gcgacactcc agatgctacg cagaagttat ggagcccagc agactacgaa 1620
aaggctggat atgttttagt tggtttatct gataatgcca aaggcgattt actcggtaag 1680
caaaccttaa ctaaggacgt tcaagatcaa tacgtttact tgaagcatgc aatcacccct 1740
tcaactgata agacacctaa agaagacgtg aaggccgaaa ctgtcagtc agtacgtact 1800
atctcatatc gggatgctga aactggtgaa aagattacag atgaattaaa gaagtacgg 1860
attactgcta atgttcttga cattacgcaa actatcgatt atgttctgtg gcctctttat 1920
gatgctttta aggttatgtt tttaggcttt gcagcaattc aaactgatgc aaaaggtttt 1980
gctaagcttg atagtaacgg taaaccagag atcaagaaa atactaatgg ccaaccaatt 2040
attgctactc gagatgataa ggcacatggt gttccaactg gtgaacatac tgactatcca 2100
gaacaaggct cacctgatgt aactaagtat ggttatgtaa aggaaagctc attagaacaa 2160
aagactaata acaaggatgg cgcacaggta gatgctaaag acggtgaccc aactcaatcc 2220
ggtggccacg tggatgttta ctacttccac gaacaagaag atatcactta tgtgaattcc 2280
aagtttaata ttgacccaaa ggtatcttga aaagacctta aaagaacgat tatctaccgt 2340
ggtaccaaag acggtcatac ttatgaagat gtaaattggt caccagatgg cactcataag 2400
tatgttcaga ctaccacctt tactcgtaag gcgattgtag atgcagtaac gaaaaaagt 2460
attaaatata ctcttgggac atcaactaaa caacttttag tagaagttat ttctaagaca 2520
cctactgaag tgggttatga caatgttgat attaaatcag tttctgcacg tactgttgat 2580
ccagataaag atccagaaga tttaggtaca acagttgtaa cttatactgt caaccaact 2640
ccaacacctg aaccaaattc aggtaatggc ggtaaacacca gcgatgggtg aaatactct 2700
gatggaggct cagaacaacc aaataatcct ggtaacaaca atgaagttcc aggtaacccg 2760
ggcggtgaca atgaaacacc taaggaaact ccaactccta aggatgataa gactacacca 2820
gaaaaaccag atgaacatga cgatttgaaa ttgaagtcac ctgacgaaca taaccatact 2880
caaagaagg aggttaacaa gacttcaaat aatactccac gtacggaacg ctggaactca 2940
aacaatctc ctaaatcaga aaacgtaaat aatgtaacag gttctaattc cgcagttaaa 3000
tctaccaata gtctgaaac agtaaaggaa aatactttac cgcagactgg ttactaggat 3060
cagtatact gtcttcagta ttccactta aataatctcc cgaatcttta ggcgttgata 3120
ctaattggga aacttcatac tttgaattat ctgtagttat taaaccttga atgtatttac 3180
ctacatcttg aagagtatca tcatttttac ctttataagt aatgcttggg agattttctg 3240
tctctccgtt ttcattagtc cagtttaaat taatagtagc tgaaaggcca tcttgcgctt 3300
tactttcagt taaagcttta gctgaaagtg agttgtact agctaatttg agagcttgag 3360
tttgaatctc ttgagtttca atccccctct tatcagaagt taaatctttg tgagactcag 3420

```

```

atttaacttc tactggattt gccttttcaa ctttagattc actagtctta tttgcttcac 3480
tcttgttttc taaggaagtc ttttgttcct ctttattatc tgttgcggtg gaaccaacag 3540
attggtcctt cttttctaata gattcagtc tcttattatt aatttcttga gttgaggtag 3600
ttctaccttc cgtagaactc tttgcttctg caggagcttg aggtgtatgg ctaacttcta 3660
catgagaaga gacttacata atttagacgt aggggacgtt aaagaaaaac aacgtttttc 3720
aattcgcaag ttaactgtag gtactgctag tgtattgctg ggtactacat tcttgtttgg 3780
tgcaggtcag actgcttacg ctgatactac tgcttcaggt gctattacta gtgaagattc 3840
ccaaaaccaa attggggggg                                     3859

```

<210> 308

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Motif

<220>

<221> MISC_FEATURE

<222> (3)...(3)

<223> Xaa = Any Amino Acid

<400> 308

Leu Pro Xaa Thr Gly

1 5

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
11 November 2004 (11.11.2004)

PCT

(10) International Publication Number
WO 2004/096992 A3

(51) International Patent Classification⁷: C07H 21/02, 21/04

(21) International Application Number:
PCT/US2004/012717

(22) International Filing Date: 23 April 2004 (23.04.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/465,621 25 April 2003 (25.04.2003) US

(71) Applicant (for all designated States except US): NORTH CAROLINA STATE UNIVERSITY [US/US]; 2401 Research Drive, Campus Box 8210, Raleigh, North Carolina 27695-8210 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): KLAENHAMMER, Todd R. [US/US]; 6509 Bakersfield Drive, Raleigh, North Carolina 27606 (US). RUSSELL, William M. [US/US]; Madison, Wisconsin (US). ALTERMAN, Eric [US/US]; Raleigh, North Carolina (US). CANO, Raul J. [US/US]; San Luis Obispo, California (US). HAMRICK, Alice [US/US]; 1610 Fifth Street, Los Osos, California 93402 (US).

(74) Agents: SPRUILL, W. Murray, et al.; Alston & Bird LLP, Bank of America Plaza, 101 South Tryon Street, Suite 4000, Charlotte, NC 28280-4000 (US).

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

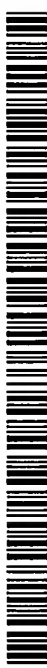
- with international search report
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

(88) Date of publication of the international search report:
16 February 2006

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: LACTOBACILLUS ACIDOPHILUS NUCLEIC ACID SEQUENCES ENCODING CELL SURFACE PROTEIN HOMOLOGUES AND USES THEREFORE

(57) Abstract: Cell wall, cell surface and secreted protein nucleic acid molecules and polypeptides and fragments and variants thereof are disclosed in the current invention. In addition, cell wall, cell surface and secreted fusion proteins, antigenic peptides, and anti-cell wall, cell surface and secreted antibodies are encompassed. The invention also provides recombinant expression vectors containing a nucleic acid molecule of the invention and host cells into which the expression vectors have been introduced. Methods for producing the polypeptides of the invention and methods for their use are further disclosed.



WO 2004/096992 A3

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US04/12717

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/02, 21/04

US CL : 536/23.1, 23.7

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : C07H 21/02, 21/04

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P	AZCARATE-PERIL et al. Identification and Inactivation of Genetic Loci Involved with Lactobacillus acidophilus Acid Tolerance. Applied and Environmental Microbiology, 2004 Vol. 70, No. 9, pages 5315-5322. See entire document.	1-5 and 9

<input type="checkbox"/> Further documents are listed in the continuation of Box C.	<input type="checkbox"/> See patent family annex.
<p>* Special categories of cited documents:</p>	
<p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier application or patent published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another claim or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p>	<p>"Y" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</p> <p>"&" document member of the same patent family</p>
Date of the actual completion of the international search	Date of mailing of the international search report
20 September 2005 (20.09.2005)	27 DEC 2005
Name and mailing address of the ISA/US	Authorized officer
Mail Stop PCT, Attn: ISA/US	Robert A. Zeman
Commissioner for Patents	Julia Jackson
P.O. Box 1450	Telephone No. (203) 308-0196
Alexandria, Virginia 22313-1450	
Facsimile No. (703) 305-3230	

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US04/12717

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of any additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-5 and 9 as they relate to SEQ ID NO:1

- Remark on Protest
- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
 - ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
 - ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US04/12717

BOX III. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Groups 1-307, claim(s) 1-5 and 9, drawn to nucleic acids, vectors comprising said nucleic acids, cells comprising said vectors and methods of producing a polypeptide using said nucleic acids wherein the nucleic acids have the sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307 or wherein said nucleic acid encodes for a polypeptide with a sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, respectively.

Groups 308-614, claim(s) 6-7, drawn to polypeptides encoded by nucleic acids with the sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307 and polypeptides with the sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, respectively.

Groups 615-921, claim(s) 8, drawn to antibodies to polypeptides encoded by nucleic acids with the sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307 and polypeptides with the sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222,

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US04/12717

224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, respectively.

Groups 922-1228, claim(s) 10-11, drawn to methods of detecting the presence of a polypeptide using a compound that binds to said polypeptide wherein said polypeptide is encoded by nucleic acids with the sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307 and polypeptides with the sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, respectively.

Groups 1229-1535, claim(s) 12-13, drawn to methods of detecting nucleic acid molecules wherein said nucleic acids molecules have the sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307 or wherein said nucleic acid encodes for a polypeptide with a sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, respectively.

Groups 1536-1842, claim(s) 14-16, drawn to methods of modulating the immune system by the administration of a polypeptide wherein said polypeptide is encoded by nucleic acids with the sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307 and polypeptides with the sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, respectively.

Groups 1843-2149, claim(s) 18-19, drawn to methods of altering the expression of a host protein or compound by introducing into a host a polypeptide wherein said polypeptide is encoded by nucleic acids with the sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307 and polypeptides with the sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, respectively.

Group 2150-2456, claim(s) 20, drawn to methods of altering the expression of a host protein or compound by introducing into a host a microorganism that expresses a polypeptide wherein said polypeptide is encoded by nucleic acids with the sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135,

International application No.
PCT/US04/12717

Groups 3685-3991, claim(s) 27, drawn to methods of preventing or reducing the occurrence of an infection comprising introducing into said subject a microorganism that expresses a polypeptide wherein said polypeptide is encoded by nucleic acids with the sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307 and polypeptides with the sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US04/12717

214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, respectively.

Groups 3992-4298, claim(s) 28-29, drawn to methods of removing detrimental compounds from the gastrointestinal tract comprising introducing into said subject a polypeptide wherein said polypeptide is encoded by nucleic acids with the sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307 and polypeptides with the sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, respectively.

Groups 4299-4605, claim(s) 30-31, drawn to methods of removing detrimental compounds from the gastrointestinal tract comprising introducing into said subject a microorganism that expresses a polypeptide wherein said polypeptide is encoded by nucleic acids with the sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307 and polypeptides with the sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, respectively.

Groups 4606-4912, claim(s) 32-39, drawn to methods of enhancing the stability of microorganism using a vector comprising a nucleic acid wherein wherein the nucleic acids have the sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307 or wherein said nucleic acid encodes for a polypeptide with a sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, respectively.

Groups 4913-5219, claim(s) 40-41, drawn to methods of enabling a microorganism to possess modified adherence properties comprising introducing into said microorganism a polypeptide wherein said polypeptide is encoded by a nucleic acid with the sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307 and polypeptides with the sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, respectively.

Groups 5220-5526, claim(s) 42, drawn to methods of protecting food from contamination by a microorganism comprising contacting food with a polypeptide wherein said polypeptide is encoded by a nucleic acid with the sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149,

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US04/12717

151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307 and polypeptides with the sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, respectively.

Groups 5527-5833, claim(s) 43-44, drawn to methods of modifying the texture of food produced by lactic acid bacteria comprising introducing into said bacteria a vector comprising a nucleic acid wherein the nucleic acids have the sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305 or 307 or wherein said nucleic acid encodes for a polypeptide with a sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, respectively.

Groups 5834-5985, claim(s) 45-53, drawn to *Lactobacillus acidophilus* that has been modified to express a polypeptide wherein said polypeptide has the sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304 or 306, respectively.

The inventions listed as Groups 1-5985 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Pursuant to 37 C.F.R. 1.475(d), the ISA/US considers that where multiple products and processes are claimed, the main invention shall consist of the first invention of the category first mentioned in the claims and the first recited invention of each of the other categories related thereto. Accordingly, the main invention (Group I) comprises the first recited product, a nucleic acid molecule with the sequence of SEQ ID NO: 1. Further pursuant to 37 C.F.R. 1.475(d), the ISA/US considers that any feature which the subsequently recited products and methods share with the main invention does not constitute a special technical feature within the meaning of PCT rule 13.2 and that each of such products and methods accordingly defines a separate invention.

The special technical features of groups 1-307 are the sequences of each individual nucleic acid.

The special technical features of groups 308-614 are the sequences of each individual polypeptide.

The special technical features of groups 615-921 are the binding specificity of each individual antibody.

The special technical features of groups 922-5833 are the method steps used and the specific reagents utilized in said method steps.

The special technical features of the groups 5834-5985 are the modification made that result in the expression of each individual polypeptide.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US04/12717

EAST, medline, Caplus, STIC

search terms: SEQ ID NO:1, lactobacillus acidophilus, adhesin